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(54) Title: METHOD FOR CLASSIFICATION OF CANCER

(57) Abstract: The present disclosure pertains to an in vitro method for the diagnostic classification of cancer based on the biological state of specific genomic sites. The disclosure provides a method that allows for a classification of a tumour sample obtained from a patient by analysing a multitude, preferably genome wide, collection of gene sites, combining the biological state of the analysed gene sites into a biological state pattern and comparing with pre-determined biological state patterns pertaining to different cancer types or tumour species. The disclosure is in particular useful for classifying cancer e.g. of the central nervous system, such as brain tumour samples and tumours of the spinal cord, since these are characterized by a large variety of distinct tumour species which have different prognostic values and require a developed treatment regime for each species in the clinical context. However, other cancers could similarly profit from the disclosure, for example sarcomas.



METHOD FOR CLASSIFICATION OF CANCER

FIELD OF THE DISCLOSURE

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The present disclosure pertains to the classification of cancer, in particular to a computer-implemented method for the diagnostic classification of cancer and/or an in vitro method for classification of cancer based on the biological state of specific genomic DNA sites or transcripts. The disclosure provides a method that allows for a classification of a cancer sample, specifically a tumour sample obtained from a patient by analysing a multitude, preferably genome wide, of gene sites, combining the biological state of the analysed gene sites into a biological state pattern and comparing it directly and/or indirectly with pre-determined biological state patterns pertaining to different cancer types or tumour species. The disclosure is in particular useful for classifying cancer of the central nervous system, i.e. brain tumour samples and/or tumours of the spinal cord, since these need to be correctly identified from a large variety of distinct tumour species which have different prognostic values and require a developed treatment regime for each species in the clinical context. However, other cancers could similarly profit from the disclosure, for example sarcomas.

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BACKGROUND

When looking at brain tumour entities alone, there are more than 100 different entities listed in the World Health Organisation classification. Many of these show complex patterns of potentially overlapping histological features. Moreover, even histologically identical tumours can belong to different molecular groups with very different treatment requirements and prognosis. The same is true for tumours of the spinal cord and tumours originating in tissues outside the central nervous system. Therefore, more advanced diagnostic tools are needed.

Epigenetic patterns, for example the epigenetic states of different gene sites, play a critical role in development, differentiation and pathogenesis of diseases such as multiple sclerosis, diabetes, schizophrenia, aging, and multiple forms of cancer including tumours of the central nervous system. Tumour entities originate from different precursor-cell populations which are transformed by genetic and epigenetic alterations. It is now recognized that many tumour entities, including the ones of the central nervous system, that are of distinct biological groups are

not always distinguishable by their histology. Most tumour entities display varied histological spectra with no clear boundaries. Epigenetic modifications, such as methylation, preserve the information of the cell of origin, its original identity. Therefore, methylation data, for example DNA methylation patterns, have a great potential to identify molecular subgroups of tumours, such as tumours of the central nervous system. Similar results can be obtained by analysing the transcripts of the respective genes of interest.

Still, treatment planning and in particular treatment success in many cancers, and in particular in cancers of the central nervous system, is highly dependent on an early and accurate diagnosis and classification of the tumour. In view of the above, new methods that overcome at least some of the problems in the art are beneficial.

SUMMARY

The present disclosure seeks to provide a strategy and method for the diagnostic classification of cancer samples with higher efficiency, specificity and sensitivity.

This object of the present invention is solved by the features of the independent claims. Preferred embodiments are defined in the dependent claims. Any “aspect”, “example” and “embodiment” of the description not falling within the scope of the claims does not form part of the invention and is provided for illustrative purposes only.

According to an independent aspect of the present disclosure, a computer-implemented method for diagnostic classification of cancer is provided. The method includes classifying a cancer using a classification algorithm based on biological states or biological state patterns of a set of gene sites of a cancer sample.

The classification algorithm is trained using biological data derived from classified cancer types, such as pre-classified cancer types. In particular, the cancer types can be pre-classified and/or can be new cancer types which are identified using the classification algorithm. For example, the classification algorithm may classify a cancer sample as unknown, wherein such unknown cancer samples can then be further analysed to determine a cancer type thereof. The further analysis may be conducted by various means, such as software and/or medical personnel.

The classification algorithm is trained using at least data pertaining to biological states of the gene sites in Table 1 (SEQ ID No. 1 to SEQ ID No. 688). By training the classification algorithm with the data of all gene sites in Table 1, an efficient and flexible classification tool can be provided.

In particular, a cancer sample can be classified using:

- (i) cancer sample data of all 688 gene sites in Table 1, or
- (ii) cancer sample data of a subset of the 688 gene sites in Table 1, such as at least 3 gene sites of the cancer sample genome.

In other words, the classification algorithm is trained with biological data pertaining to all 688 gene sites in Table 1, but for the classification of a cancer sample, it might not be necessary to provide cancer sample data of all 688 gene sites. The number of gene sites used to classify the cancer sample can be selected depending on circumstances, such as data available from the cancer sample (e.g., it could be that only data pertaining to a subset of the 688 gene sites are available for analysis), time constraints (the fewer the gene sites, the faster the analysis), sensitivity requirements (the higher the number of gene sites, the higher the accuracy of the analysis), and the like.

In view of the above, the computer-implemented method for the diagnostic classification of cancer may reduce the processing resources used by a GPU and/or reduce the power consumed by a GPU. Moreover, by using cancer sample data of a subset of the 688 gene sites in Table 1, such as at least 3 gene sites of the cancer sample genome, the performance, power consumption, and/or programming flexibility of a GPU that performs the method for the diagnostic classification of cancer may be improved.

Preferably, the set of gene sites comprises at least 3 gene sites of the cancer sample genome selected from a list consisting of the gene sites in Table 1 of this document.

Preferably, the biological states of the gene sites comprise the biological states of the gene sites as listed in Table 1 of this document and preferably up to 20 (or 15 or 12 kb) upstream and/or downstream of each of said gene sites. For example, the biological states of the gene sites comprise the biological states of the gene sites as listed in Table 1 and up to 10 kb, pref-

erably up to 8 kb or up to 6 kb or up to 4 kb or up to 2 kb, upstream and/or downstream of the gene sites.

According to some embodiments, which can be combined with other embodiments described herein, the method further includes determining biological states pertaining to the at least 3 gene sites of the cancer sample genome.

Additionally, or alternatively, the method further includes determining a biological state pattern of the set of gene sites based on the determined biological state(s) of each of the at least 3 gene sites.

According to another independent aspect of the present disclosure, a method for diagnostic classification of cancer is provided.

According to some embodiments, which can be combined with other embodiments described herein, the method for diagnostic classification of cancer is an *in-vitro* method.

In a preferred embodiment, the method includes:

- providing a cancer sample,
- determining biological states pertaining to at least 3 gene sites of the cancer sample genome, wherein the gene sites are selected from a list consisting of the gene sites in Table 1,
- determining a biological state pattern based on the determined biological state(s) of each of the at least 3 gene sites, and
- classifying a cancer type based on the determined biological state pattern and pre-determined biological state patterns pertaining to different cancer types.

Preferably, the biological states of the gene sites comprise the biological states of the gene sites as listed in Table 1 of this document and preferably up to 20 kb (or 15 or 12 kb) upstream and/or downstream of each of said gene sites. For example, the biological states of the gene sites comprise the biological states of the gene sites as listed in Table 1 and preferably up to 10 kb, preferably up to 8 kb or up to 6 kb or up to 4 kb or up to 2 kb, upstream and/or downstream of the gene sites.

Preferably, the step of determining a biological state pattern comprises combining the biological state(s) of the gene sites into the biological state pattern.

Preferably, classifying a cancer type comprises comparing the biological state pattern of the set of gene sites with pre-determined biological state patterns derived from the biological state data pertaining to different cancer types.

Preferably, the cancer is classified as a specific cancer type if the biological state pattern of the set of gene sites differs from the biological state data derived from the pre-classified cancer type by at most 5 %, preferably at most 4 % or at most 3 % or at most 2 % or at most 1 %.

Preferably, the biological state is selected from a group including, or consisting of, epigenetic state, mutation state, copy number and RNA expression.

Preferably, the epigenetic state is a methylation state.

Preferably, the set of gene sites comprises at least 10, preferably at least 20 or at least 30 or at least 40 or at least 50 or at least 60 or at least 70 or at least 80 or at least 90 or at least 100 or all gene sites of the cancer sample genome in Table 1.

Preferably, the at least one of the at least 3 gene sites are the ones with the highest values of variable importance (imp_sum) in Tables 3 to 172 of this document. Most preferred, at least one of the at least 3 gene sites is selected from the group including (or consisting) of PTPRN2 (SEQ ID No. 491), PRDM16 (SEQ ID No.477), HDAC4 (SEQ ID No.249), PAX6 (SEQ ID No. 431) and MAD1L1 (SEQ ID No. 349).

Preferably, the biological states of the gene sites comprise exclusively the biological states of the gene sites as listed in Table 1 without any bases upstream and/or downstream of the gene sites.

Preferably, the biological state is a methylation state and/or the biological state pattern is a methylation state pattern.

Preferably, the cancer is a cancer of the central nervous system or a sarcoma. However, the present disclosure is not limited thereto, and other cancer types, such as carcinomas, sarcomas, myelomas, neural crest lineage tumors (e.g., melanoma), leukaemia, lymphoma and mixed types can be classified using the method according to the present invention.

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Preferably, the cancer is a cancer listed in Table 2.

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Preferably, the method further includes determining a further (second) biological state different from the (first) biological state and pertaining to at least one of the gene sites pertaining to the cancer sample genome.

Preferably, the method further includes correlating the further (second) biological state of the at least one gene site pertaining to the cancer sample genome with the classified cancer type.

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Preferably, the method further includes defining the at least one gene site with the determined further (second) biological state as an alternative or additional biomarker in the diagnosis of the classified cancer types.

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Preferably, the further (second) biological state is selected from the group including, or consisting of, epigenetic state, mutation state, RNA expression and copy number.

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According to another independent aspect of the present disclosure, a computer-readable storage medium is provided. The computer-readable storage medium has computer-executable instructions stored, that, when executed, cause a computer to perform the methods described herein.

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The term “computer-readable storage medium” may refer to any storage device used for storing data accessible by a computer, as well as any other means for providing access to data by a computer. Examples of a storage device-type computer-readable medium include: a magnetic hard disk; a floppy disk; an optical disk, such as a CD-ROM and a DVD; a magnetic tape; a memory chip.

According to another independent aspect of the present disclosure, a system for diagnosing cancer is provided. The system includes one or more processors and a memory coupled to the

one or more processors and comprising instructions executable by the one or more processors to implement the methods described herein.

The system may be a computer system. The term a “computer system” may refer to a system having a computer, where the computer comprises a computer-readable storage medium embodying software to operate the computer.

The term “software” is used interchangeably herein with “program” and refers to prescribed rules to operate a computer. Examples of software include: software; code segments; instructions; computer programs; and programmed logic.

The embodiments of the present disclosure provide a classification of cancer samples in cancer diagnosis using a classification algorithm, which is a machine learning (ML) algorithm.

The term “classification” refers to a procedure and/or algorithm in which individual items are placed into groups or classes based on quantitative information on one or more characteristics inherent in the items (referred to as traits, variables, characters, features, etc.) and based on a statistical model and/or a training set of previously labelled items. Specifically in the context of the present disclosure, classification preferably means determining which specific cancer type, for example determined by its epigenetic features, a cancer sample belongs to.

The term “machine learning algorithm” as used throughout the present application refers to an algorithm that builds a model based on training data, in order to make predictions or decisions without being explicitly programmed to do so. In particular, the term “classification” refers to a machine learning algorithm in which individual items are placed into groups or classes based on quantitative information on one or more characteristics inherent in the items (referred to as traits, variables, characters, features, etc.) and based on a statistical model and/or a training data set of previously labelled items. Specifically in the context of the present invention, classification preferably means determining which specific cancer type, for example determined by its epigenetic state pattern, a cancer sample belongs to.

The term “training data set” in context of the invention refers to a set of biological state data, such as genomic methylation data, of a multitude of tumours that were classified by prior art methods, and therefore are of known tumour species.

The classification algorithm can be any appropriate algorithm for establishing a correlation between datasets, namely the biological state(s) or biological state pattern(s) of the cancer sample and the biological state data derived from pre-classified cancer types, which can be pre-determined biological state(s) or biological state patterns. Methods for establishing correlation between datasets include, but are not limited to, discriminant analysis (DA) (e.g., linear-, quadratic-, regularized-DA), Discriminant Functional Analysis (DFA), Kernel Methods (e.g., SVM), Multidimensional Scaling (MDS), Nonparametric Methods (e.g., k-Nearest-Neighbour Classifiers), PLS (Partial Least Squares), Tree-Based Methods (e.g., Logic Regression, CART, Random Forest Methods, Boosting/Bagging Methods), Generalized Linear Models (e.g., Logistic Regression), Principal Components based Methods (e.g., SIMCA), Generalized Additive Models, Fuzzy Logic based Methods, Neural Networks and Genetic Algorithms based methods.

The person skilled on the art will have no problem in selecting an appropriate method/algorithm to establish the correlation between the biological state(s) or biological state pattern(s) of the cancer sample and the biological state data derived from pre-classified cancer types of the present invention. In one embodiment, the method/algorithm used in correlating the biological state(s) or biological state pattern(s) of the cancer sample and the biological state data derived from pre-classified cancer types of the present invention is selected from the group including (or consisting of) DA (e.g., Linear-, Quadratic-, Regularized Discriminant Analysis), DFA, Kernel Methods (e.g., SVM), MDS, Nonparametric Methods (e.g., k-Nearest-Neighbour Classifiers), PLS (Partial Least Squares), Tree-Based Methods (e.g., Logic Regression, CART, Random Forest Methods, Boosting Methods), Generalized Linear Models (e.g., Logistic Regression), and Principal Components Analysis.

In an exemplary embodiment, the classification algorithm uses random forest analysis. As used herein the term “random forest analysis” refers to a computational method that is based on the idea of using multiple different decision trees to compute the overall most predicted class (the mode). In a specific application, the mode will be either tumour species or class based on how many decision trees predicted the samples to match a specific class. The class predicted by the majority is selected as the predicted class for the sample. The different decision trees used in this algorithm are trained on a randomly generated subset of the training data set and on a randomly selected set of the variables. This is why this algorithm relies on

two hyperparameters: the number of random trees to use, and the number of random variables used to train the different trees.

The term “biological state” may refer to an epigenetic state, mutation state, RNA expression or copy number of a gene or gene site.

The term “epigenetic state” refers to a measure for epigenetic changes (or for functionally relevant changes of an upregulation and/or downregulation) of the gene activity of a particular gene site and/or gene in the genome of a cancer sample. The epigenetic state comprises an epigenetic downregulation and/or upregulation of the gene site’s activity in the cancer sample in comparison to that same gene site’s activity in physiological tissue. Such downregulation and/or upregulation can for example be due to DNA methylation, histone modification or other epigenetic effects.

The term “epigenetic state pattern” refers to a combination of the epigenetic state(s) of a plurality of gene sites and/or genes. It comprises an overview of the epigenetic state(s) of the gene sites and/or genes. An epigenetic state pattern can therefore in its simplest form comprise information about which of the gene sites and/or genes of the plurality in question have an activation which is epigenetically modified in comparison to the physiological state and which do not. The epigenetic state pattern could also comprise information about which of the gene sites and/or genes are epigenetically upregulated and/or downregulated, for example in terms of hypermethylation (resulting in downregulation) or hypomethylation (resulting in upregulation) when DNA methylation is used as measure for epigenetic influence on gene or gene site activity.

In some embodiments, the classification algorithm of the present disclosure can be trained using epigenetic data derived from classified cancer types, such as pre-classified cancer types. The epigenetic data may be provided in the form of a predetermined pattern or predetermined epigenetic state pattern. The term “predetermined pattern” or “predetermined epigenetic state pattern” refers to an epigenetic state pattern that has been determined beforehand and that is typical of a specific cancer type, for example one of the types mentioned in Table 2 (and, for example, Tables 3 to 172). The first iteration of predetermined patterns has been determined by the inventors and has been used to train the classification algorithm.

In a preferred embodiment of the disclosure, the predetermined epigenetic state patterns pertain to the cancer types listed in Table 2 (and, for example, Tables 3 to 172, respectively). Furthermore, the predetermined epigenetic state pattern comprises essentially the same gene sites as the set of gene sites of the cancer sample being analysed. If, by determining the epigenetic state of the set of gene sites, as explained in more detail below, an epigenetic state pattern is obtained that corresponds to one of the predetermined patterns, the cancer pertaining to the sample can be classified as pertaining to this cancer type. The predetermined epigenetic state patterns are preferably determined by the classification algorithm. This means that the predetermined epigenetic state patterns are not in itself accessible by a user, but contained in the results of the classification algorithm, which, for example, employs machine learning and continually updates its own reference material. The predetermined epigenetic state patterns determined by the classification algorithm therefore change over time in an effort to increase sensitivity and specificity even further. It is therefore neither feasible nor useful to give an example of the predetermined patterns used in the invention as they are subject to continuous change. On the other hand, the skilled person is familiar with these aspects of machine learning and can easily provide for a classification algorithm to establish its own predetermined epigenetic state patterns as used herein.

Biological changes, such as epigenetic changes, in cancer tissue are known to be specific for certain cancer types or subtypes. The biological state(s) of a gene site can be determined using different methods known to the skilled person. For example, the biological state, such as the epigenetic state, of a gene site can be determined by assaying histone modifications, proteomics or transcriptomics. One approach could, for example, be based on an Assay for Transposase-Accessible Chromatin using sequencing (ATAC-seq). Another approach is assaying DNA methylation. As there are robust and reliable DNA methylation assays established and readily available, determining the epigenetic state of gene sites through determining methylation is the preferred approach used in the disclosure. However, it is not a single data point determined by any of the mentioned assays that determines the type of the cancer. The type of the cancer is determined by the epigenetic downregulation or upregulation of its gene sites, which in turn determines the metabolism and phenotype of the cancer. Gene site activation can, however, be determined by a number of different epigenetic approaches, as outlined above. To classify cancer types, it is therefore more prudent to determine the effect of the epigenetic changes on gene site activity rather than rely on the specific epigenetic changes measured by a specific type of assay. In theory, all of the epigenetic approaches should in the

end imply the same gene sites as having a pathological activity, provided that all gene sites and their activity are equally accessible through the various assays. This pathological gene site activity is what makes and defines the cancer types.

- 5 In view of the above, the methods of the present disclosure classify a cancer based on the biological state of specific genomic DNA sites or transcripts.

In one embodiment of the disclosure, the inventors used DNA methylation to find gene sites with pathological activity within the cancer genome. The epigenetic state of these gene sites
10 was then used to find patterns typical for different cancer types. Thus, the inventors found a set of gene sites having the biggest impact on differentiating between different cancer types.

To this end the inventors tested their approach using an Illumina methylation bead chip with which a multitude of classically classified tumour specimen were tested. Illumina's Hu-
15 manMethylation450 (450k) BeadChip allows to assays DNA methylation at 482,421 CpG dinucleotides. The platform measures DNA methylation by genotyping sodium bisulfite treated DNA. To run the assay only a small amount of DNA is needed and it is possible to use both frozen and paraffin (FFPE) material. So far, approximately 90000 tumour samples have been profiled by the inventors and allowed the verification of the surprisingly superior ap-
20 proach of the herein disclosed disclosure.

As readily apparent to the skilled person, the classification according to the disclosure also means that a stratification and/or a diagnosis of the cancer is achieved. In the context of the present disclosure the term "stratification" refers to the classification or grouping of patients
25 according to one or more predetermined criteria. In certain embodiments stratification is performed in a diagnostic setting in order to group a patient according to the prognosis of disease progression, either with or without treatment. In particular embodiments stratification is used in order to distribute patients enrolled for a clinical study according to their individual characteristics. In particular embodiments stratification is used in order to identify the best suitable
30 treatment option for a patient.

The term "diagnosis" or "diagnostic" is used herein to refer to the identification or classification of a molecular or pathological state, disease or condition. For example, "diagnosis" may refer to identification of a particular type of cancer, e.g., a lung cancer. "Diagnosis" may also

refer to the classification of a particular type of cancer, e.g., by histology (e.g., a non-small cell lung carcinoma), by molecular features (e.g., a lung cancer characterized by nucleotide and/or amino acid variation(s) in a particular gene or protein), or both. However, it is important to note that the disclosure is directed to a strictly in vitro method in all its embodiments. None of the method steps of any embodiment are performed on the human or animal body.

The term “cancer type”, “tumour species” or “tumour class” shall refer to a specific kind of a tumour or subcategory of a tumour that can be classified based on its tissue origin, genetic makeup, histology etc. In particular in the field of brain tumours various distinct tumour species or classes of the central nervous system exist that can be differentiated via for example histopathology (1. Acta Neuropathol. 2007 Aug; 114(2):97-109. Epub 2007 Jul 6. “The 2007 WHO classification of tumours of the central nervous system.” Louis DN(1), Ohgaki H, Wiestler OD, Cavenee WK, Burger PC, Jouvet A, Scheithauer BW, Kleihues P.). Specifically, the disclosure pertains to the cancer types as listed in Table 2.

The term “cancer sample” or “tumour sample” as used herein refers to a sample obtained from a patient. The tumour sample can be obtained from the patient by routine measures known to the person skilled in the art, i.e., biopsy (taken by aspiration or punctuation, excision or by any other surgical method leading to biopsy or resected cellular material). For those areas not easily reached via an open biopsy a surgeon can, through a small hole made in the skull, use stereotaxic instrumentation to obtain a “closed” biopsy. Stereotaxic instrumentation allows the surgeon to precisely position a biopsy probe in three-dimensional space to allow access almost anywhere in the brain. Therefore, it is possible to obtain tissue for the diagnostic method of the present disclosure. The actual removal of the sample from the patient is, however, not part of the inventive method. “Providing a cancer sample” therefore merely pertains to making a sample available for laboratory use without the step of obtaining it from a patient in the first place.

The term “cancer” or “tumour” is not limited to any stage, grade, histomorphological feature, invasiveness, aggressiveness or malignancy of an affected tissue or cell aggregation. In particular stage 0 cancer, stage I cancer, stage II cancer, stage III cancer, stage IV cancer, grade I cancer, grade II cancer, grade III cancer, malignant cancer, primary carcinomas, and all other types of cancers, malignancies etc. are included.

As used herein, the term “gene site” refers to a region of DNA comprising or consisting of a gene, particularly a gene or gene site as listed in Table 1. In particular, the term “gene site” refers to a DNA sequence with a genetic locus as defined in Table 1. A gene site may comprise additional base pairs upstream and/or downstream of a gene, for example up to 12 kb, preferably up to 10 kb up to 8 kb or up to 6 kb or up to 4 kb or up to 2 kb upstream and/or downstream. A biological state, such as an epigenetic state, of a gene site may therefore refer to the biological state of the gene itself and additionally to the biological state of the additional string of base pairs upstream and/or downstream of the gene. In preferred embodiments of the disclosure, the biological state of the gene sites in the set comprises the biological state of the gene sites as listed in Table 1 and up to 10 kb, preferably up to 8 kb or up to 6 kb or up to 4 kb or up to 2 kb, upstream and/or downstream of the genes. In a further preferred embodiment, the biological state of the gene sites comprises exclusively the biological state of the gene sites as listed in Table 1 without any bases upstream and/or downstream of the gene sites. In this case, only the biological state of the gene sites themselves are being used and the gene sites do not comprise any bases outside of the gene sites as listed in Table 1.

The term “set of gene sites” refers to a number of gene sites being grouped together. For example, it is the epigenetic state(s) of this set of gene sites that is being evaluated in the disclosure, then combined into a pattern and analysed by the classification algorithm.

As used herein, the term “CpG site” or “CpG position” refers to a region of DNA where a cytosine nucleotide occurs next to a guanine nucleotide in the linear sequence of bases along its length, the cytosine (C) being separated by only one phosphate (p) from the guanine (G). About 70% of human gene promoters have a high CpG content. Regions of the genome that have a higher concentration of CpG sites are known as “CpG islands”. Cytosines in CpG dinucleotides can be methylated to form 5-methylcytosine. Methylation of (i.e., introduction of a methyl group in) the cytosines of CpG site within the promoters of genes can lead to gene silencing, a feature found in a number of human cancers. In contrast, the hypomethylation of CpG sites has generally been associated with the over-expression of oncogenes within cancer cells. The term “independent genomic CpG positions” shall in the context of the present disclosure mean that each CpG position of a group of genomic CpG positions can be probed separately for its methylation state.

The term “methylation state”, as used herein describes the state of methylation of a CpG position, thus refers to the presence or absence of 5-methylcytosine at one CpG site within genomic DNA. When none of the DNA of an individual is methylated at one given CpG site, the position is 0% methylated. When all the DNA of the individual is methylated at that given CpG site, the position is 100% methylated. When only a portion, e.g., 50%, 75%, or 80%, of the DNA of the individual is methylated at that CpG site, then the CpG position is said to be 50%, 75%, or 80%, methylated, respectively. The term “methylation state” reflects any relative or absolute amount of methylation of a CpG position. Methylation of CpG positions can be assessed by any method used in the art. The terms “methylation” and “hypermethylation” are used herein interchangeably. When used in reference to a CpG positions, they refer to the methylation state corresponding to an increased presence of 5-methylcytosine at a CpG site within the DNA of a biological sample obtained from a patient, relative to the amount of 5-methylcytosine found at the CpG site within the same genomic position of a biological sample obtained from a healthy individual, or alternatively from an individual suffering from a tumour of a different class or species.

The term “biological sample” is used herein in its broadest sense. In the practice of the present disclosure, a biological sample is generally obtained from a subject. A sample may be any biological tissue or fluid with which the biological state(s) of gene sites of the present disclosure may be assayed. Frequently, a sample will be a “clinical sample” (i.e., a sample obtained or derived from a patient to be tested). The sample may also be an archival sample with known diagnosis, treatment, and/or outcome history. Examples of biological samples suitable for use in the practice of the present disclosure include, but are not limited to, bodily fluids, e.g., blood samples (e.g., blood smears), and cerebrospinal fluid, brain tissue samples, spinal cord tissue samples or bone marrow tissue samples such as tissue or fine needle biopsy samples. Biological samples may also include sections of tissues such as frozen sections taken for histological purposes. The term “biological sample” also encompasses any material derived by processing a biological sample. Derived materials include, but are not limited to, cells (or their progeny) isolated from the sample, as well as nucleic acid molecules (DNA and/or RNA) extracted from the sample. Processing of a biological sample may involve one or more of: filtration, distillation, extraction, concentration, inactivation of interfering components, addition of reagents, and the like.

The method according to some embodiments of the present disclosure includes a step of “determining an epigenetic state” of a set of gene sites. This can be achieved through any means suitable to assay epigenetically modified activity of the gene sites. In a preferred embodiment of the disclosure the epigenetic state of a set of gene sites is determined by assessing the DNA methylation state of a multitude of independent genomic CpG positions, particularly CpG positions within the gene sites as mentioned above, preferably within the gene sites listed in Table 1, in a biological sample obtained from a patient. Determination of the methylation state may be performed using any method known in the art to be suitable for assessing the methylation of cytosine residues in DNA. Such methods are known in the art and have been described; and one skilled in the art will know how to select the most suitable method depending on the number of samples to be tested, the quantity of sample available, and the like.

Thus, the methylation state of a genomic CpG position or a combination of genomic CpG positions according to the disclosure can be determined using any of a wide variety of methods that are generally divided into strategies based on methylation-specific PCR (MSP), and strategies employing PCR performed under methylation-independent conditions (MIP). Methylation-independent PCR (MIP) primers are used in most of the available PCR-based methods. They are designed for proportional amplification of methylated and unmethylated DNA. In contrast, methylation-specific PCR (MSP) primers are designed for the amplification of methylated template only.

Examples of methylation-independent PCR based techniques include, but are not limited to, direct bisulfite direct sequencing (Frommer et al., PNAS USA, 1992, 89: 1827-1831), pyrosequencing (Collela et al., Biotechniques, 2003, 35: 146-150; Uhlmann et al., Electrophoresis, 2002, 23: 4072-4079; Tost et al., Biotechniques, 2003, 35: 152-156), Combined Bisulfite Restriction Analysis or “COBRA” (Xiong et al., Nucleic Acids Res., 1997, 25: 2532-2534), Methylation-Sensitive Single-Nucleotide Primer Extension or “MS-SnuPE” (Gonzalzo et al., Nucleic Acids Res., 1997, 25: 2529-2531), Methylation-Sensitive Melting Curve Analysis or “MS-MSA” (Worm et al., Clin. Chem., 2001, 47: 1183-1189), Methylation-Sensitive High-Resolution Melting or “MS-HRM” (Wojdacz et al., Nucleic Acids Res., 2007, 35:e41), MALDI-TOF mass spectrometry with base-specific cleavage and primer extension (Ehrich et al., PNAS USA, 2005, 102: 15785-15790), and HeavyMethyl (Cottrell et al., Nucleic Acids Res., 2004, 32: e10).

Examples of methylation-specific PCR based techniques include for example methylation specific PCR or “MSP” (Herman et al., PNAS USA, 1996, 93: 9821-9826; Mackay et al., Hum. Genet., 2006, 120: 262-269; Mackay et al., Hum. Genet., 2005, 116: 255-261; Palmisano et al., Cancer Res., 2000, 60: 5954-5958; Voso et al., Blood, 2004, 103: 698-700),
5 MethylLight (Eads et al., Nucleic Acids Res., 2000, 28:e32; Eads et al., Cancer Res., 1999, 59: 2302-2306; Lo et al., Cancer Res., 1999, 59: 3899-3903), Melting curve Methylation Specific PCR or “McMSP” (Akey et al., Genomics, 2002, 80: 376-384), Sensitive Melting Analysis after Real-Time MSP or “SMART-MSP” (Kristensen et al., Nucleic Acids Res., 2008, 36: e42), and Methylation-Specific Fluorescent Amplicon Generation or “MS-FLAG” (Bonnanno et al., Clin. Chem., 2007, 53: 2119-2127).
10

Many of these methods rely on the prior treatment of DNA with sodium bisulphite. This treatment leads to the conversion of unmethylated cytosine to uracil, while methylated cytosine remains unchanged (Clark et al., Nucleic Acids Res., 1994, 22: 2990-2997). This change
15 in the DNA sequence following bisulphite conversion can be detected using a variety of methods, including PCR amplification followed by DNA sequencing. It is safe to say that the use of bisulphite-converted DNA for DNA methylation analysis has surpassed almost every other methodology for DNA methylation analysis, thereby becoming the gold standard for detecting changes in DNA methylation. The protocol described by Frommer et al. (PNAS
20 USA, 1992, 89: 1827-1831) has been widely used for sodium bisulphite treatment of DNA, and a variety of commercial kits are now available for this purpose.

Thus, in a method according to the disclosure, the step of determining the epigenetic state can be achieved by determining the methylation state of a gene promoter, or of a combination of
25 gene promoters of the disclosure. It may be performed using any of the techniques described above or any combination of these techniques. One skilled in the art will recognized that when the methylation state of a combination of gene promoters has to be determined, the determinations may be performed using the same DNA methylation analysis technique or different DNA methylation analysis techniques. Other methods include oligonucleotide methylation tiling arrays, BeadChip assays, HPLC/MS methods, methylation-specific multiplex ligation-dependent probe amplification (MS-MPLA), bisulphite sequencing, and assays using
30 antibodies to DNA methylation, i.e., ELISA assays.

By using the statistical model as described herein, the inventors found that the gene sites comprising the gene sites listed in Table 1 are sufficient to classify cancer samples into a large number of different cancer types. While it may be possible to classify even more cancer types by analysing the named gene sites, this has been validated for the cancer types listed in Table

5 2. To classify a cancer type, according to the disclosure, it is therefore only necessary to determine the epigenetic state of these selected gene sites, in particular of at least 3 gene sites. A full analysis of the whole genome of the cancer type can therefore be avoided. For a sufficiently specific classification, only those gene sites listed in Table 1 must be analysed, resulting in quicker and less laborious diagnosis.

10 The inventors further found that a set of gene sites comprising at least 3 of the gene sites listed in Table 1 is sufficient for the classification of the cancer sample. However, larger sets provide more accuracy. In preferred embodiments of the disclosure, the set of gene sites thus comprises at least 10, preferably at least 20 or at least 30 or at least 40 or at least 50 or at least

15 60 or at least 70 or at least 80 or at least 90 or at least 100, genes of the sample genome of the cancer being classified. A set of gene sites preferably comprising 100 or less, 90 or less, 80 or less, 70 or less, 60 or less, 50 or less, 40 or less, 30 or less, 20 or less, or 10 or less gene sites provide for a good balance between accuracy and work necessary. The embodiments of the present disclosure are not limited thereto, and the set may comprise more than 100 gene sites

20 or all gene sites listed in Table 1.

While all of the gene sites or genes listed in Table 1 could be used to classify the cancer types as described herein in Table 2, the inventors identified subsets of the genes with higher importance, meaning resulting in more accuracy, when used to classify specific cancer types. It

25 is therefore preferred that the predetermined pattern for a cancer type as listed in Table 2 comprises at least 3 gene sites for that specific cancer type. It is further preferred that the predetermined pattern for a cancer type comprises at least 3 gene sites for that specific cancer type selected from the gene sites listed in Tables 3 to 172, respectively. In a preferred embodiment the set of gene sites of the cancer sample genome being analysed comprises the exact

30 same gene sites or genes as the predetermined pattern.

In a preferred embodiment, the statistical model employed by the inventors provides for a measure of the variable importance of the gene sites for each cancer.

As can be seen from Tables 3 to 172, the different gene sites have different importance for the classification. To improve the accuracy of the classification, it is therefore preferred that the epigenetic data for a cancer type comprises those gene sites listed in Tables 3 to 172 for that cancer type that are the ones with the highest values of variable importance for that cancer type.

As stated before, it is preferred that the set of gene sites of the cancer sample genome being analysed comprises the same genes or gene sites as the epigenetic data derived from pre-classified cancer types (predetermined pattern). The set of gene sites of the cancer sample genome being analysed, and the epigenetic data derived from pre-classified cancer types therefore preferably also comprise the same number of genes or gene sites.

While analysing gene sites of a set of genes comprising 3 genes is advantageous for being less laborious, the accuracy of the classification increases with more genes being analysed per cancer type. It is therefore preferred that the predetermined pattern for a cancer type listed in Table 2 comprises at least 10, preferably at least 20 or at least 30 or at least 40 or at least 50 or at least 60 or at least 70 or at least 80 or at least 90 or at least 100, gene sites or genes listed in Table 1. The preferred gene sites or genes “for a cancer type” are the ones listed for each cancer type in in Tables 3 to 172, respectively. As explained above for the set, 80 to 100 genes provide for a good balance between accuracy and workload.

The classification may include a direct or indirect comparison of the epigenetic state pattern of the set of gene sites with predetermined epigenetic state patterns, e.g. by determining the overlap of the two patterns, i.e., how much the two patterns are similar to or different from each other. This may, for example, be statistically determined and may be represented as a numerical value. Specifically, the difference between the patterns may be represented by a percentage. The accuracy of the classification can be influenced by allowing patterns with higher or lower difference from a predetermined pattern to still be classified as the cancer type the predetermined pattern pertains to. For a suitable accuracy, it is preferred that the cancer is classified as the cancer to which the predetermined pattern pertains if the epigenetic state pattern of the set of gene sites differs from the predetermined pattern by at most 5 %, preferably at most 4 % or at most 3 % or at most 2 % or at most 1 %. These values are both useful in practice and achievable by the inventive method.

As explained above, the predetermined epigenetic state patterns used for comparison have been determined by the inventors by analysing more than 90000 cancer samples from a range of different sources. As this process is also part of the present disclosure, it is explained in detail below.

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In all embodiments the method of the disclosure is performed as an *ex-vivo* or *in-vitro* method.

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In another preferred aspect of the present invention, the invention then relates to a method of treating cancer in a patient, comprising performing a method according to the present invention, and providing a suitable treatment to said patient, wherein said treatment is based, at least in part, on the results of the method according to the present invention.

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In another preferred aspect of the present invention, the invention relates to a method of developing a treatment regime for the cancer (e.g., a tumour species) classified using the method according to the present invention. Preferably, the method further includes providing a suitable treatment to a patient based on the developed treatment regime.

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“Treatment” shall mean a reduction and/or amelioration of the symptoms of the disease. An effective treatment achieves, for example, a shrinking of the mass of a tumor and the number of cancer cells. A treatment can also avoid (prevent) and reduce the spread of the cancer, such as, for example, affect metastases and/or the formation thereof. A treatment may be a naive treatment (before any other treatment of a disease had started), or a treatment after the first round of treatment (e.g. after surgery or after a relapse). The treatment can also be a combined treatment, involving, for example, chemotherapy, surgery, and/or radiation treatment. The treatment can also modulate auto-immune response, infection and inflammation.

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Most preferably the methods according to the disclosure are used for the classification of tumours of the central nervous system, therefore, the tumour preferably is a brain tumour or a spinal cord tumour, and the tumour species is a brain tumour species or a spinal cord tumour species. As already noted herein before, these tumours are characterized by a huge epigenetic variety which has a significant impact on the development of treatment regimes in order to allow for the best treatment of the patient. If the tumour disease is a tumour of the central nervous system (CNS), it is preferred that said tumour species comprises at least 184 different

classes of CNS tumours. Additionally, the disclosure is also applicable to sarcomas. In a preferred embodiment said CNS tumours are selected from the list of cancer types or tumour species of Table 2.

- 5 The determination of DNA methylation levels of the disclosure is performed preferably with a genomic array or chip comprising probes which are specific for the methylation of at least 1000 CpG positions. It is preferred to test as many positions as possible in order to allow for the generation of a highly specific classification. Genome-wide DNA methylation assays are therefore preferred, such as the HumanMethylation450k-chip (Illumina®).

10

The classification algorithm may be based on random forest (RF). The training of the RF-based classification algorithm according to some embodiments of the disclosure may comprise a preceding step of selecting CpG position which of all CpG positions used provide the purest splitting rules, and using said selected CpG positions as a training-data-optimization-set to train a classification rule.

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In other embodiments of the disclosure the training of the RF-based classification algorithm may comprise a step of down-sampling for each tumour species the number of bootstrap samples to the minority class, the minority class being the lowest sample size of a tumour species in the training dataset.

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Another embodiment of the disclosure provides the above method and comprises the further step of including the methylation data of the tumour sample as classified into the training-data-set to obtain an enhanced-training-data-set and computing an enhanced-classification-rule by random forest analysis based on the enhanced-training-dataset. Optionally the classification of said tumour sample may be repeated with the enhanced-classification-rule. This embodiment serves the continuous development and improvement of the original training data set. Each further classified tumour species will have a genomic DNA methylation profile or epigenetic state pattern that further enhances the classification for that tumour species and that can then be used as a predetermined epigenetic state pattern in the present disclosure. Therefore, the disclosure in one preferred embodiment provides a classification system characterized by a self-learning classification rule.

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In order to provide a classification rule with good specificity and sensitivity, the pre-determined methylation data / epigenetic state pattern used in context of the present disclosure includes for each pre-classified cancer type the methylation state/levels at said CpG position of at least one, two, three, four, five, six or more independent samples.

5

Another aspect of the present disclosure then pertains to a method for stratifying the treatment of a tumour patient, comprising the classification of the tumour species / cancer type of the tumour of the patient according to the classification methods of the disclosure and stratifying the treatment of the patient in accordance with the diagnosed tumour species.

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Yet a further aspect of the disclosure pertains to a computer-implemented method for generating a classification-rule for aiding the classification of tumour samples in cancer diagnosis, the method comprising providing DNA methylation data of a multitude of independent genomic CpG positions of genomes of a multitude of diverse pre-classified tumour species of the same tumour type (for example brain cancer, lung cancer, leukaemia, etc.); computing a random forest of binary decision trees from the DNA methylation data, wherein in each binary decision tree of said random forest each node is a CpG position, and each terminal leave a specific tumour species, and each binary splitting rule is a methylation state at said CpG position. This method can be used to create the predetermined epigenetic state patterns as explained above.

20

To learn a classification rule that allows predicting the class assignment of future diagnostic cases the inventor's applied the machine learning algorithm RandomForest (RF; Breiman, 2001). The RF algorithm is a so-called ensemble method that combines the predictions of several 'weak' classifiers to achieve improved prediction accuracy. The RF uses binary classification trees (Classification and Regression Trees (CART); Breiman et al., 1983) as 'weak' classifiers. Each of these trees is a sequence of binary splitting rules that are learned by recursive binary splitting. The CART algorithm starts with all samples assigned to a 'root' node and tries to find the variable, e.g., a measured CpG probe, and a corresponding cut-off that results in the purest split into the different classes. To measure this gain in class 'purity' the Gini index, a classical statistical measure for inequality, may be used. To fit a tree the CART algorithm iteratively repeats these steps until no further improvements can be made, i.e., only samples of the same class are assigned to the final 'leaf' node, or a pre-specified node size is achieved. To predict the class of a new diagnostic case the binary splitting rules are compared

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with the new data starting in the root node down to one of the leaf nodes. The tree then predicts or votes for the class dominating that leaf node.

Decision trees have the advantage that they are non-parametric and do not rely on any distributional assumptions. Moreover, trees allow to learn complex non-linear relationships and interactions, they are easy to interpret and can be efficiently fitted in large data sets. The main disadvantages of decision trees are that they often tend to overfit the data and that they have a weak prediction performance.

10 However, to improve the prediction accuracy of a single tree the RF algorithm combines thousands of trees by bootstrap aggregation (bagging). In brief, each tree is fitted using training data sets that are generated by drawing bootstrap samples, i.e., randomly selecting two-third of the data with replacement. In addition, at each node only a random subset of the available variables is used to find an optimal splitting rule. This additional source of randomi-
15 zation allows selecting variables with lower predictive value that would otherwise be ruled out by the most prominent variables. This feature guarantees that the resulting trees are decorrelated, i.e., they use different variables to find an optimal prediction rule. Taking the majority vote over thousands of bootstrap aggregated and decorrelated trees greatly improves the prediction accuracy of the RF. The majority vote, i.e., the proportion of trees voting for a class,
20 can be used as empirical class probabilities or scores that turned out to be a very useful tool for diagnosis.

To validate the resulting RF classifier, a repeated five-fold cross-validation is applied. In each cross-validation the reference set is randomly split into five parts. Then four-fifth of the data
25 is used to train the RF classifier and one-fifth is used for prediction. Currently the estimated test error of the classifier is around 3.1%.

Alternatively, the resulting RF classifier is validated by a repeated threefold cross-validation. In each cross validation the reference set is randomly split into three parts. Then two-third of
30 the data is used to train the RF classifier and one-third is used for prediction. Currently the estimated test error of the classifier is around 4.9%.

The classification scores generated by the RF, i.e., the proportion of trees voting for a class, are typically unequally distributed between classes. Furthermore, if interpreted as class prob-

abilities, the scores often fail to estimate the actual class probabilities and are thus said to be not well-calibrated. However, to judge the classification of a single case in the context of clinical diagnosis, the uncertainties associated with an individual prediction in terms of a confidence scores, or estimated class probability is needed. To receive recalibrated scores that are comparable between classes and that are improved estimates of the certainty of individual predictions, the inventors fit a calibration model to raw RF scores. This calibration model is a multinomial logistic regression model, which takes the tumour subclasses as response variable and the 'raw' RF scores as explanatory variables. In addition, this model is fitted by incorporating a small ridge-penalty on the likelihood to prevent the model from over fitting as well as to stabilize estimation in situations where classes are perfectly separable. The amount of this regularization, i.e., the penalization parameter, is determined by running a ten-fold cross-validation and choosing the value that minimizes the misclassification error. To fit this model independent, 'raw' RF scores are needed, i.e., the scores need to be generated by an RF classifier that was not trained using the same samples, otherwise the RF scores will be systematically biased and not comparable to scores of unseen cases. To generate such independent 'raw' scores, the inventors apply a three-fold cross validation.

To validate the class predictions generated by using the recalibrated scores of the calibration model a three-fold nested cross-validation is applied. In each cross validation the reference set is randomly split into three parts. Then two-third of the data is used to train the RF classifier and one-third is used for prediction. Within each of these three cross-validation runs a nested three-fold cross-validation is applied to generate independent RF scores, which are used to train a calibration model. The predicted RF scores resulting from the outer cross-validation loop are then recalibrated by using the suitable calibration model, i.e. a model that was fitted using the RF scores generated by using the other two-third of the data in the inner loop. Currently the estimated test error of the classifier when using the recalibrated scores for prediction is around 3.2%.

Some embodiments of the disclosure pertain to a method where the diverse tumour species are selected from metastatic tumours, tumours stemming from specific tissues, tumours in a specific stage, recurrent tumours, tumours having a specific genetic mutation, tumours of patients having different gender, age or genetic background.

BRIEF DESCRIPTION OF THE DRAWINGS

The present disclosure will now be further described in the following examples with reference to the accompanying figures and sequences, nevertheless, without being limited thereto. For the purposes of the present disclosure, all references as cited herein are incorporated by reference in their entireties. In the Figures:

Figure 1: Heatmap representation of the reference set. The colour code indicates the different tumour classes, FFPE and frozen samples as well as samples that are misclassified in the cross validation. The heatmap shows the methylation profile of 10,000 CpG probes most important for the classification (highest average gain in Gini purity).

Figure 2: Example of a binary decision tree. At each node a CpG probe and corresponding cut-off is used to make a binary decision. The final leaf nodes display the abbreviation of the tumour subclass, i.e., EPN_PFA means posterior fossa ependymoma subtype A.

Figure 3: Median test error estimated by three five-fold cross validation runs.

Figure 4: The left panel shows a symbolically the histology of a WNT medulloblastoma and a Group 3 medulloblastoma which are not distinguishable. The right panel shows a multidimensional scaling (MDS) analysis of 107 medulloblastoma samples of all molecular subtypes using the 21,092 most variable CpG probes. WNT medulloblastoma are coloured in blue, SHH medulloblastoma in red, Group 3 medulloblastoma in yellow and Group 4 medulloblastoma in green.

Figure 5: A shows the result of the histology of the patient. B shows the classifier scores. Highlighted is the highest score entry.

Figure 6: A and B show the result of the histology of the patient. C shows the classifier scores. Highlighted is the highest score entry.

Figure 7: Schematic overview how the classifier is trained and validated by the three-fold nested-cross validation. In each outer cross validation run the training data is used for an inner three-fold cross-validation that generates independent RF scores. These scores are used to fit a calibration model which can then be applied to recalibrate the RF scores generated by predicting the test data in the outer loop. To fit a calibration model using all the data in the reference set, which is later used for new diagnostic cases, the RF scores generated in the outer loop can be used.

Figure 8: Genome plot showing the *PTPRN2* gene, CpG sites and RF variable importance measure.

Figure 9: Heatmap showing the methylation values of 100 CpGs located on *PAX6*, *PTPRN2* and *OSTM1* with highest standard deviation across 75 ATRT samples. Rows and columns have been reordered by applying hierarchical clustering with Euclidean distance as distance metric and complete linkage as linkage method. The class annotation colour code shows the previously known molecular subtypes, the gene annotation indicates the gene on which the CpGs are located.

Figure 10A: 75 ATRT tumour samples projected on to the first two PCs resulting from PCA.

Figure 10B: 75 ATRT tumour samples projected on to coordinates calculated by tSNE analysis.

Figure 10C: CART tree with two sequential splitting rules.

Figure 10D: Scatterplot of 75 ATRT tumour samples, the x and y-axes are the methylation value of the two CpG sites selected by the CART tree. The corresponding splitting rule cut-offs are displayed as dashed lines.

Figure 11: tSNE of 1167 samples for which DNA-methylation as well as gene expression data is available. The tSNE coordinates were calculated on the gene expression

data of the 688 most important genes or gene sites. The class labels and colours correspond to classes predicted by the methylation classifier.

Figures 12A and B: Confusion matrices that show the results of a 3-fold cross validation to validate the RF and the multinomial logistic regression model. Like for classifiers trained on methylation data, most errors occur between closely related entities such as the MB group 3 and 4 subtypes.

Figure 13: Simulation study to investigate brain tumor classifier performance for classifiers trained using CpG-probes located on random subsets of signature genes and random hg19 genes.

Figure 14: tSNE dimension reduction of DNA-methylation profiles of 9084 TCGA cases from 33 different projects where each project focused on specific tumor entity.

Figure 15: Left: confusion matrix which shows the result of the 3-fold cross-validation; right: tSNE dimension reduction highlighting the samples that were falsely predicted in the cross-validation.

Figure 16: Confusion matrices for four different statistical or machine learning models trained on the TCGA cohort shown in Figure 14.

DETAILED DESCRIPTION OF EMBODIMENTS

Infinium Methylation Assay

Genome-wide screening of DNA methylation patterns was performed by using the Infinium HumanMethylation450 BeadChips (Illumina, San Diego, US), allowing the simultaneous quantitative measurement of the methylation state at 485,577 CpG sites. By combining Infinium I and Infinium II assay chemistry technologies, the BeadChip provides coverage of 99% of RefSeq genes and 96 % of CpG islands.

DNA concentrations were determined using PicoGreen (Life Technologies, Darmstadt, Germany). The quality of genomic DNA samples was checked by agarose-gel analysis, and samples with an average fragment size >3kb were selected for methylation analysis. For formalin-

fixed paraffin-embedded (FFPE) DNA samples the quality was evaluated by real-time PCR analysis on Light Cycler 480 Real-Time PCR System (Roche, Mannheim, Germany) using the Infinium HD FFPE QC Kit (Illumina). The laboratory work was done in the Genomics and Proteomics Core Facility at the German Cancer Research Center, Heidelberg, Germany (DKFZ).

DNA (500 ng genomic DNA and 250 ng FFPE DNA, respectively) from each sample was bisulfite converted using the EZ-96 DNA Methylation Kit (Zymo Research Corporation, Orange, US) according to the manufacturer recommendations. Bisulfite treatment leads to the deamination of non-methylated cytosines to uracils, while methylated cytosines are refractory to the effects of bisulfite and remain cytosine. After bisulfite conversion, FFPE samples were treated with the Infinium HD DNA Restoration Kit (Illumina) according to the manufacturer recommendations. By using enzymatic reactions, degraded FFPE DNA is restored in preparation for the whole genome amplification.

Each sample was whole genome amplified and enzymatically fragmented following the instructions in the Illumina Infinium HD Assay Methylation Protocol Guide (genomic DNA) or Infinium HD FFPE Methylation Guide (FFPE DNA), respectively. The DNA was applied to Infinium HumanMethylation450 BeadChip and hybridization is performed for 16-24h at 48°C. During hybridization, the DNA molecules anneal to locus-specific DNA oligomers linked to individual bead types. One or two probes are used to interrogate CpG locus, depending on the probe design for a particular CpG site.

Allele-specific primer annealing is followed by single-base extension using DNP- and Biotin-labeled ddNTPs. For Infinium I assay design, both bead types (one each for the methylated and unmethylated states) for the same CpG locus incorporate the same type of labeled nucleotide, determined by the base preceding the interrogated "C" in the CpG locus, and therefore are detected in the same color channel. Infinium II uses only one bead type with a unique type of probe allowing detection of both alleles. The methylated and unmethylated signals are generated respectively in the green and the red channels.

After extension, the array is fluorescently stained, scanned, and the intensities at each CpGs were measured. Microarray scanning was done using an iScan array scanner (Illumina). DNA methylation values, described as beta values, are recorded for each locus in each sample.

DNA methylation beta values are continuous variables between 0 and 1, representing the percentage of methylation of a given cytosine corresponding to the ratio of the methylated signal over the sum of the methylated and unmethylated signals.

5 Data pre-processing

All data analysis was performed using the open-source statistical programming language R (R Core Team, 2014). Raw data files generated by the iScan array scanner were read and pre-processed using the capabilities of the Bioconductor package minfi (Aryee et al, 2014). With the minfi package the same pre-processing steps as recommended in Illumina's BeadStudio
10 software were performed.

In addition, the following filtering criteria were applied: Removal of probes targeting the X and Y chromosomes ($n = 11,551$), removal of probes containing a single nucleotide polymorphism (dbSNP132 Common) within five base pairs of and including the targeted CpG-site ($n = 24,536$), and probes not mapping uniquely to the human reference genome (hg19) allowing
15 for one mismatch ($n = 9,993$). In total, 438,370 probes were kept for analysis.

Training the classifier

To learn a classification of 1899 samples that were assigned to 72 different brain tumour sub-
20 types the Random Forest (RF) algorithm implemented in the R package randomForest (Liaw and Wiener, 2002) was used. The RF algorithm is a so-called ensemble method that combines the predictions of several 'weak' classifiers to achieve improved prediction accuracy. The RF uses binary classification trees (Classification and Regression Trees (CART); Breiman et al., 1983) as 'weak' classifiers. Each of these trees represents a sequence of binary splitting rules
25 that are learned by recursive binary splitting. The CART algorithm starts with all samples assigned to a 'root' node and tries to find the variable, e.g., a measured CpG probe, and a corresponding cut-off that results in the purest split into the different classes. To measure this gain in class 'purity' the Gini index, a classical statistical measure for inequality, is used. To fit a tree the CART algorithm iteratively repeats these steps until no further improvements can be
30 made, i.e., only samples of the same class are assigned to the final 'leaf' node, or a pre-specified node size is achieved. To predict the class of a new diagnostic case the binary splitting rules are compared with the new data starting in the root node down to one of the leaf nodes. The tree then predicts or votes for the class dominating that leaf node. However, to improve the prediction accuracy of a single tree the RF algorithm combines thousands of trees

by bootstrap aggregation (bagging). In brief, each tree is fitted using training data sets that are generated by drawing bootstrap samples, i.e., randomly selecting two-third of the data with replacement. In addition, at each node only a random subset of the available variables are used to find an optimal splitting rule. To predict the class of a diagnostic sample the RF takes the majority vote of all trees in the forest.

To learn the classification the default parameter settings of the randomForest function were used and 10,000 decision trees were fitted. In addition, to take the highly imbalanced class sizes into account a down-sampling strategy was followed, i.e., to fit a decision tree the number of bootstrap samples drawn from each class was equal to the number of samples in the minority class. To further improve prediction performance of the classifier a variable selection was performed, i.e. in a first step the algorithm is used to calculate the variable importance, e.g. the average improvement in Gini purity of a CpG probe when used for a splitting rule. The final classifier was trained using only the 30,000 CpG probes with highest variable importance measure.

An overview of the training of the classifier is provided in Figure 7.

Internal validation

To validate the resulting classifier and estimate its performance in predicting future diagnostic cases a repeated five-fold cross-validation was applied. In example, in each cross-validation run the reference set is randomly split into five parts. Then four-fifth of the data is used to train the RF classifier as described above and one-fifth is used for prediction. Currently the estimated test error of the classifier is around 3.1%.

Example 1: Distinguishing WNT medulloblastoma from Group 3 medulloblastoma

Medulloblastoma is the most common malignant paediatric brain tumour and comprises four distinct molecular variants. These variants are known as WNT, SHH, Group 3, and Group 4. These variants are histologically indistinguishable, but clearly separable by DNA methylation patterns (see Figure 4). WNT tumours show activated Wnt signalling pathway and carry a favourable prognosis. SHH medulloblastoma show Hedgehog signalling pathway activation and are known to have an intermediate to good prognosis. While both WNT and SSH variants

are molecularly already well characterised, the genetic programs driving the pathogenesis of Group 3 and Group 4 medulloblastoma remain largely unknown.

Example 2: Change of Diagnosis of an anaplastic astrocytoma WHO III

A 1944 born female brain tumour patient was diagnosed based on histology (see Figure 5A) to suffer from an anaplastic astrocytoma WHO III. Using the inventive classification procedure, a classifier score of 0.335 changed the diagnosis to Glioblastoma WHO IV (see Figure 5B).

Example 3: Change of Diagnosis of Schwannoma

A 1969 born male patient was based on the histology diagnosed with Schwannoma (Figures 6A and 6B). The classification procedure of the present disclosure however was able to diagnose the patient to suffer from Meningioma WHO I (see Figure 6C).

Example 4: DNA methylation-based classification of tumour entities using three gene sites

Atypical teratoid rhabdoid tumour (ATRT) is a rare paediatric brain tumour that can be subdivided into three molecular subgroups: ATRT-TYR, ATRT-SHH and ATRT-MYC (Ho et al. 2020, PMID: 31889194).

The inventors have identified genes that include CpG sites that are most important for the classification of brain tumours and molecular subtypes. The importance of these CpGs for the classification has been measured by applying the permutation-based variable importance measure of the Random Forest (RF) algorithm (Strobl et al. 2007, PMID: 17254353). Among others the three genes *PAX6*, *PTPRN2* and *OSTM1* include many important CpGs for the classification. Figure 8 displays the *PTPRN2* gene and the CpG sites located on it. Most of the CpGs have a positive variable importance measure, indicating that these CpGs are predictive for the classification of brain tumours.

In the following it is demonstrated how the CpGs located on the three genes *PAX6*, *PTPRN2* and *OSTM1* can be used to classify ATRTs into their three molecular subtypes by applying

different unsupervised and supervised statistical methods. After pre-processing, the inventors identified 1022 CpGs located on the three genes. Applying unsupervised, hierarchical clustering to the methylation values of the 100 CpGs with highest standard deviation across 75 ATRT samples, an almost perfect separation into the three molecular subtypes of ATRT can be found (Figure 9).

Next principal component analysis (PCA) is applied as an example for a linear dimension reduction method to the methylation values of all 1022 CpGs. Projecting the samples on the first two principal components (PC) that explain most of the variability in the data, a grouping into the three molecular subtypes can be found (Figure 10A). In addition, t-distributed stochastic neighbour embedding (t-SNE) has been applied, as an example for a non-linear dimension reduction method, to the methylation data and the resulting projection also shows a clustering of the three ATRT subtypes (Figure 10B). Other linear and non-linear dimension reduction methods that can be applied to achieve similar results are for example multi-dimensional scaling (MDS), factor analysis (FA), non-negative matrix factorization (NMF), truncated singular value decomposition (SVD), stochastic neighbour embedding (SNE), uniform manifold approximation and projection for dimension reduction (UMAP) and linear discriminant analysis (LDA).

To show how supervised statistical methods can be applied to fit a model that predicts ATRT subtypes, a classification and regression tree (CART) has been applied to methylation data (Figure 10C). At each node, the CART algorithm automatically tries out all available 1022 CpGs probes and possible cut-offs and selects the CpG probe and corresponding cut-off that leads to the purest split into the ATRT subtypes. The algorithm stops, as soon as the class purity measured by the Gini coefficient cannot be further improved. Here the CART algorithm found two sequential splitting rules (Figure 10D) that involve only two CpG probes that result in an almost perfect separation of the ATRT subclasses. Random Forests usually combine hundreds or thousands of CART trees by bootstrap aggregation (bagging) to achieve an improved prediction accuracy. Other supervised methods that can be applied to fit models with comparable prediction performance, are for example gradient boosting machines (GBM), support vector machines (SVM), multinomial logistic regression models and (deep) neural nets.

Example 5: Gene expression data used for the classification of tumour entities originally identified in DNA-methylation data

By analysing DNA-methylation data and training machine learning models for the classification of brain tumours, 688 genes have been identified that include CpG sites that can be considered most important for the classification of molecular brain tumour types. To show that these brain tumour entities can also be recognized in gene expression data and that this data can be used to train similarly performing machine learning models, 1167 brain tumour samples were analysed for which both DNA-methylation as well as gene expression data is available. This paired gene expression and methylation data set includes samples from 79 of the in total 184 classes that were defined on the DNA-methylation level.

Figure 11 shows the 1167 samples projected onto a t-distributed stochastic neighbour embedding (tSNE) that was applied to the gene expression data of the 688 most important genes identified in the methylation data. The colouring and the labelling of the groups are according to the class, and the samples are classified by the DNA-methylation classifier. The general clustering of the classes is very similar to a tSNE performed on DNA-methylation and even new sub-entities such as the medulloblastoma (MB) group 3 and 4 subtypes I-VIII can be identified. This proves that the gene expression data of the 688 identified genes is highly predictive for the 184 classes.

To show that the gene expression data can also be used to train supervised machine learning models, the gene expression data set was reduced to 1057 samples belonging to 50 classes with a minimal class sample size of 7 samples. The inventors then trained a basic random forest (RF) model and a lasso-penalized multinomial logistic regression model to this data set and validated the performance of both models by 3-fold cross-validation (CV). The CV estimated an accuracy of 0.788 for the RF (Figure 12B) and an accuracy 0.766 for the logistic regression model (Figure 12A), what proves that gene expression can be used to train similar classification models.

Accordingly, it has been shown by the inventors that the biological state used to train the classification algorithm is not limited to methylation, but can also be another biological state such as gene expression.

Example 6: Simulation study to investigate brain tumor classifier performance for classifiers trained using CpG-probes located on random subsets of signature genes and random hg19 genes

5 To show that subsets of the 688 signature genes are already predictive for defined brain tumor methylation classes, the inventors performed a simulation study. In this study Random Forest classifiers were trained using CpG probes located on different random subsets of the 688 signature genes. The number of genes were varied from 3 to 688 in 20 equal steps and for each number of genes training was repeated at least 3 times. In addition, the inventors also trained
10 classifiers using CpG probes located on genes randomly sampled from all known genes available in the hg19 genome. For each trained classifier the performance was measured by the overall accuracy and the number of classes for which the class wise accuracy was greater 0.8.

Figure 13 shows the results of this simulation study. For subsets of three genes the difference
15 between genes selected from the signature gene list in Table 1 compared to randomly selected genes is most distinct, i.e. the overall accuracy for the signature genes is around 0.8 while for the random gene classifiers it is always below 0.5. When increasing the number of genes, the overall accuracy for both the signature gene classifiers as well as the random gene classifiers increases to levels around 0.90 accuracy and above. The signature gene classifiers perform
20 always better as the classifiers trained on random genes. When considering the number of classes for which a class accuracy of greater 0.8 was achieved, the simulation shows, that the genes in Table 1 are important to reliably predict more specific classes.

Example 7: Classifiers for other pan-cancer tumors

25 To show that the signature gene list can also be used to train well performing classification models to predict other cancer types, the inventors trained a RF classifier on a large cohort of publicly available DNA-methylation array samples from the Cancer Genome Atlas Project (TCGA).

30 Figure 14 shows a tSNE of 9084 sample from 31 different TCGA projects that investigated different cancer types, e.g. LUAD is the abbreviation lung adenocarcinoma, BRCA for breast cancer etc. A complete list of the TCGA projects and their abbreviations can be found under the following link: <https://portal.gdc.cancer.gov/projects>. The inventors defined for each pro-

ject a tumor and control tissue class where possible, resulting in total 53 classes. Training a RF classifier using all CpGs located on genes listed on the signature list of Table 1 on this data set, the resulting classifier achieves an overall accuracy of 0.9226, as measured by a 3-fold statistical cross-validation (Figure 15: the confusion matrix on the left shows the result of the 3-fold cross-validation; the right plot shows the tSNE dimension reduction highlighting the samples that were falsely predicted in the cross-validation. Errors typically occur between related entities, such as Lung Squamous Cell Carcinoma (LUSC) and Lung Adenocarcinoma (LUAD)).

Applying other statistical or machine learning algorithms, that are suitable for multiclass classification tasks, prediction models with a comparable accuracy can be fitted, as it is shown in Figure 16. Figure 16 shows confusion matrices for four different statistical or machine learning models trained on the TCGA cohort shown in Figure 14. The regularized logistic regression model showed the best overall accuracy of 0.9343, followed by the linear-kernel support vector machine (SVM) with accuracy 0.9299, the extreme gradient boosted trees (XGBoost) classifier with accuracy 0.9239 and a radial basis function kernel SVM with an accuracy of 0.9101. More careful hyper-parameter tuning might improve the performance of all presented prediction models.

References:

R Core Team (2014). R: A language and environment for statistical computing. R Foundation for Statistical Computing, Vienna, Austria. URL <http://www.R-project.org/>.

MJ Aryee, AE Jaffe, H Corrada-Bravo, C Ladd-Acosta, AP Feinberg, KD Hansen, RA Irizarry. Minfi: A flexible and comprehensive Bioconductor package for the analysis of Infinium

DNA Methylation microarrays. Bioinformatics 2014, In press. doi: 10.1093/bioinformatics/btu049.

A. Liaw and M. Wiener (2002). Classification and Regression by randomForest. R News 2(3), 18--22.

Bioconductor: Open software development for computational biology and bioinformatics R.

Gentleman, V. J. Carey, D. M. Bates, B. Bolstad, M. Dettling, S. Dudoit, B. Ellis, L. Gautier, Y. Ge, and others 2004, Genome Biology, Vol. 5, R80.

Tables:

Table 1: List of gene sites according to the disclosure including their genetic locus and Sequence ID in the sequence listing. The sequence listing associated with this application is filed in electronic format and hereby incorporated by reference into the specification in its entirety.

5

Seq. ID No.	Gene site	Chromosome	Sequence start	Sequence end
1	ABAT	chr16	8766944	8879932
2	ABLIM2	chr4	7965537	8162059
3	ABR	chr17	905258	1092116
4	ACAD10	chr12	112122357	112196411
5	ACMSD	chr2	135594686	135661102
6	ACOT7	chr1	6322832	6455326
7	ACOX3	chr4	8366509	8443952
8	ACSL1	chr4	185675249	185748715
9	ACTR3C	chr7	149942801	150022258
10	ADAMTS17	chr15	100510143	100883683
11	ADAMTS2	chr5	178536352	178773931
12	ADARB2	chr10	1221753	1781170
13	ADGRA1	chr10	134882933	134946679
14	ADGRB1	chr8	143543877	143627868
15	ADGRD1	chr12	131436952	131627508
16	AFF3	chr2	100162216	100760537
17	AGAP1	chr2	236401233	237041944
18	AGAP2	chr12	58116576	58137444
19	AGO2	chr8	141539764	141647146
20	AIRE	chr21	45704221	45719602
21	AK1	chr9	130627259	130641522
22	AKAP13	chr15	85922347	86294089
23	ANAPC16	chr10	73619647	73997118
24	ANK1	chr8	41509244	41755780
25	ANK2	chr4	113737739	114306396
26	ANKLE2	chr12	133300754	133339951
27	ANKRD11	chr16	89332529	89558469
28	ANKRD33B	chr5	10562935	10659428
29	ANKS1A	chr6	34855538	35086820
30	ANKS1B	chr12	99127069	100379932
31	AP2A2	chr11	924309	1013745
32	APBA2	chr15	29129668	29412016
33	ARHGAP18	chr6	129896740	130184192
34	ARHGAP22	chr10	49652568	49865810
35	ARHGAP23	chr17	36583220	36670128
36	ARHGAP25	chr2	68905246	69055457
37	ARHGAP26	chr5	142148792	142610072
38	ARHGAP27P1	chr17	62744280	62779617

39	ARHGAP45	chr19	1064422	1088127
40	ARHGEF10	chr8	1770649	1908307
41	ARHGEF7	chr13	111766124	111959581
42	ARL6IP6	chr2	153572907	153619267
43	ARMC2	chr6	109168119	109296852
44	ASAP1	chr8	131062851	131457406
45	ASAP2	chr2	9345394	9547312
46	ASIC2	chr17	31338606	32485325
47	ASPSCR1	chr17	79933926	79976782
48	ATG4B	chr2	242575527	242614771
49	ATP11A	chr13	113343143	113542982
50	ATP2B4	chr1	203594415	203714709
51	ATXN7L1	chr7	105243721	105518531
52	AUTS2	chr7	69062405	70259385
53	AXIN2	chr17	63523183	63638683
54	BACH2	chr6	90634747	91008127
55	BAHCC1	chr17	79372040	79434858
56	BAIAP2	chr17	79007447	79092732
57	BCAR1	chr16	75261428	75303451
58	BCAT1	chr12	24961458	25103893
59	BCL11B	chr14	99634125	99739322
60	BFSP2	chr3	133117290	133195556
61	BOC	chr3	112928912	113007805
62	BOLA2	chr16	29452726	30207127
63	BTBD11	chr12	107710697	108054919
64	BTBD9	chr6	38134727	38609424
65	C10orf105	chr10	73469958	73499081
66	C10orf90	chr10	128112074	128360579
67	C19orf25	chr19	1460262	1480728
68	C1orf94	chr1	34631124	34686231
69	C6orf223	chr6	43966837	43975194
70	C7orf50	chr7	1035123	1179393
71	CABLES1	chr18	20713028	20841934
72	CACHD1	chr1	64934976	65160241
73	CACNA1C	chr12	2160916	2808615
74	CACNA1D	chr3	53527576	53847992
75	CACNA1H	chr16	1201741	1273272
76	CACNA1I	chr22	39965258	40087240
77	CACNA2D2	chr3	50398731	50542392
78	CACNA2D3	chr3	54155193	55110084
79	CACNA2D4	chr12	1899623	2029370
80	CACNB2	chr10	18428106	18832188
81	CADM1	chr11	115038451	115376741
82	CALD1	chr7	134462664	134656980
83	CAMK4	chr5	110558447	110822248
84	CAMTA1	chr1	6843884	7831266
85	CAPG	chr2	85620371	85642697

86	CASC15	chr6	21663503	22216234
87	CASP8	chr2	202096666	202153934
88	CASZ1	chr1	10695166	10858233
89	CBFA2T3	chr16	88939763	89045004
90	CCDC140	chr2	223161366	223171436
91	CCDC167	chr6	37449197	37469200
92	CCDC177	chr14	70035031	70043100
93	CCDC85C	chr14	99976103	100072227
94	CCDC88C	chr14	91736167	91885688
95	CCND2	chr12	4381402	4416022
96	CCR6	chr6	167411316	167554129
97	CDC42BPB	chr14	103397216	103525242
98	CDH4	chr20	59825982	60517173
99	CDK6	chr7	92232735	92467441
100	CDYL	chr6	4704893	4957278
101	CELF4	chr18	34821508	35147500
102	CELSR1	chr22	46755231	46934567
103	CFAP46	chr10	134620396	134757589
104	CFLAR	chr2	201979377	202038911
105	CHID1	chr11	865857	916558
106	CHN2	chr7	29184700	29555444
107	CHST11	chr12	104849192	105157292
108	CHTF18	chr16	837122	849574
109	CLDN10	chr13	96084353	96233510
110	CLYBL	chr13	100257419	100550888
111	CMIP	chr16	81477275	81746867
112	CNMD	chr13	53275900	53315447
113	CNP	chr17	40117259	40131254
114	CNPY1	chr7	155292453	155328039
115	COL23A1	chr5	177663117	178019056
116	COL26A1	chr7	101004622	101203804
117	COL4A1	chr13	110799810	110960996
118	COLEC11	chr2	3640922	3693734
119	COQ8A	chr1	227083089	227176746
120	CORO1C	chr12	109037385	109126826
121	CORO2B	chr15	68869808	69021644
122	CPE	chr4	166298597	166420982
123	CPEB1-AS1	chr15	83315021	83363072
124	CPEB4	chr5	173313831	173388813
125	CPNE4	chr3	131252077	132005754
126	CPQ	chr8	97655999	98157222
127	CPZ	chr4	8580717	8622988
128	CRACR2A	chr12	3714818	3863866
129	CRADD	chr12	94069651	94290116
130	CRB2	chr9	126116948	126142532
131	CRISPLD2	chr16	84852087	84944616
132	CSMD1	chr8	2791375	4853828

133	CSRNPI	chr3	39181842	39197553
134	CTBP2	chr10	126674918	126851124
135	CTNNA2	chr2	79410857	80877488
136	CUEDC1	chr17	55937104	56034184
137	CUX1	chr7	101457684	101928750
138	CXXC5	chr5	139026801	139064180
139	CYBA	chr16	88708197	88718992
140	CYREN	chr7	134775617	134857078
141	CYTH1	chr17	76668630	76779876
142	DAGLB	chr7	6447247	6525349
143	DDA1	chr19	17418837	17435606
144	DDT	chr22	24312054	24323519
145	DDX31	chr9	135468176	135547288
146	DENND11	chr7	141355028	141403453
147	DENND2B	chr11	8713399	8933998
148	DENND3	chr8	142137220	142207406
149	DERL3	chr22	24175190	24182815
150	DGKD	chr2	234261653	234382243
151	DGKG	chr3	185863490	186081523
152	DICER1	chr14	95551065	95625847
153	DIP2C	chr10	318630	737108
154	DISC1	chr1	231761061	232178519
155	DLEU1	chr13	50654914	51104170
156	DLG4	chr17	7091710	7124869
157	DLL1	chr6	170589794	170601197
158	DLX5	chr7	96648202	96655643
159	DLX6-AS1	chr7	96596327	96644877
160	DMRTA2	chr1	50881723	50890619
161	DNAAF5	chr7	764838	827616
162	DNAJB6	chr7	157128210	157211633
163	DNAJC17	chr15	41058567	41101176
164	DNAJC27	chr2	25165005	25196463
165	DNM3	chr1	171809118	172389067
166	DNMT3A	chr2	25454330	25566959
167	DONSON	chr21	34946283	35286203
168	DPP6	chr7	153582919	154587495
169	DPY19L1P1	chr7	32619053	32760280
170	DSE	chr6	116573836	116760942
171	DTNA	chr18	32071754	32473308
172	DUSP5	chr10	112256125	112272802
173	DUSP6	chr12	89740337	89747796
174	DUSP7	chr3	52081437	52091961
175	EBF1	chr5	158121423	158528288
176	EBF2	chr8	25697746	25904140
177	EBF3	chr10	131631996	131763591
178	EDNRB	chr13	78468116	78551164
179	EGFR	chr7	55085225	55276531

180	EML1	chr14	100202569	100409895
181	EMX2OS	chr10	119242304	119306079
182	EOGT	chr3	69022868	69064274
183	EPAS1	chr2	46523041	46615342
184	EPHA10	chr1	38178053	38232324
185	EPHB1	chr3	134512599	134980807
186	ERI3	chr1	44685242	44822439
187	ESR1	chr6	151976330	152425908
188	ESRRG	chr1	216675088	217312597
189	ETS1	chr11	128327156	128458953
190	EXPH5	chr11	108374658	108465874
191	EXT1	chr8	118810102	119125558
192	EXT2	chr11	44095576	44268480
193	F11R	chr1	160963501	161010274
194	FAM181A	chr14	94383740	94397454
195	FAM53B	chr10	126304149	126480407
196	FAM83E	chr19	49102357	49118194
197	FBRSL1	chr12	133065657	133163273
198	FBXL17	chr5	107193234	107719299
199	FBXL18	chr7	5513928	5554899
200	FEZ1	chr11	125314141	125367706
201	FGFR2	chr10	123236344	123359472
202	FHIT	chr3	59733536	61238633
203	FLJ12825	chr12	54450538	54517518
204	FMN1	chr15	33056245	33488434
205	FMNL2	chr2	153190251	153507848
206	FOXK1	chr7	4681888	4812574
207	FOXO1	chr13	41046631	41242234
208	FOXP1	chr3	71002365	71634640
209	FOXP4	chr6	41512664	41571622
210	FRMD4A	chr10	13684206	14505643
211	FRMPD2	chr10	49363101	49484441
212	FYN	chr6	111980035	112196155
213	GABRB3	chr15	26787194	27186186
214	GAK	chr4	841565	927674
215	GALK2	chr15	49446476	49623502
216	GALNT2	chr1	230192036	230419375
217	GALNT9	chr12	132679417	132907405
218	GAREM2	chr2	26394460	26414032
219	GAS7	chr17	9812426	10103368
220	GATA4	chr8	11532968	11619009
221	GATA6	chr18	19747904	19783991
222	GCK	chr7	44182370	44230522
223	GCSAML	chr1	247668894	247741348
224	GDF6	chr8	97153058	97174520
225	GDNF	chr5	37811279	37841282
226	GLI2	chr2	121491699	121751729

227	GLI3	chr7	41999048	42278118
228	GLT8D2	chr12	104381265	104459461
229	GLUD1P2	chr10	46763168	48959583
230	GNA12	chr7	2766241	2885459
231	GNAO1	chr16	56223751	56392856
232	GNAS	chr20	57413295	57487750
233	GNB5	chr15	52411623	52485065
234	GNG7	chr19	2509718	2704246
235	GPC6	chr13	93877578	95061773
236	GPR39	chr2	133172647	133405669
237	GRHL2	chr8	102503168	102683452
238	GRID1	chr10	87357812	88127750
239	GRIK2	chr6	101845169	102519458
240	GRIN1	chr9	140032109	140064714
241	GRIN2B	chr12	13712910	14134522
242	GRIP1	chr12	66739711	67199394
243	GRK5	chr10	120965697	121216631
244	GRTP1	chr13	113977005	114019963
245	GSE1	chr16	85643529	85711312
246	GSG1	chr12	13234971	13258130
247	GTF2E2	chr8	30434531	30517238
248	HBG2	chr11	5268002	5668511
249	HDAC4	chr2	239968364	240324846
250	HDAC7	chr12	48175007	48215263
251	HHEX	chr10	94448181	94456908
252	HIVEP3	chr1	41970536	42503096
253	HK1	chr10	71028256	71163137
254	HLX	chr1	221051243	221059900
255	HMGA2	chr12	66215937	66361571
256	HMGCR	chr5	74630654	74659426
257	HNF1B	chr17	36044934	36106596
258	HOTAIR	chr12	54354592	54370240
259	HOTTIP	chr7	27238540	27247630
260	HOXA-AS3	chr7	27178483	27197047
261	HOXA10-HOXA9	chr7	27200557	27221380
262	HOXA3	chr7	27144309	27168139
263	HOXB-AS1	chr17	46620213	46630103
264	HOXB-AS3	chr17	46666323	46685274
265	HOXB3	chr17	46624732	46669131
266	HOXB6	chr17	46671599	46683854
267	HOXC4	chr12	54409142	54451314
268	HOXD3	chr2	177027305	177039326
269	HOXD4	chr2	177014613	177019449
270	ICAM5	chr19	10399155	10408954
271	IDI2	chr10	1063347	1073299
272	IFFO1	chr12	6646039	6666749
273	IFT80	chr3	159943741	160169126

274	IGDCC4	chr15	65672325	65716910
275	IGF1R	chr15	99191261	99509259
276	IGF2BP1	chr17	47073274	47135007
277	IGF2BP3	chr7	23348328	23511495
278	IGFBPL1	chr9	38405025	38425944
279	IGSF21	chr1	18432740	18706477
280	IL17D	chr13	21275982	21298737
281	INPP5A	chr10	134349853	134598484
282	IQCE	chr7	2597132	2655868
283	IQSEC1	chr3	12937042	13116117
284	IRF6	chr1	209957468	209981020
285	ISLR2	chr15	74420215	74430643
286	ITGA5	chr12	54787545	54814550
287	ITPK1	chr14	93401759	93583763
288	ITPKB	chr1	226817891	226928376
289	JAKMIP1	chr4	6026426	6203818
290	JPH3	chr16	87633941	87733261
291	JUP	chr17	39678369	39944464
292	KAZN	chr1	14923713	15446044
293	KCNAB2	chr1	6050858	6162753
294	KCNB1	chr20	47987005	48101990
295	KCNH2	chr7	150640544	150676902
296	KCNIP1	chr5	169779381	170165136
297	KCNIP4	chr4	20728739	21951874
298	KCNMA1	chr10	78627859	79399077
299	KCNQ1	chr11	2464721	2871840
300	KCNV2	chr9	2716026	2731537
301	KDM4B	chr19	4967624	5155108
302	KIAA1522	chr1	33206012	33242071
303	KIF21B	chr1	200937014	200994328
304	KIF26A	chr14	104603560	104648735
305	KIF26B	chr1	245316787	245867928
306	KIFC3	chr16	57790629	57898233
307	KIRREL3	chr11	126291896	126874855
308	KLHL25	chr15	86301059	86339689
309	KLHL26	chr19	18746338	18782802
310	KLHL29	chr2	23606798	23932983
311	KNDC1	chr10	134972471	135041416
312	LAIR1	chr19	54863735	54883665
313	LBX1-AS1	chr10	102987851	103000116
314	LDLRAD4	chr18	13217229	13654253
315	LHPP	chr10	126148841	126304210
316	LHX2	chr9	126772389	126796942
317	LHX4	chr1	180197933	180245688
318	LHX5	chr12	113899194	113911377
319	LHX9	chr1	197880135	197903215
320	LIMCH1	chr4	41361304	41703561

321	LIN28A	chr1	26735769	26757719
322	LINC00311	chr16	85315064	85323185
323	LINC00461	chr5	87835097	87982120
324	LINC00856	chr10	80006882	80312612
325	LINC01140	chr1	87457190	87636386
326	LINC01551	chr14	29240410	29265500
327	LINC01749	chr20	61639235	61717923
328	LIPE-AS1	chr19	42899800	43158007
329	LMF1	chr16	902135	1032818
330	LMX1B	chr9	129375222	129464811
331	LOC100130872	chr4	1188071	1204250
332	LOC100132215	chr2	63269600	63277156
333	LOC145845	chr15	37155144	37180234
334	LOC339874	chr3	131042436	131101819
335	LOC606724	chr16	29459166	30202075
336	LOC613038	chr16	29474789	30219748
337	LOXL3	chr2	74758446	74782562
338	LPCAT1	chr5	1460042	1525576
339	LPIN1	chr2	11816205	11969033
340	LPP	chr3	187870163	188609960
341	LRBA	chr4	151184311	151938149
342	LRMDA	chr10	77541019	78318626
343	LRP2	chr2	169982119	170220622
344	LRRRC61	chr7	150005130	150036745
345	LRRFIP1	chr2	238534724	238691790
346	LTF	chr3	46475996	46528224
347	LYPD1	chr2	133400837	133430570
348	MACROD1	chr11	63764530	63935085
349	MAD1L1	chr7	1853928	2274083
350	MAML2	chr11	95709940	96077844
351	MAML3	chr4	140636046	141076733
352	MAP2K3	chr17	21186468	21220051
353	MAP3K3	chr17	61698275	61775170
354	MAPK8IP1	chr11	45905547	45929516
355	MAPK8IP3	chr16	1754721	1821818
356	MBP	chr18	74689289	74846274
357	MCC	chr5	112356296	112826027
358	MCF2L	chr13	113621314	113755553
359	MCIDAS	chr5	54513925	54524643
360	MCPH1	chr8	6262613	6502640
361	MDM4	chr1	204484007	204679161
362	MECOM	chr3	168799787	169383063
363	MEGF6	chr1	3403006	3529559
364	MEIS1	chr2	66661032	66801391
365	MEIS2	chr15	37181722	37395000
366	METAP1D	chr2	172863304	172947087
367	MGMT	chr10	131263954	131567283

368	MIR100HG	chr11	121958311	122239967
369	MIR124-2HG	chr8	65284275	65297342
370	MIR548F5	chr13	36046426	36516882
371	MIR548G	chr3	99271653	99718559
372	MIR548H4	chr15	69114803	69491362
373	MIR9-3HG	chr15	89909830	89943218
374	MIRLET7BHG	chr22	46448226	46511308
375	MLC1	chr22	50496320	50525858
376	MLLT1	chr19	6208892	6281459
377	MNX1	chr7	156785245	156804847
378	MOB2	chr11	1489185	1787001
379	MPP7	chr10	28338423	28593495
380	MRC2	chr17	60703262	60772462
381	MSC-AS1	chr8	72753858	72970047
382	MSI2	chr17	55331712	55758799
383	MSRA	chr8	9910330	10287901
384	MTHFR	chr1	11844287	11867660
385	MYO16	chr13	109247000	109861855
386	MYT1	chr20	62781644	62875106
387	MYT1L	chr2	1791385	2336545
388	NAV1	chr1	201615950	201797602
389	NAV2	chr11	19370771	20144647
390	NBEA	chr13	35514924	36248374
391	NCOR2	chr12	124807457	125053510
392	NDRG4	chr16	58496049	58549023
393	NDST1	chr5	149875840	149939273
394	NDUFA13	chr19	19625519	19647453
395	NEAT1	chr11	65188769	65213528
396	NFATC1	chr18	77154272	77290823
397	NFIB	chr9	14080342	14400482
398	NFIX	chr19	13105084	13211110
399	NHSL1	chr6	138741681	138895168
400	NKD2	chr5	1007577	1040427
401	NOTCH1	chr9	139387396	139441738
402	NPHP4	chr1	5921370	6054033
403	NR1D1	chr17	38247537	38258478
404	NR2E1	chr6	108485715	108511513
405	NR2F1-AS1	chr5	92743565	92918503
406	NR5A2	chr1	199995230	200148050
407	NRCAM	chr7	107786571	108098341
408	NRG1	chr8	31495411	32624058
409	NRXN1	chr2	50144143	51261174
410	NRXN3	chr14	78635216	80336133
411	NTM	chr11	131238871	132208216
412	NUDT1	chr7	2280357	2292280
413	NUMA1	chr11	71712411	71793073
414	NXN	chr17	701053	884498

415	NXPH1	chr7	8472085	8794093
416	OBI1-AS1	chr13	78492324	79192960
417	OLFM1	chr9	137965589	138014530
418	OLIG2	chr21	34396716	34403003
419	ONECUT2	chr18	55101417	55160030
420	OPCML	chr11	132283375	133403903
421	OSBPL3	chr7	24834664	25021260
422	OTP	chr5	76923037	76936022
423	OTX1	chr2	63275692	63286466
424	OTX2-AS1	chr14	57277224	57399050
425	PACRG	chr6	163146664	163738024
426	PACS2	chr14	105765670	105865984
427	PARD3	chr10	34396988	35105753
428	PARD3B	chr2	205409016	206486386
429	PAX1	chr20	21684797	21700624
430	PAX3	chr2	223063106	223165215
431	PAX6	chr11	31804840	31841009
432	PAX6-AS1	chr11	31836614	31910087
433	PBX1	chr1	164527097	164855800
434	PCCA	chr13	100739769	101184191
435	PCDHA1	chr5	140164376	140393429
436	PCDHA2	chr5	140172944	140393429
437	PCDHA3	chr5	140179283	140393429
438	PCDHA4	chr5	140185172	140393429
439	PCDHGA1	chr5	140708752	140894048
440	PCDHGA10	chr5	140791243	140894048
441	PCDHGA11	chr5	140799037	140894048
442	PCDHGA12	chr5	140808658	140894048
443	PCDHGA2	chr5	140716854	140894048
444	PCDHGA3	chr5	140722101	140894048
445	PCDHGA4	chr5	140733268	140894048
446	PCDHGA5	chr5	140742398	140894048
447	PCDHGA6	chr5	140752151	140894048
448	PCDHGA7	chr5	140760967	140894048
449	PCDHGA8	chr5	140765952	140894048
450	PCDHGA9	chr5	140781020	140894048
451	PCDHGB1	chr5	140728328	140894048
452	PCDHGB2	chr5	140738203	140894048
453	PCDHGB3	chr5	140748462	140894048
454	PCDHGB4	chr5	140765952	140894048
455	PCDHGB5	chr5	140776195	140894048
456	PCDHGB6	chr5	140786270	140894048
457	PCDHGB7	chr5	140795714	140894048
458	PCDHGC3	chr5	140854069	140894048
459	PCSK9	chr1	55503649	55532026
460	PDE4B	chr1	66256693	66841762
461	PDE4D	chr5	58263366	59785425

462	PDE6B	chr4	617863	666181
463	PDGFRA	chr4	54242320	55165912
464	PER2	chr2	239151179	239200243
465	PHF19	chr9	123616431	123641106
466	PITPNC1	chr17	65371897	65694879
467	PITX2	chr4	111537080	111564779
468	PITX3	chr10	103988446	104002731
469	PLEC	chr8	144987821	145052413
470	PLEKHM1P1	chr17	62773689	62834802
471	PLEKHO2	chr15	65132582	65161701
472	PLXNC1	chr12	94540999	94702951
473	POU6F2	chr7	39016109	39505890
474	PPM1H	chr12	63036263	63330165
475	PPP2R2A	chr8	25228575	26231695
476	PPP2R2B	chr5	145967567	146462583
477	PRDM16	chr1	2984242	3356685
478	PRDM2	chr1	14025235	14153074
479	PRDM6	chr5	122423341	122525245
480	PRDM8	chr4	81103939	81126982
481	PRKAG2	chr7	151251701	151575816
482	PRKCA	chr17	64297426	64808362
483	PRKCE	chr2	45877543	46416629
484	PRKCH	chr14	61652787	62019198
485	PRKCZ	chr1	1980409	2118334
486	PRKN	chr6	161767090	163150334
487	PRR5L	chr11	36316225	36488254
488	PSD3	chr8	18383313	18872696
489	PTPN20	chr10	46548623	48829424
490	PTPRG	chr3	61545743	62282073
491	PTPRN2	chr7	157330250	158381982
492	PVT1	chr8	128805303	129114999
493	PWWP2B	chr10	134209202	134232858
494	RAB11FIP3	chr16	474168	573981
495	RABGAP1L	chr1	174127052	174965945
496	RAD51B	chr14	68284996	69198435
497	RADIL	chr7	4832785	4924835
498	RAI1	chr17	17583287	17716265
499	RALGAPA2	chr20	20368772	20694766
500	RAPGEF4	chr2	173599025	173919120
501	RASA3	chr13	114745694	114899595
502	RASGRP3	chr2	33659916	33791298
503	RBFOX1	chr16	6067632	7764840
504	RBFOX3	chr17	77083927	77513730
505	RBM20	chr10	112402655	112600727
506	RBMS1	chr2	161127162	161351818
507	RBMS3	chr3	29321303	30053386
508	RCN1	chr11	31836614	32128772

509	RERE	chr1	8410964	8879199
510	REXO1	chr19	1813745	1849952
511	RFX4	chr12	106975185	107158082
512	RGL1	chr1	183603708	183899166
513	RGL3	chr19	11492273	11531518
514	RGS12	chr4	3293255	3443140
515	RGS20	chr8	54762868	54873363
516	RIMBP2	chr12	130879181	131202326
517	RNF216	chr7	5658172	5822861
518	RNF4	chr4	2469295	2519086
519	RNLS	chr10	89890557	90344582
520	ROR1	chr1	64238190	64648679
521	RORA	chr15	60778983	61523002
522	RPS6KA2	chr6	166821354	167277271
523	RPTOR	chr17	78517125	78941673
524	RREB1	chr6	7106330	7253713
525	RTKL1	chr20	62287663	62330044
526	RTKL1-TNFRSF6B	chr20	62287663	62331551
527	RUBCN	chr3	197396759	197478068
528	RUNDC3A	chr17	42384427	42397538
529	RUNX1	chr21	36158598	37358547
530	RXRA	chr9	137207444	137333931
531	SASH1	chr6	148662229	148874684
532	SATB2	chr2	200132723	200337489
533	SATB2-AS1	chr2	200331321	200338981
534	SBNO2	chr19	1106133	1175782
535	SCG5	chr15	32932370	32990798
536	SCOC	chr4	141176940	141305210
537	SDK1	chr7	3339580	4310131
538	SDK2	chr17	71329023	71641727
539	SEPTIN9	chr17	75275992	75498178
540	SFXN5	chr2	73167665	73300465
541	SH3BP4	chr2	235859128	235965858
542	SH3RF3	chr2	109744497	110263707
543	SHANK2	chr11	70312461	70937342
544	SHOX2	chr3	157812300	157825452
545	SHROOM3	chr4	77354753	77705905
546	SIM1	chr6	100835250	100914305
547	SIM2	chr21	38070491	38124010
548	SKI	chr1	2158634	2243152
549	SKOR1	chr15	68110542	68127674
550	SLC12A9	chr7	100448841	100466134
551	SLC1A7	chr1	53551351	53609789
552	SLC22A18	chr11	2919451	2947976
553	SLC22A18AS	chr11	2907827	2926675
554	SLC25A10	chr17	79668900	79689546
555	SLC25A22	chr11	788975	799769

556	SLC38A10	chr17	79217299	79270596
557	SLC4A8	chr12	51783601	51911047
558	SLC6A9	chr1	44455672	44498664
559	SLC7A5	chr16	87862129	87904600
560	SLC8A2	chr19	47929779	47976807
561	SLC9A3	chr5	471834	526049
562	SLX1A	chr16	29464322	30210387
563	SLX1B-SULT1A4	chr16	29464371	30217150
564	SMAD3	chr15	67356695	67489033
565	SMAGP	chr12	51637633	51665702
566	SMG1P2	chr16	29452726	30283698
567	SMURF1	chr7	98623558	98743243
568	SND1	chr7	127290702	127734159
569	SNTG2	chr2	945054	1372884
570	SNX29	chr16	12069102	12669646
571	SOGA1	chr20	35404345	35493587
572	SORBS2	chr4	186505098	186879370
573	SORCS2	chr4	7192874	7746064
574	SOX10	chr22	38366819	38384929
575	SOX2-OT	chr3	180772968	181461513
576	SOX6	chr11	15986495	16761690
577	SPATA13	chr13	24552339	24898169
578	SPECC1	chr17	19911149	20219572
579	SPON2	chr4	1159221	1204250
580	SPPL2B	chr19	2268020	2356600
581	SPTBN1	chr2	54681954	54900083
582	SPTBN4	chr19	40970648	41083865
583	SRCIN1	chr17	36684759	36763683
584	SRGAP3	chr3	9020776	9292869
585	SRRM3	chr7	75829716	75918105
586	SSBP3	chr1	54689604	54873568
587	STAP2	chr19	4322540	4344283
588	STARD13	chr13	33675772	34252432
589	STK10	chr5	171467574	171616846
590	STK24	chr13	99100955	99230896
591	STK32C	chr10	134019496	134147563
592	STON1-GTF2A1L	chr2	48755564	49005156
593	STOX2	chr4	184825009	184940375
594	STRA6	chr15	74470308	74503546
595	SYCP2L	chr6	10746495	10976041
596	SYNJ2	chr6	158401388	158521707
597	TACC2	chr10	123747189	124015557
598	TAFA2	chr12	62100529	62655425
599	TBC1D16	chr17	77904642	78011157
600	TBC1D7	chr6	13265274	13330287
601	TBC1D9	chr4	141540436	141678971
602	TBCD	chr17	80708440	80902562

603	TBR1	chr2	162271120	162283073
604	TBX15	chr1	119424166	119533679
605	TBX4	chr17	59528279	59563971
606	TBX5	chr12	114790235	114847747
607	TEAD1	chr11	12694469	12967784
608	TENM2	chr5	166710343	167692662
609	TENM3	chr4	183063640	183725677
610	TENM3-AS1	chr4	183058659	183067168
611	TENM4	chr11	78362828	79153195
612	TET1	chr10	70318617	70455739
613	TFAP2A	chr6	10395416	10421297
614	TFAP2B	chr6	50784939	50816826
615	TG	chr8	133877705	134148643
616	TGFB3	chr14	76422942	76449592
617	THRA	chr17	38216663	38251620
618	THRB	chr3	24157145	24537953
619	TK1	chr17	76168660	76184785
620	TLX1NB	chr10	102847578	102892403
621	TMBIM1	chr2	219137417	219158780
622	TMEM132C	chr12	128750448	129193960
623	TMEM132D	chr12	129554771	130389712
624	TNRC18P1	chr4	141560845	141565734
625	TNS3	chr7	47313252	47623242
626	TOLLIP	chr11	1294098	1332392
627	TOM1L2	chr17	17745322	17877284
628	TOX2	chr20	42541992	42699754
629	TP73	chr1	3567629	3654265
630	TRABD2B	chr1	48224700	48464062
631	TRAK1	chr3	42131246	42268882
632	TRAPPC12	chr2	3381946	3490357
633	TRAPPC9	chr8	140741086	141470178
634	TRIM2	chr4	154072770	154261974
635	TRIM34	chr11	5639674	5667125
636	TRIM6-TRIM34	chr11	5616365	5667125
637	TRIM65	chr17	73883541	73894584
638	TRIM71	chr3	32858010	32935271
639	TRIO	chr5	14142329	14510958
640	TRIP6	chr7	100463450	100472576
641	TSC2	chr16	2096490	2140213
642	TSNAX-DISC1	chr1	231662899	232178519
643	TSPAN14	chr10	82212538	82283891
644	TSPAN4	chr11	841324	868616
645	TSPAN9	chr12	3185021	3397230
646	TSPEAR	chr21	45916275	46132995
647	TSTD1	chr1	161005922	161010274
648	TTC12	chr11	113183751	113245518
649	TTLL10	chr1	1107786	1134813

650	TTLL11	chr9	124582704	124857385
651	TUBA1C	chr12	49620209	49668613
652	TULP4	chr6	158732192	158934356
653	TXNRD1	chr12	104604988	104745585
654	UFSP2	chr4	186319194	186348639
655	UHRF1	chr19	4908010	4963665
656	UNQ6494	chr9	92253198	92336174
657	USP20	chr9	132596196	132645617
658	UTRN	chr6	144605990	145175670
659	VAV2	chr9	136625516	136858946
660	VAX1	chr10	118886532	118899312
661	VAX2	chr2	71126220	71162075
662	VEPH1	chr3	156976032	157222915
663	VGLL4	chr3	11596044	11763720
664	VOPP1	chr7	55536806	55641700
665	VPS13D	chr1	12288613	12573598
666	VRK2	chr2	58133286	58388555
667	WDR81	chr17	1618317	1643393
668	WFIKN2	chr17	48910511	48921209
669	WNT16	chr7	120963921	120982658
670	WNT5A	chr3	55498243	55523170
671	WNT6	chr2	219723046	219740454
672	WT1	chr11	32407822	32458581
673	WWOX	chr16	78131827	79248064
674	WWP2	chr16	69794687	69977144
675	YJEFN3	chr19	19625519	19649893
676	ZAR1	chr4	48490809	48497922
677	ZBTB16	chr11	113928931	114122897
678	ZBTB20	chr3	114055447	114867627
679	ZC3H12D	chr6	149767266	149807648
680	ZC3H3	chr8	144518325	144625120
681	ZIC4	chr3	147102335	147126096
682	ZIC5	chr13	100613775	100625678
683	ZMIZ1	chr10	80827292	81077785
684	ZNF280D	chr15	56920874	57212197
685	ZNF423	chr16	49523015	49893330
686	ZNF536	chr19	30861828	31050465
687	ZNF664-RFLNA	chr12	124456262	124802070
688	ZNF833P	chr19	11749091	11798884

Table 2: List of cancer types according to the disclosure

Column 1 lists the abbreviations of the cancer types used herein. The WHO 2020 entity or cancer type names are shown in Column 2. Column 3 provides a descriptor for the molecular class and Column 4 lists the PubMed Number (PMID). Where no PMID number appears in Column 4 the method according to the disclosure uncovered cancer subspecies that were not known or published before and thus have no PMID.

Cancer Type	WHO_2020_entity	Molecular.class	PMID
A_IDH	Astrocytoma, IDH-mutant	diffuse glioma, IDH-mutant and 1p19q retained [astroglial type]	29539639
A_IDH_HG	Astrocytoma, IDH-mutant	diffuse glioma, IDH-mutant and 1p19q retained [astroglial type], high grade	29539639
ANTCON	Anaplastic neuroepithelial tumour with condensed nuclei	anaplastic neuroepithelial tumour with condensed nuclei	
ATRT_MYC	Atypical teratoid/rhabdoid tumour	Atypical teratoid rhabdoid tumour, MYC activated	29539639
ATRT_SHH	Atypical teratoid/rhabdoid tumour	Atypical teratoid rhabdoid tumour, SHH activated	29539639
ATRT_TYR	Atypical teratoid/rhabdoid tumour	Atypical teratoid rhabdoid tumour, Tyrosinase activated	29539639
CHGL	Chordoid glioma	chordoid glioma of the 3rd ventricle	29539639
CHORDM	Chordoma (including poorly differentiated chordoma)	chordoma	29539639
CN	Central neurocytoma	central neurocytoma	29539639
CNS_NB_FOXR2	CNS embryonal tumour (or CNS neuroblastoma), FOXR2-altered	CNS neuroblastoma, FOXR2-altered	29539639
CNS_SARC_DICER	Primary intracranial sarcoma, DICER1-mutant	CNS DICER1-associated sarcoma	29881993
CPC_A	Choroid plexus carcinoma	choroid plexus carcinoma	29539639
CPC_B	Choroid plexus carcinoma	choroid plexus carcinoma	33249490
CPH_ADM	Adamantinomatous Craniopharyngioma	adamantinomatous craniopharyngioma	29539639
CPH_PAP	Papillary Craniopharyngioma	papillary craniopharyngioma	29539639
CPP_AD	Choroid plexus papilloma	choroid plexus papilloma	29539639
CPP_INF	Choroid plexus papilloma	choroid plexus papilloma	29539639

CRINET	Cribriform neuroepithelial tumour	cribriform neuroepithelial tumour	
CTRL_ADENOPIT	Control tissue, pituitary gland (anterior lobe)	normal pituitary gland, anterior lobe	29539639
CTRL_BLOOD	Normal WBCs	control tissue, blood	
CTRL_CBM	Control tissue, cerebellum	control tissue, cerebellar hemisphere	29539639
CTRL_CORPCAL	Control tissue, corpus callosum	control tissue, white matter (corpus callosum)	29539639
CTRL_HEMI	Control tissue, cerebral hemisphere	control tissue, hemispheric cortex	29539639
CTRL_HYPOTHAL	Control tissue, hypothalamus	control tissue, hypothalamus	29539639
CTRL_INFLAM	Glioblastoma, IDH-wildtype	control tissue, inflammatory tumour microenvironment	29539639
CTRL_OPTIC	Control tissue, optic pathway	control tissue, optic pathway	
CTRL_PIN	Control tissue, pineal gland	control tissue, pineal gland	29539639
CTRL_PONS	Control tissue, pons	control tissue, pons	29539639
CTRL_REACTIVE	Control tissue, reactive tumour microenvironment	control tissue, reactive tumour microenvironment	29539639
DGONC	Diffuse glioneuronal tumour with oligodendroglioma-like features and nuclear clusters (DGONC)	Diffuse glioneuronal tumour with oligodendroglioma-like features and nuclear clusters	31867747
DLBCL	Diffuse large B-cell lymphoma of the CNS	diffuse large B cell lymphoma	29539639
DLGNT_1	Diffuse leptomeningeal glioneuronal tumour	diffuse leptomeningeal glioneuronal tumour	29539639
DLGNT_2	Diffuse leptomeningeal glioneuronal tumour	diffuse leptomeningeal glioneuronal tumour	29766299
DMG_EGFR	Bithalamic glioma, EGFR-mutant	diffuse midline glioma [(bi-)thalamic, EGFR altered]	33130881
DMG_K27	Diffuse midline glioma, H3 K27M-mutant	diffuse midline glioma, H3 K27-mutant / EZHIP over-expressing	29539639
DMT_SMARCB1	Desmoplastic myxoid tumour of the pineal region, SMARCB1-mutant	desmoplastic myxoid tumour, SMARCB1-altered	
DNET	Dysembryoplastic neuroepithelial tumour	dysembryoplastic neuroepithelial tumour	29539639
EFT_CIC	CIC sarcoma	Ewing family tumour with CIC alteration	29539639
EMB_ND_A	Embryonal tumour not otherwise specified, subtype A	embryonal tumour [non defined, type A]	
ENB	Esthesioneuroblastoma, IDH-wildtype	esthesioneuroblastoma	29730775
EPN_MPE	Myxopapillary ependymoma	myxopapillary ependymoma	29539639

EPN_PF_SE	Subependymoma	posterior fossa subependymoma	29539639
EPN_PFA_1a	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A1	29909548
EPN_PFA_1b	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A1	29909548
EPN_PFA_1c	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A1	29909548
EPN_PFA_1d	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A1	29909548
EPN_PFA_1e	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A1	29909548
EPN_PFA_1f	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A1	29909548
EPN_PFA_2a	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A2	29909548
EPN_PFA_2b	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A2	29909548
EPN_PFA_2c	Posterior fossa ependymoma Group PFA	posterior fossa ependymoma group A2	29909548
EPN_PFB_1	Posterior fossa ependymoma Group PFB	posterior fossa ependymoma group B1-B3	30019219
EPN_PFB_2	Posterior fossa ependymoma Group PFB	posterior fossa ependymoma group B1-B3	30019219
EPN_PFB_3	Posterior fossa ependymoma Group PFB	posterior fossa ependymoma group B1-B3	30019219
EPN_PFB_4	Posterior fossa ependymoma Group PFB	posterior fossa ependymoma group B4	30019219
EPN_PFB_5	Posterior fossa ependymoma Group PFB	posterior fossa ependymoma group B5	30019219
EPN_RELA_Like_A	Supratentorial ependymoma C11orf95 fusion-positive	supratentorial ependymoma, c11orf95:RELA-like	33879448
EPN_RELA_Like_B	Supratentorial ependymoma C11orf95 fusion-positive	supratentorial ependymoma, c11orf95:RELA-like	33879448
EPN_RELA_Like_C	Supratentorial ependymoma C11orf95 fusion-positive	supratentorial ependymoma, c11orf95:RELA-like	33879448
EPN_SPINE	Spinal ependymoma	spinal ependymoma	29539639
EPN_SPINE_MYCN	Spinal ependymoma, MYCN-amplified	spinal ependymoma, MYCN-amplified	31414211
EPN_SPINE_SE_A	Subependymoma	spinal subependymoma [sub-type B]	31414211
EPN_SPINE_SE_B	Subependymoma	spinal subependymoma [sub-type A]	29539639
EPN_ST_ND_A	Supratentorial ependymoma	supratentorial ependymoma [non-defined type]	
EPN_ST_SE	Subependymoma	supratentorial subependymoma	29539639

EPN_YAP	Supratentorial ependymoma, YAP1 fusion-positive	supratentorial ependymoma, YAP1-fused	29539639
ERMS	Rhabdomyosarcoma	embryonal rhabdomyosarcoma	33479225
ETMR_Atyp	Embryonal tumour with multilayered rosettes	embryonal tumour with multilayered rosettes-like	31802000
ETMR_C19MC	Embryonal tumour with multilayered rosettes	embryonal tumour with multilayered rosettes, C19MC altered	29539639
EVNCYT	Extraventricular neurocytoma	extraventricular neurocytoma	
EWS	Ewing sarcoma	Ewing sarcoma	29539639
GBM_CBM	Glioblastoma, IDH-wildtype	high-grade diffuse glioma of the midline/posterior fossa; H3/IDH-wildtype	
GBM_G34	Diffuse hemispheric glioma, H3 G34-mutant	high-grade diffuse glioma, H3 G34-mutant	29539639
GBM_MES_Atyp	Glioblastoma, IDH-wildtype	glioblastoma, IDH-wildtype, mesenchymal type	
GBM_MES_Typ	Glioblastoma, IDH-wildtype	glioblastoma, IDH-wildtype, mesenchymal type	29539639
GBM_ped_ND_A	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type; non-defined A]	
GBM_ped_ND_B	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type; non-defined B]	
GBM_pedMYCN	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type, MYCN activated]	29539639
GBM_pedRTK1a	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type, RTK1]	28401334
GBM_pedRTK1b	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type, RTK1]	28401334
GBM_pedRTK1c	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type, RTK1]	28401334
GBM_pedRTK2a	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type, RTK2]	28401334
GBM_pedRTK2b	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	glioblastoma [pediatric-type, RTK2]	28401334
GBM_PNC	Glioblastoma, IDH-wildtype	glioblastoma, IDH-wildtype, with primitive neuronal component	
GBM_RTK1	Glioblastoma, IDH-wildtype	glioblastoma, IDH-wildtype, RTK1 type	29539639
GBM_RTK2	Glioblastoma, IDH-wildtype	glioblastoma, IDH-wildtype, RTK2 type	29539639

GCT_GERM_A	Germinoma	germinoma, type A	
GCT_GERM_B	Germinoma	germinoma, type B (KIT-mutant)	
GCT_TERA	Mature teratoma	teratoma	
GCT_YOLKSAC	Yolk sac tumour	yolk sac tumour	
GG	Ganglioglioma	ganglioglioma	29539639
GNT_ND	Glioneuronal tumour, not otherwise specified, subtype A	diffuse glioneuronal tumour, non defined type	
HGAP	High-grade astrocytoma with piloid features	high-grade astrocytoma with piloid features	29539639
HGNET_BCOR_Fus	CNS tumour with BCOR internal tandem duplication	neuroepithelial tumour with EP300:BCOR(L1) fusion	
HGNET_BCOR_ITD	CNS tumour with BCOR internal tandem duplication	neuroepithelial tumour with BCOR internal tandem duplication	29539639
HGNET_BEND2	Astroblastoma	high-grade neuroepithelial tumour with MN1:BEND2 fusion	29539639
HGNET_CXXC5	Astroblastoma	high-grade neuroepithelial tumour with MN1:CXXC5 fusion	
HGNET_ND_B	Glioblastoma, IDH-wildtype	diffuse high-grade neuroepithelial tumour [adult-type, non-defined type B]	
HGNET_ND_C	Glioblastoma, IDH-wildtype	diffuse high-grade neuroepithelial tumour [adult-type, non-defined type C]	
HGNET_ND_D	Glioblastoma, IDH-wildtype	diffuse high-grade neuroepithelial tumour [adult-type, non-defined type D]	
HGNET_PATZ	Neuroepithelial tumour, PATZ1 fusion-positive	neuroepithelial tumour with PATZ1 fusion	
HGNET_PLAG	Diffuse paediatric-type high grade glioma, H3 wildtype and IDH wild type	diffuse high-grade neuroepithelial tumour, PLAG-family amplified	
HMB	Haemangioblastoma	haemangioblastoma	29539639
IDH_B	Astrocytoma, IDH-mutant	diffuse glioma, IDH-mutant and 1p19q retained [astroglial type]	
IHG	Infant-type hemispheric glioma, H3-wildtype	infantile hemispheric glioma	29539639
IO_MEPL	Medulloepithelioma	intraocular medulloepithelioma	
LCH	Langerhans cell histiocytosis	Langerhans cell histiocytosis	
LGG_DIG_DIA	Desmoplastic infantile astrocytoma and ganglioglioma	desmoplastic infantile ganglioglioma/astrocytoma	29539639
LGG_MYB_A	Angiocentric glioma	diffuse glioma, MYB(L1)-altered, subtype A [angiocentric glioma-type]	29539639

LGG_MYB_B	Diffuse astrocytoma, MYB or MYBL1-altered	diffuse glioma, MYB(L1)-altered, subtype B [infratentorial-type]	
LGG_MYB_C	Diffuse astrocytoma, MYB or MYBL1-altered	diffuse glioma, MYB(L1)-altered, subtype C [isomorphic diffuse glioma-type]	
LGG_MYB_D	Diffuse astrocytoma, MYB or MYBL1-altered	diffuse glioma, MYB(L1)-altered, subtype D	
LIPN	Cerebellar liponeurocytoma	liponeurocytoma	29539639
MB_G34_I	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 3	31076851
MB_G34_II	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 3	31076851
MB_G34_III	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 3	31076851
MB_G34_IV	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 3	31076851
MB_G34_V	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 4	31076851
MB_G34_VI	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 4	31076851
MB_G34_VII	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 4	31076851
MB_G34_VIII	Medulloblastoma, non-WNT/non-SHH	medulloblastoma Group 4	31076851
MB_MYO	Medulloblastoma, non-WNT/non-SHH	medullomyoblastoma	
MB_SHH_AD	Medulloblastoma, SHH-activated	medulloblastoma, SHH-activated [childhood/adult type]	28609654
MB_SHH_AD	Medulloblastoma, SHH-activated	medulloblastoma, SHH-activated [childhood/adult type]	28609654
MB_SHH_AD	Medulloblastoma, SHH-activated	medulloblastoma, SHH-activated [childhood/adult type]	28609654
MB_SHH_AD	Medulloblastoma, SHH-activated	medulloblastoma, SHH-activated [childhood/adult type]	28609654
MB_SHH_IDH	Medulloblastoma, SHH-activated	medulloblastoma, SHH-activated, IDH-mutant	
MB_WNT	Medulloblastoma, WNT-activated	medulloblastoma, WNT-activated	29539639
MELN	Meningeal melanocytosis and melanomatosis	melanocytoma	29539639
MET_MEL	Metastases to the brain and spinal cord parenchyma	melanoma [metastatic]	29539639
MMNST	Malignant melanotic nerve sheath tumour	malignant melanotic nerve sheath tumour	29539639

MNG_ben-1	Meningioma	meningioma, benign	28314689
MNG_ben-2	Meningioma	meningioma, benign	28314689
MNG_ben-3	Meningioma	meningioma, benign	28314689
MNG_int-A	Meningioma	meningioma, intermediate	28314689
MNG_int-B	Meningioma	meningioma, intermediate	28314689
MNG_mal	Meningioma	meningioma, malignant	28314689
MNG_SMARCE1	Meningioma	meningioma, SMARCE1-altered	
MPNST_Atyp	Malignant peripheral nerve sheath tumour (MPNST)	malignant peripheral nerve sheath tumour [spinal or atypical type]	
MPNST_Typ	Malignant peripheral nerve sheath tumour (MPNST)	malignant peripheral nerve sheath tumour [typical type]	
MYXGNT	Myxoid glioneuronal tumour	myxoid glioneuronal tumour of the 3rd ventricle / septum pellucidum	
NB_MYCN	NB, MYCN	neuroblastoma	27635046
NB_TMMneg	NB, no-TMM	neuroblastoma	27635046
NB_TMMpos	NB, TERT	neuroblastoma	27635046
NFIB_PLEX	Hybrid nerve sheath tumours	plexiform neurofibroma	
O_IDH	Oligodendroglioma, IDH-mutant and 1p/19q-codeleted	diffuse glioma, IDH-mutant and 1p19q co-deleted [oligodendroglial type]	29539639
OLIGOSARC_IDH	Oligodendroglioma, IDH-mutant and 1p/19q-codeleted	diffuse glioma, IDH-mutant and 1p19q co-deleted [oligodendroglial type]	
PA_CORT	Pilocytic astrocytoma	supratentorial pilocytic astrocytoma	29539639
PA_INF	Pilocytic astrocytoma	infratentorial pilocytic astrocytoma	29539639
PA_INF_FGFR	Pilocytic astrocytoma	infratentorial pilocytic astrocytoma	
PA_MID	Pilocytic astrocytoma	supratentorial midline pilocytic astrocytoma	29539639
PB_FOXR2	Pineoblastoma	pineoblastoma, MYC/FOXR2-activated	31768671
PB_Grp1A	Pineoblastoma	pineoblastoma, miRNA pathway altered, group 1	31768671
PB_Grp1B	Pineoblastoma	pineoblastoma, miRNA pathway altered, group 1	31768671
PB_Grp2	Pineoblastoma	pineoblastoma, miRNA pathway altered, group 2	31768671

PGG	Paraganglioma	spinal paraganglioma	29539639
PGNT	Papillary glioneuronal tumour	papillary glioneuronal tumour	
PIN_CYT	Pineocytoma	pineocytoma	31768671
PIN_RB	Pineoblastoma	pineal retinoblastoma	29539639
PITAD_ACTH	Pituitary adenoma /PitNET	pituitary adenoma, ACTH-producing	29539639
PITAD_GON	Pituitary adenoma /PitNET	pituitary adenoma, gonadotrophin-producing	29539639
PITAD_PRL	Pituitary adenoma /PitNET	pituitary adenoma, prolactin-producing	29539639
PITAD_STH_DENSE1	Pituitary adenoma /PitNET	pituitary adenoma, STH-producing	29539639
PITAD_STH_DENSE2	Pituitary adenoma /PitNET	pituitary adenoma, STH-producing	29539639
PITAD_STH_SPARSE	Pituitary adenoma /PitNET	pituitary adenoma, STH-producing	29539639
PITAD_TSH	Pituitary adenoma /PitNET	pituitary adenoma, TSH-producing	29539639
PITUI	Pituicytoma	pituicytoma	29539639
PLASMACYT	Miscellaneous rare lymphomas in the CNS	plasmacytoma	29539639
PLNTY	Polymorphous low-grade neuroepithelial tumour of the young	polymorphous low-grade neuroepithelial tumour of the young	27812792
PPTID_A	Pineal parenchymal tumour of intermediate differentiation	pineal parenchymal tumour of intermediate differentiation	31768671
PPTID_B	Pineal parenchymal tumour of intermediate differentiation	pineal parenchymal tumour of intermediate differentiation	31768671
PTPR_A	Papillary tumour of the pineal region	papillary tumour of the pineal region	29539639
PTPR_B	Papillary tumour of the pineal region	papillary tumour of the pineal region	29539639
PXA	Pleomorphic xanthoastrocytoma	pleomorphic xanthoastrocytoma(-like)	29539639
RB	Retinoblastoma	retinoblastoma	29539639
RB_MYCN	Retinoblastoma, subtype MYCN-altered	retinoblastoma, MYCN-activated	33879448
RGNT	Rosette forming glioneuronal tumour	rosette-forming glioneuronal tumour	29539639
SCHW	Schwannoma	schwannoma	29539639

SEGA	Subependymal giant cell astrocytoma	subependymal giant cell astrocytoma	29539639
SFT_HMPC	Solitary fibrous tumour	solitary fibrous tumour / haemangiopericytoma	29539639
SNUC_IDH2	Esthesioneuroblastoma, IDH-mutant	Sinonasal undifferentiated carcinoma, IDH2-mutant	29730775
ST_EPN_REL_A	Supratentorial ependymoma C11orf95 fusion-positive	supratentorial ependymoma, c11orf95:RELA-fused	29539639
ST_EPN_REL_B	Supratentorial ependymoma C11orf95 fusion-positive	supratentorial ependymoma, c11orf95:RELA-fused	33879448
VGLL	Low grade neuroepithelial tumour, subtype VGLL fused	intracranial schwannoma, VGLL-altered	

Tables 3 to 172: Classification of cancer types listed in Table 2 according to the disclosure.

The classification data for each cancer type as listed in Table 2 is shown in an individual table. Each table comprises the following columns:

Column 1 shows the selected gene sites for the classification of the cancer type.

- 5 Column 2 shows the overall statistical importance (imp_sum) of a specific gene site for the classification of the cancer type. The overall importance of the specific gene site (imp_sum) is calculated by multiplying the number of single measurement points (n_probes) of Column 4 with the mean variable importance (imp_mean) of Column 3. Higher values represent more important gene sites.
- 10 Column 3 shows the mean variable importance (imp_mean) of all of the single measurement points (n_probes) of the specific gene sites according to the statistical model used (e.g. based on Random Forest)

Column 4 shows the number of single measurement points (n_probes; CpG site methylation probes that fall within the gene site).

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TABLE 3: Cancer Type A_IDH							
Gene site	imp_sum	imp_mean	n				
PTPRN2	18.78638	0.229102	82	SDK1	5.072705	0.253635	20
PRDM16	15.88426	0.223722	71	ABR	4.501446	0.225072	20
HDAC4	11.38158	0.30761	37	MAD1L1	11.21992	0.590522	19
PAX6	7.719922	0.220569	35	SMG1P2	5.771893	0.303784	19
RBFOX3	5.391468	0.154042	35	BOLA2	5.771893	0.303784	19
DIP2C	11.84772	0.370241	32	LOC613038	5.771893	0.303784	19
SOX2-OT	9.378707	0.323404	29	CASZ1	4.031351	0.212176	19
GALNT9	4.056375	0.150236	27	FOXK1	6.749132	0.374952	18
ADARB2	6.339109	0.243812	26	ANKRD11	4.824927	0.268051	18
SHANK2	4.920743	0.189259	26	TBC1D16	4.176223	0.232012	18
AGAP1	7.296626	0.291865	25	SEPTIN9	3.781195	0.210066	18
CAMTA1	5.092806	0.203712	25	MCF2L	3.725642	0.20698	18
PDGFRA	4.139033	0.165561	25	OPCML	7.22948	0.425264	17
SATB2	5.319752	0.221656	24	FOXP1	7.461073	0.466317	16
MEIS1	4.304819	0.179367	24	NAV2	4.408791	0.275549	16
RPTOR	11.20222	0.487053	23	GLI2	8.586287	0.572419	15
NCOR2	4.696695	0.204204	23	BAIAP2	4.850054	0.323337	15
INPP5A	3.980493	0.173065	23	KNDC1	4.040584	0.269372	15
RIMBP2	3.715073	0.161525	23	NFATC1	3.893129	0.259542	15
SKI	9.355866	0.445517	21	RPS6KA2	5.709661	0.407833	14
FRMD4A	6.390597	0.31953	20	IQSEC1	4.288682	0.306334	14
				ARHGEF10	4.250505	0.303607	14
				PRKAG2	4.116933	0.294067	14

CUX1	3.667762	0.261983	14	RBMS3	4.328619	1.082155	4
GNG7	3.48551	0.248965	14	DTNA	3.8923	0.973075	4
MSI2	6.236622	0.47974	13	VOPP1	3.405106	0.851277	4
MYT1L	4.125383	0.317337	13	SRRM3	3.823662	1.274554	3
CMIP	4.831247	0.402604	12	DAGLB	3.455348	1.151783	3
ADGRD1	4.598185	0.383182	12	ANKLE2	4.083121	2.04156	2
ZC3H3	4.555928	0.379661	12	SLC25A10	3.753383	1.876692	2
MIRLET7BHG	4.206607	0.350551	12	SOX10	3.463676	1.731838	2
RASA3	3.881123	0.323427	12	Table 4			
MEGF6	3.49592	0.291327	12				
FGFR2	3.946181	0.358744	11	Gene site	imp_sum	imp_mean	n
SPON2	3.782265	0.343842	11	PTPRN2	13.16665	0.160569	82
ZC3H12D	3.768599	0.3426	11	PRDM16	11.2564	0.158541	71
VGLL4	3.446999	0.313364	11	PCDHGA1	6.017158	0.101986	59
ACOT7	4.628745	0.462874	10	PCDHGA2	5.700772	0.100014	57
SH3RF3	3.971742	0.397174	10	PCDHGA3	5.384386	0.099711	54
RGS12	3.917101	0.39171	10	PCDHGB1	5.384386	0.101592	53
AKAP13	3.404835	0.340483	10	PCDHGA4	5.384386	0.105576	51
SND1	6.763759	0.751529	9	PCDHGB2	5.068	0.103429	49
ATP11A	5.979014	0.664335	9	PCDHGA5	5.068	0.10783	47
ADAMTS2	5.342213	0.593579	9	PCDHGB3	5.068	0.11786	43
TSPAN9	4.494867	0.49943	9	PCDHGA6	5.068	0.1267	40
AXIN2	4.478168	0.497574	9	HDAC4	12.55202	0.339244	37
TRAPPC12	4.45643	0.495159	9	PCDHGA7	4.751614	0.128422	37
SLC22A18	4.308821	0.478758	9	PAX6	9.136798	0.261051	35
NEAT1	3.415812	0.379535	9	RBFOX3	9.124187	0.260691	35
ASAP1	3.398391	0.377599	9	PCDHGB4	4.751614	0.13576	35
MSRA	4.796431	0.599554	8	PCDHGA8	4.751614	0.13576	35
DNMT3A	4.299295	0.537412	8	DIP2C	9.649572	0.301549	32
AFF3	4.03016	0.50377	8	PCDHGB5	4.435228	0.138601	32
RORA	3.933212	0.491652	8	PCDHGA9	4.435228	0.143072	31
DLEU1	3.641639	0.455205	8	SOX2-OT	10.27019	0.354145	29
DUSP6	5.017101	0.716729	7	PCDHGA10	3.846128	0.137362	28
VPS13D	4.243833	0.606262	7	GALNT9	4.09556	0.151687	27
NAV1	4.237089	0.605298	7	ADARB2	5.791898	0.222765	26
LINC00461	4.202952	0.600422	7	AGAP1	8.559905	0.342396	25
C19orf25	3.637842	0.519692	7	PDGFRA	6.841003	0.27364	25
FBXL18	4.410866	0.735144	6	CAMTA1	5.65441	0.226176	25
CRADD	4.042402	0.673734	6	MEIS1	11.15091	0.464621	24
STK10	3.58235	0.597058	6	SATB2	8.839103	0.368296	24
LRRFIP1	3.445461	0.574243	6	PCDHGB7	3.846128	0.160255	24
RUNDC3A	4.649823	0.929965	5	RPTOR	7.902877	0.343603	23
ARHGEF7	4.081638	0.816328	5	INPP5A	5.966938	0.259432	23
TSNAX-DISC1	4.017901	0.80358	5	RIMBP2	5.064586	0.220199	23
MRC2	3.944978	0.788996	5	HOXB3	3.589754	0.156076	23
BCAR1	3.588348	0.71767	5	PRKCZ	5.390894	0.245041	22
TK1	3.547527	0.709505	5	SKI	6.459381	0.30759	21
STAP2	4.426476	1.106619	4				

ZIC4	4.94215	0.23534	21	NR2E1	3.648623	0.456078	8
SIM2	3.756501	0.178881	21	NAV1	4.624354	0.660622	7
FRMD4A	3.866106	0.193305	20	VPS13D	3.796267	0.542324	7
MAD1L1	10.17086	0.535308	19	C19orf25	3.791917	0.541702	7
ZNF423	5.772862	0.303835	19	LINC01140	3.549345	0.507049	7
SMG1P2	5.633616	0.296506	19	FBXL18	4.832711	0.805452	6
BOLA2	5.633616	0.296506	19	SRGAP3	4.349279	0.72488	6
LOC613038	5.633616	0.296506	19	CRACR2A	3.642366	0.607061	6
CASZ1	4.639517	0.244185	19	RUNDC3A	5.364042	1.072808	5
FOXK1	5.824185	0.323566	18	MRC2	4.240738	0.848148	5
ANKRD11	5.042924	0.280162	18	TSNAX-DISC1	4.221202	0.84424	5
SEPTIN9	4.66177	0.258987	18	ARHGEF7	4.089307	0.817861	5
TBC1D16	3.842806	0.213489	18	STAP2	7.704487	1.926122	4
RBFOX1	3.695191	0.205288	18	RBMS3	4.25923	1.064808	4
OPCML	7.050041	0.414708	17	VOPP1	3.764	0.941	4
PAX6-AS1	4.863903	0.286112	17	SRRM3	5.500931	1.833644	3
RCN1	4.863903	0.286112	17	TABLE 5: Cancer Type ANTCON			
TBX15	3.726216	0.219189	17	Gene site	imp_sum	imp_mean	n
NAV2	4.581486	0.286343	16	PTPRN2	7.483021	0.091256	82
FOXP1	4.081864	0.255117	16	PRDM16	4.367174	0.061509	71
GLI2	10.28032	0.685355	15	PCDHGA1	2.965166	0.050257	59
RPS6KA2	5.678692	0.405621	14	PCDHGA2	2.965166	0.05202	57
CUX1	4.301523	0.307252	14	PCDHGA3	2.965166	0.05491	54
IQSEC1	3.938498	0.281321	14	PCDHGB1	2.965166	0.055947	53
MSI2	5.975883	0.459683	13	PCDHGA4	2.965166	0.058141	51
MYT1L	5.311196	0.408554	13	PCDHGB2	2.965166	0.060514	49
SPTBN4	4.376569	0.336659	13	PCDHGA5	2.531088	0.053853	47
CMIP	4.991631	0.415969	12	PCDHGB3	2.531088	0.058863	43
ZC3H3	4.560729	0.380061	12	PCDHGA6	2.214702	0.055368	40
MIRLET7BHG	4.517836	0.376486	12	HDAC4	5.100359	0.137848	37
GLUD1P2	4.213095	0.383009	11	PCDHGA7	2.214702	0.059857	37
VGLL4	3.803764	0.345797	11	PAX6	4.939121	0.141118	35
RAD51B	3.543642	0.322149	11	PCDHGB4	2.214702	0.063277	35
ACOT7	5.348642	0.534864	10	PCDHGA8	2.214702	0.063277	35
NR2F1-AS1	4.332052	0.433205	10	PCDHGB5	2.214702	0.069209	32
ATP11A	6.242261	0.693585	9	PCDHGA9	2.214702	0.071442	31
SND1	5.421156	0.602351	9	SOX2-OT	5.824753	0.200854	29
TRAPPC12	4.750868	0.527874	9	SHANK2	2.07689	0.07988	26
ASAP1	4.177354	0.46415	9	CAMTA1	3.156495	0.12626	25
ADAMTS2	3.748026	0.416447	9	AGAP1	2.633589	0.105344	25
RUNX1	3.706722	0.411858	9	PDGFRA	2.134721	0.085389	25
APBA2	3.609137	0.401015	9	SATB2	4.601253	0.191719	24
ADGRB1	3.604336	0.400482	9	RPTOR	4.447377	0.193364	23
TXNRD1	3.556455	0.395162	9	NXN	2.150077	0.093482	23
DNMT3A	5.65658	0.707073	8	PRKCZ	2.51794	0.114452	22
LINC00311	4.894521	0.611815	8	SKI	2.796501	0.133167	21
MSRA	4.026572	0.503321	8	ZNF423	4.010188	0.211063	19
PPP2R2B	3.77597	0.471996	8				

MAD1L1	3.859638	0.203139	19	VPS13D	2.207261	0.315323	7
SMG1P2	3.770753	0.198461	19	RBMS1	1.957648	0.279664	7
BOLA2	3.770753	0.198461	19	EPHA10	1.996731	0.332788	6
LOC613038	3.770753	0.198461	19	MYO16	1.956058	0.32601	6
CASZ1	1.910046	0.100529	19	SLC22A18AS	1.912184	0.318697	6
ANKRD11	1.917186	0.10651	18	RUNDC3A	3.204346	0.640869	5
OPCML	3.205323	0.188548	17	SLC8A2	2.163285	0.432657	5
TBX15	1.941086	0.114182	17	ARHGEF7	2.052253	0.410451	5
FOXP1	3.221398	0.201337	16	CNMD	1.973732	0.394746	5
NAV2	2.538252	0.158641	16	THRB	1.940011	0.388002	5
GLI2	6.990535	0.466036	15	ONECUT2	2.858992	0.714748	4
NFATC1	2.039808	0.135987	15	STAP2	2.282702	0.570675	4
TBX5	2.788694	0.199192	14	RBMS3	2.014411	0.503603	4
CUX1	2.302986	0.164499	14	LINC00856	1.991078	0.49777	4
ARHGEF10	2.283155	0.163083	14	SRRM3	3.72052	1.240173	3
IQSEC1	2.078601	0.148472	14	GRIN2B	3.033253	1.011084	3
RPS6KA2	1.916508	0.136893	14	DICER1	2.143218	0.714406	3
MSI2	3.663853	0.281835	13	SOX10	3.646176	1.823088	2
MYT1L	3.019476	0.232267	13	SLC25A10	2.213726	1.106863	2
CMIP	2.634173	0.219514	12	KCNB1	2.174145	1.087073	2
MIRLET7BHG	2.582972	0.215248	12	CFLAR	2.014526	1.007263	2
ZC3H12D	2.029367	0.184488	11	GRIN1	1.944439	0.972219	2
VGLL4	2.027528	0.184321	11	MAPK8IP1	1.980944	1.980944	1
RAD51B	1.977181	0.179744	11				
LBX1-AS1	3.913136	0.391314	10				
SPPL2B	3.257854	0.325785	10				
GRID1	2.263188	0.226319	10				
TSPAN4	2.108335	0.210833	10				
SKOR1	1.946083	0.194608	10				
RGS12	1.934755	0.193475	10				
ATP11A	3.784347	0.420483	9				
ADGRB1	3.322193	0.369133	9				
RUNX1	3.083942	0.34266	9				
SND1	2.935944	0.326216	9				
ZNF833P	2.584271	0.287141	9				
AXIN2	2.468323	0.274258	9				
ADAMTS2	2.162573	0.240286	9				
ASAP1	2.085051	0.231672	9				
NOTCH1	2.064723	0.229414	9				
NEAT1	1.974612	0.219401	9				
VRK2	2.995784	0.374473	8				
LINC00311	2.230276	0.278785	8				
NXPH1	2.151553	0.268944	8				
MBP	2.102791	0.262849	8				
NR2E1	1.898316	0.237289	8				
DUSP6	2.822265	0.403181	7				
NAV1	2.582267	0.368895	7				
TOX2	2.386634	0.340948	7				

				TABLE 6.	Cancer Type			
					ATRT_MYC			
				Gene site	imp_sum	imp_mean	n	
				PTPRN2	17.73723	0.216308	82	
				PRDM16	13.36136	0.188188	71	
				PCDHGA1	11.41704	0.193509	59	
				PCDHGA2	10.35292	0.18163	57	
				PCDHGA3	9.908546	0.183492	54	
				PCDHGB1	9.908546	0.186954	53	
				PCDHGA4	9.908546	0.194285	51	
				PCDHGB2	9.168339	0.187109	49	
				PCDHGA5	9.168339	0.195071	47	
				PCDHGB3	7.663836	0.178229	43	
				PCDHGA6	7.34745	0.183686	40	
				HDAC4	20.61752	0.55723	37	
				PCDHGA7	7.031064	0.190029	37	
				PCDHGB4	7.031064	0.200888	35	
				PCDHGA8	7.031064	0.200888	35	
				PAX6	5.397601	0.154217	35	
				DIP2C	10.77775	0.336805	32	
				PCDHGB5	6.27593	0.196123	32	
				PCDHGA9	6.27593	0.202449	31	
				SOX2-OT	6.391698	0.220403	29	
				PCDHGB6	5.959544	0.205502	29	

PCDHGA10	5.959544	0.212841	28	GNA12	5.032973	0.419414	12
SHANK2	4.056797	0.156031	26	TNS3	4.957592	0.413133	12
AGAP1	11.14937	0.445975	25	FBRSL1	4.5699	0.380825	12
CAMTA1	5.943709	0.237748	25	TBX4	4.111141	0.342595	12
PDGFRA	5.604404	0.224176	25	CTNNA2	4.073641	0.33947	12
PCDHGB7	5.535067	0.230628	24	ADGRD1	4.025228	0.335436	12
RPTOR	11.41745	0.496411	23	ZC3H12D	4.849544	0.440868	11
NCOR2	8.405351	0.36545	23	CTBP2	4.362049	0.39655	11
NXN	7.435412	0.323279	23	ACOT7	4.431353	0.443135	10
PCDHGA11	5.535067	0.240655	23	NBEA	3.965625	0.396562	10
PRKCZ	5.398038	0.245365	22	SND1	8.53951	0.948834	9
SKI	11.2062	0.533629	21	ADAMTS2	6.888579	0.765398	9
HOXA-AS3	4.54373	0.216368	21	ATP11A	6.762114	0.751346	9
SDK1	5.016131	0.250807	20	KCNH2	5.308144	0.589794	9
FRMD4A	4.007902	0.200395	20	TRAPPC12	4.83608	0.537342	9
ABR	3.959355	0.197968	20	CACNA2D4	4.766338	0.529593	9
MAD1L1	12.71891	0.669416	19	MGMT	4.576613	0.508513	9
ZNF423	6.244655	0.328666	19	ASAP1	4.566396	0.507377	9
SMG1P2	5.741184	0.302168	19	ZNF833P	4.242022	0.471336	9
BOLA2	5.741184	0.302168	19	TSPAN9	4.038929	0.44877	9
LOC613038	5.741184	0.302168	19	VRK2	4.017195	0.502149	8
KCNQ1	5.021333	0.264281	19	SYNJ2	3.989878	0.498735	8
CASZ1	5.018076	0.264109	19	ITPKB	5.378408	0.768344	7
CFAP46	4.552203	0.23959	19	NAV1	5.039236	0.719891	7
FOXK1	10.48601	0.582556	18	RXRA	4.298066	0.614009	7
TBC1D16	7.537054	0.418725	18	CRADD	4.812334	0.802056	6
ANKRD11	6.677221	0.370957	18	FBXL18	4.670889	0.778482	6
RBFOX1	4.311269	0.239515	18	TSNAX-DISC1	5.461204	1.092241	5
SEPTIN9	4.091576	0.22731	18	ARHGEF7	5.319103	1.063821	5
OPCML	4.016549	0.236268	17	RUNDC3A	4.452929	0.890586	5
FOXP1	4.010279	0.250642	16	NHSL1	4.604302	1.151075	4
GLI2	6.717306	0.44782	15	RALGAPA2	4.665413	2.332707	2
BAIAP2	6.057075	0.403805	15				
SLX1B-SULT1A4	5.70781	0.380521	15	TABLE 7: Cancer Type ATRT_SHH			
SLX1A	5.70781	0.380521	15	Gene site	imp_sum	imp_mean	n
LOC606724	5.70781	0.380521	15	PTPRN2	24.89162	0.303556	82
ZBTB20	4.322333	0.288156	15	PRDM16	15.79215	0.222425	71
MIR548F5	5.757953	0.411282	14	PCDHGA1	8.715701	0.147724	59
IQSEC1	5.167301	0.369093	14	PCDHGA2	8.202776	0.143908	57
C7orf50	5.156157	0.368297	14	PCDHGA3	8.202776	0.151903	54
RPS6KA2	4.986439	0.356174	14	PCDHGB1	8.202776	0.154769	53
ARHGEF10	4.555787	0.325413	14	PCDHGA4	7.88639	0.154635	51
PRKAG2	4.408054	0.314861	14	PCDHGB2	7.298762	0.148954	49
MSI2	7.594149	0.584165	13	PCDHGA5	7.298762	0.155293	47
MYT1L	4.818631	0.370664	13	PCDHGB3	6.282316	0.1461	43
CMIP	7.520737	0.626728	12	PCDHGA6	5.834838	0.145871	40
ZC3H3	5.633656	0.469471	12	HDAC4	18.17436	0.491199	37

PCDHGA7	5.202066	0.140596	37	PRKAG2	5.378981	0.384213	14
PAX6	5.810192	0.166005	35	IQSEC1	4.92666	0.351904	14
RBFOX3	4.941735	0.141192	35	MSI2	8.50001	0.653847	13
PCDHGB4	4.88568	0.139591	35	GSE1	5.467176	0.420552	13
PCDHGA8	4.88568	0.139591	35	MYT1L	5.392954	0.414843	13
DIP2C	10.64599	0.332687	32	CMIP	5.995666	0.499639	12
GALNT9	7.350354	0.272235	27	ADGRD1	5.49992	0.458327	12
SHANK2	5.282632	0.203178	26	FBRSL1	5.377398	0.448117	12
AGAP1	11.67873	0.467149	25	GNA12	4.901687	0.408474	12
CAMTA1	10.30116	0.412046	25	ZC3H3	4.777128	0.398094	12
PDGFRA	5.066539	0.202662	25	ZC3H12D	5.069794	0.46089	11
RPTOR	13.54718	0.589008	23	ANAPC16	4.337299	0.3943	11
INPP5A	8.11614	0.352876	23	CTBP2	4.211653	0.382878	11
NXN	8.036403	0.349409	23	AKAP13	5.934512	0.593451	10
NCOR2	7.002394	0.304452	23	TSPAN4	5.465636	0.546564	10
RIMBP2	4.968555	0.216024	23	ACOT7	4.63607	0.463607	10
PRKCZ	6.218634	0.282665	22	RGS12	4.236383	0.423638	10
SKI	9.977176	0.475104	21	GAS7	4.190349	0.419035	10
HOXA-AS3	5.84487	0.278327	21	ATP11A	8.092174	0.89913	9
ABR	5.093333	0.254667	20	SND1	7.130321	0.792258	9
SDK1	4.517652	0.225883	20	ADAMTS2	6.985639	0.776182	9
MAD1L1	12.65219	0.665905	19	TSPAN9	5.699636	0.633293	9
SMG1P2	7.06765	0.371982	19	KCNH2	5.598484	0.622054	9
BOLA2	7.06765	0.371982	19	TRAPPC12	5.177346	0.575261	9
LOC613038	7.06765	0.371982	19	MGMT	5.073455	0.563717	9
ZNF423	5.716777	0.300883	19	ASAP1	4.968154	0.552017	9
CASZ1	5.598989	0.294684	19	DNMT3A	4.980074	0.622509	8
KCNQ1	4.405857	0.231887	19	DLEU1	4.929789	0.616224	8
FOKK1	9.609548	0.533864	18	SYNJ2	4.464514	0.558064	8
TBC1D16	7.431807	0.412878	18	VPS13D	5.363926	0.766275	7
MCF2L	6.035987	0.335333	18	ITPKB	5.030327	0.718618	7
ANKRD11	5.04371	0.280206	18	C19orf25	4.429583	0.632798	7
SEPTIN9	4.418339	0.245463	18	NAV1	4.398237	0.62832	7
OPCML	5.149965	0.302939	17	RXRA	4.217134	0.602448	7
EBF3	5.495662	0.343479	16	CRADD	4.749641	0.791607	6
NAV2	4.483761	0.280235	16	FBXL18	4.234717	0.705786	6
FOXP1	4.190478	0.261905	16	ARHGEF7	5.396565	1.079313	5
GLI2	7.394108	0.492941	15	TSNAX-DISC1	5.184178	1.036836	5
BAIAP2	5.826734	0.388449	15	RUNDC3A	4.527973	0.905595	5
SLX1B-				BCAR1	4.171778	0.834356	5
SULT1A4	4.969677	0.331312	15	NHSL1	5.159373	1.289843	4
SLX1A	4.969677	0.331312	15				
LOC606724	4.969677	0.331312	15				
KIRREL3	4.942031	0.329469	15				
NFATC1	4.188296	0.27922	15				
RPS6KA2	8.057203	0.575514	14				
CUX1	5.824604	0.416043	14				
C7orf50	5.488536	0.392038	14				

TABLE 8.

Cancer Type
ATRT_TYR

Gene site	imp_sum	imp_mean	n
PTPRN2	17.17779	0.209485	82
PRDM16	13.19798	0.185887	71
PCDHGA1	7.447791	0.126234	59

PCDHGA2	7.050652	0.123696	57	RCN1	4.816456	0.283321	17
PCDHGA3	6.919764	0.128144	54	FOXP1	7.32639	0.457899	16
PCDHGB1	6.919764	0.130562	53	GLI2	7.809527	0.520635	15
PCDHGA4	6.603378	0.129478	51	KIRREL3	7.209825	0.480655	15
PCDHGB2	6.603378	0.134763	49	BAIAP2	6.29041	0.419361	15
PCDHGA5	6.286992	0.133766	47	ZBTB20	5.342014	0.356134	15
PCDHGB3	5.970606	0.138851	43	SLX1B-			
PCDHGA6	5.724475	0.143112	40	SULT1A4	5.163699	0.344247	15
HDAC4	20.70341	0.559552	37	SLX1A	5.163699	0.344247	15
PCDHGA7	5.091703	0.137614	37	LOC606724	5.163699	0.344247	15
RBFOX3	6.927478	0.197928	35	RPS6KA2	6.698645	0.478475	14
PAX6	6.599989	0.188571	35	IQSEC1	6.069825	0.433559	14
PCDHGB4	5.091703	0.145477	35	PRKAG2	5.738334	0.409881	14
PCDHGA8	5.091703	0.145477	35	CUX1	5.302633	0.378759	14
DIP2C	11.60772	0.362741	32	C7orf50	4.746734	0.339052	14
PCDHGB5	4.775317	0.149229	32	MIR548F5	4.480361	0.320026	14
PCDHGA9	4.775317	0.154042	31	MSI2	6.390182	0.491552	13
SOX2-OT	8.196193	0.282627	29	MYT1L	5.351189	0.41163	13
PCDHGB6	4.458931	0.153756	29	GSE1	4.631692	0.356284	13
PCDHGA10	4.458931	0.159248	28	CMIP	7.168856	0.597405	12
GALNT9	4.845115	0.179449	27	FBRSL1	6.380225	0.531685	12
SHANK2	7.031974	0.270461	26	ZC3H3	5.577344	0.464779	12
ADARB2	4.425699	0.170219	26	MAML3	5.348197	0.445683	12
AGAP1	13.75814	0.550325	25	GNA12	5.327119	0.443927	12
CAMTA1	8.294735	0.331789	25	ADGRD1	5.196335	0.433028	12
MEIS1	6.612173	0.275507	24	TNS3	4.431316	0.369276	12
RPTOR	13.07668	0.568551	23	RAD51B	4.560009	0.414546	11
NXN	10.20379	0.443643	23	TSPAN4	6.463955	0.646395	10
INPP5A	6.643652	0.288854	23	AKAP13	5.713526	0.571353	10
NCOR2	6.499293	0.282578	23	ACOT7	5.249279	0.524928	10
RIMBP2	4.784154	0.208007	23	SND1	7.870976	0.874553	9
PRKCZ	8.619356	0.391789	22	ATP11A	7.260096	0.806677	9
SKI	11.00712	0.524148	21	ADAMTS2	6.931892	0.77021	9
FRMD4A	7.127492	0.356375	20	TSPAN9	4.861158	0.540129	9
ABR	5.1764	0.25882	20	KCNH2	4.764548	0.529394	9
SDK1	4.96091	0.248046	20	CACNA2D4	4.710694	0.52341	9
MAD1L1	12.46744	0.656181	19	DNMT3A	4.897363	0.61217	8
SMG1P2	6.447881	0.339362	19	DLEU1	4.821535	0.602692	8
BOLA2	6.447881	0.339362	19	SYNJ2	4.589362	0.57367	8
LOC613038	6.447881	0.339362	19	VPS13D	5.492812	0.784687	7
KCNQ1	5.898287	0.310436	19	NAV1	5.347137	0.763877	7
CASZ1	5.485553	0.288713	19	RXRA	4.834905	0.690701	7
ZNF423	5.462272	0.287488	19	CXXC5	4.78724	0.683891	7
CFAP46	5.159089	0.271531	19	FBXL18	4.838799	0.806467	6
FOKK1	10.70561	0.594756	18	CRADD	4.809103	0.801517	6
TBC1D16	6.899829	0.383324	18	TSNAX-DISC1	5.422562	1.084512	5
ANKRD11	5.454725	0.30304	18	ARHGEF7	4.794453	0.958891	5
PAX6-AS1	4.816456	0.283321	17	RUNDC3A	4.504949	0.90099	5

NHSL1	5.116568	1.279142	4	ANKRD11	3.55617	0.197565	18
RALGAPA2	4.45333	2.226665	2	MCF2L	3.27087	0.181715	18
TABLE 9: Cancer Type CHGL				OPCML	3.559998	0.209412	17
Gene site	imp_sum	imp_mean	n	TBX15	3.539969	0.208233	17
PTPRN2	14.79861	0.180471	82	FOXP1	5.668133	0.354258	16
PRDM16	12.8778	0.181377	71	NAV2	4.20854	0.263034	16
PCDHGA1	5.515199	0.093478	59	GLI2	6.894022	0.459601	15
PCDHGA2	5.198813	0.091207	57	NFIX	4.539748	0.30265	15
PCDHGA3	5.198813	0.096274	54	RPS6KA2	5.924986	0.423213	14
PCDHGB1	5.198813	0.098091	53	PRKAG2	5.161181	0.368656	14
PCDHGA4	4.767947	0.093489	51	C7orf50	4.374604	0.312472	14
PCDHGB2	4.451561	0.090848	49	CUX1	4.301476	0.307248	14
PCDHGA5	4.135175	0.087982	47	IQSEC1	4.248587	0.30347	14
PCDHGB3	3.502403	0.081451	43	MSI2	5.792215	0.445555	13
PCDHGA6	3.502403	0.08756	40	GSE1	4.661854	0.358604	13
HDAC4	12.87305	0.34792	37	MYT1L	3.970198	0.3054	13
PCDHGA7	3.502403	0.09466	37	CMIP	4.801019	0.400085	12
PAX6	7.160987	0.2046	35	MIRLET7BHG	4.003606	0.333634	12
RBFOX3	3.818802	0.109109	35	FBRSL1	3.821366	0.318447	12
PCDHGB4	3.502403	0.100069	35	ZC3H3	3.753333	0.312778	12
PCDHGA8	3.502403	0.100069	35	RASA3	3.657104	0.304759	12
DIP2C	8.043739	0.251367	32	ZC3H12D	3.612422	0.328402	11
PCDHGB5	3.502403	0.10945	32	CTBP2	3.525179	0.320471	11
PCDHGA9	3.502403	0.112981	31	CACNA1C	3.372955	0.306632	11
SOX2-OT	4.335995	0.149517	29	AKAP13	5.056953	0.505695	10
SHANK2	5.495176	0.211353	26	CHST11	3.124458	0.312446	10
ADARB2	4.218601	0.162254	26	RGS12	3.122263	0.312226	10
AGAP1	8.389655	0.335586	25	TSPAN4	3.114551	0.311455	10
CAMTA1	7.901409	0.316056	25	TRAPPC12	4.011072	0.445675	9
PDGFRA	4.726646	0.189066	25	ATP11A	3.780115	0.420013	9
SATB2	5.128386	0.213683	24	SND1	3.550011	0.394446	9
RPTOR	10.87751	0.472935	23	RUNX1	3.508329	0.389814	9
NCOR2	4.219558	0.183459	23	CACNA2D4	3.410833	0.378981	9
INPP5A	4.041	0.175696	23	MGMT	3.143697	0.3493	9
RIMBP2	3.839015	0.166914	23	ADAMTS2	3.099666	0.344407	9
PRKCZ	4.948854	0.224948	22	NOTCH1	3.071767	0.341307	9
SKI	8.260395	0.393352	21	DNMT3A	4.219117	0.52739	8
ZIC4	3.647669	0.173699	21	DLEU1	4.091619	0.511452	8
SDK1	6.056386	0.302819	20	ESRRG	3.813668	0.476709	8
ABR	5.322552	0.266128	20	MCC	3.480227	0.435028	8
FRMD4A	4.655164	0.232758	20	MSRA	3.13775	0.392219	8
MAD1L1	9.009302	0.474174	19	AFF3	3.097254	0.387157	8
ZNF423	7.063639	0.37177	19	LINC00311	3.083062	0.385383	8
CASZ1	4.550555	0.239503	19	NAV1	4.437205	0.633886	7
SEPTIN9	5.657282	0.314293	18	LHPP	3.999415	0.571345	7
TBC1D16	5.558976	0.308832	18	C19orf25	3.883883	0.55484	7
FO XK1	4.715776	0.261988	18	MIR548H4	3.465819	0.495117	7
				FOXP4	3.315285	0.473612	7

LINC01140	3.25579	0.465113	7	SKI	9.865213	0.469772	21
RXRA	3.076949	0.439564	7	FRMD4A	6.525814	0.326291	20
SLC22A18AS	4.438269	0.739711	6	SDK1	5.35532	0.267766	20
FBXL18	3.916143	0.65269	6	MAD1L1	13.4089	0.705732	19
RUNDC3A	4.641016	0.928203	5	CASZ1	6.812935	0.358576	19
TSNAX-DISC1	3.590508	0.718102	5	ZNF423	6.718331	0.353596	19
STAP2	3.380822	0.845206	4	SMG1P2	5.821967	0.306419	19
IGDCC4	3.084475	0.771119	4	BOLA2	5.821967	0.306419	19
DAGLB	3.187697	1.062566	3	LOC613038	5.821967	0.306419	19

TABLE 10: Cancer Type CHORDM

Gene site	imp_sum	imp_mean	n				
PTPRN2	16.55238	0.201858	82	ANKRD11	5.957897	0.330994	18
PRDM16	14.25707	0.200804	71	SEPTIN9	5.504379	0.305799	18
PCDHGA1	7.664046	0.129899	59	OPCML	4.593892	0.270229	17
PCDHGA2	7.34766	0.128906	57	FOXP1	6.10553	0.381596	16
PCDHGA3	7.031274	0.130209	54	SORBS2	6.052013	0.378251	16
PCDHGB1	7.031274	0.132666	53	EBF3	5.932069	0.370754	16
PCDHGA4	7.031274	0.137868	51	NAV2	5.279409	0.329963	16
PCDHGB2	7.031274	0.143495	49	ZBTB20	6.598775	0.439918	15
PCDHGA5	6.714888	0.14287	47	GLI2	5.800381	0.386692	15
PCDHGB3	6.082116	0.141445	43	NFIX	5.646003	0.3764	15
PCDHGA6	6.398502	0.159963	40	SLX1B-			
HDAC4	21.54355	0.582258	37	SULT1A4	5.321711	0.354781	15
PCDHGA7	7.031274	0.190034	37	SLX1A	5.321711	0.354781	15
PAX6	10.37192	0.296341	35	LOC606724	5.321711	0.354781	15
RBFOX3	8.759702	0.250277	35	BAIAP2	4.860121	0.324008	15
PCDHGB4	7.031274	0.200894	35	KNDC1	4.851891	0.323459	15
PCDHGA8	7.031274	0.200894	35	CUX1	7.205997	0.514714	14
DIP2C	12.96907	0.405283	32	RPS6KA2	6.180081	0.441434	14
PCDHGB5	6.714888	0.20984	32	IQSEC1	5.85971	0.418551	14
PCDHGA9	6.714888	0.216609	31	C7orf50	5.675578	0.405398	14
PCDHGB6	6.398502	0.220638	29	PRKAG2	5.473467	0.390962	14
SOX2-OT	6.1506	0.21209	29	ARHGEF10	4.720729	0.337195	14
PCDHGA10	5.967975	0.213142	28	MSI2	7.483359	0.575643	13
GALNT9	6.874988	0.254629	27	MYT1L	5.628405	0.432954	13
SHANK2	6.202549	0.23856	26	GSE1	5.108727	0.392979	13
AGAP1	12.407	0.49628	25	RFX4	5.022644	0.386357	13
CAMTA1	5.741739	0.22967	25	CMIP	6.303599	0.5253	12
SATB2	5.401018	0.225042	24	FBRSL1	5.567028	0.463919	12
PCDHGB7	5.335203	0.2223	24	RASA3	5.536303	0.461359	12
RPTOR	11.37436	0.494538	23	ZC3H3	5.072695	0.422725	12
NCOR2	10.30472	0.448031	23	MIRLET7BHG	4.778244	0.398187	12
INPP5A	6.682606	0.290548	23	TNS3	4.728176	0.394015	12
NXN	5.454332	0.237145	23	ZC3H12D	5.34907	0.486279	11
PCDHGA11	5.335203	0.231965	23	RAD51B	5.248837	0.477167	11
RIMBP2	5.27324	0.229271	23	CTBP2	4.770185	0.433653	11
PRKCZ	6.818188	0.309918	22	ACOT7	6.555788	0.655579	10
				TSPAN4	5.56361	0.556361	10

KLHL29	4.70729	0.470729	10	SKI	11.48203	0.546763	21
ATP11A	8.056261	0.89514	9	ZIC4	3.924716	0.186891	21
SND1	6.661356	0.740151	9	SIM2	3.534931	0.16833	21
ADAMTS2	6.218541	0.690949	9	ABR	7.657151	0.382858	20
CACNA2D4	5.379067	0.597674	9	FRMD4A	6.170234	0.308512	20
TSPAN9	4.561383	0.50682	9	SDK1	4.298032	0.214902	20
MSRA	4.804979	0.600622	8	MAD1L1	10.78128	0.567436	19
SMAD3	4.791134	0.598892	8	ZNF423	7.597013	0.399843	19
DNMT3A	4.742032	0.592754	8	SMG1P2	6.87194	0.361681	19
SYNJ2	4.676059	0.584507	8	BOLA2	6.87194	0.361681	19
C19orf25	5.429518	0.775645	7	LOC613038	6.87194	0.361681	19
GAK	5.087383	0.726769	7	CASZ1	5.104204	0.268642	19
VPS13D	4.969722	0.70996	7	TBC1D16	6.092089	0.338449	18
FBXL18	5.310933	0.885156	6	FOXK1	6.044418	0.335801	18
TSNAX-DISC1	6.356626	1.271325	5	SEPTIN9	4.550265	0.252792	18
RUNDC3A	5.285637	1.057127	5	OPCML	7.381886	0.434229	17
ARHGEF7	5.257238	1.051448	5	TBX15	3.551385	0.208905	17
				FOXP1	4.744313	0.29652	16
				NAV2	4.17554	0.260971	16
				GLI2	9.66338	0.644225	15
				SLX1B-			
				SULT1A4	4.42696	0.295131	15
				SLX1A	4.42696	0.295131	15
				LOC606724	4.42696	0.295131	15
				BAIAP2	4.293779	0.286252	15
				ZBTB20	3.970811	0.264721	15
				NFIX	3.576827	0.238455	15
				PRKAG2	5.562683	0.397335	14
				RPS6KA2	4.538682	0.324192	14
				MOB2	3.632116	0.259437	14
				IQSEC1	3.623361	0.258811	14
				MSI2	7.276147	0.559704	13
				GSE1	4.103655	0.315666	13
				MYT1L	3.811088	0.293161	13
				CLYBL	3.726201	0.286631	13
				MAML3	5.722683	0.47689	12
				MIRLET7BHG	4.931143	0.410929	12
				ZC3H3	4.921139	0.410095	12
				CMIP	4.50246	0.375205	12
				TNS3	4.033096	0.336091	12
				MEGF6	3.679307	0.306609	12
				ZC3H12D	5.752693	0.522972	11
				VGLL4	4.195828	0.381439	11
				SPON2	4.119606	0.37451	11
				GLUD1P2	3.612424	0.328402	11
				ACOT7	4.552161	0.455216	10
				ATP11A	5.824264	0.64714	9
				TRAPPC12	4.941906	0.549101	9

Cancer Type							
CN							
Gene site	imp_sum	imp_mean	n				
PTPRN2	17.41315	0.212355	82				
PRDM16	18.11757	0.255177	71				
PCDHGA1	4.439372	0.075244	59				
PCDHGA2	4.439372	0.077884	57				
PCDHGA3	4.755758	0.08807	54				
PCDHGB1	4.755758	0.089731	53				
PCDHGA4	4.755758	0.09325	51				
PCDHGB2	4.439372	0.090599	49				
PCDHGA5	4.122986	0.087723	47				
PCDHGB3	3.501677	0.081434	43				
HDAC4	9.842804	0.266022	37				
PAX6	8.660398	0.24744	35				
RBFOX3	8.540415	0.244012	35				
DIP2C	8.478792	0.264962	32				
SOX2-OT	9.240267	0.31863	29				
GALNT9	4.333948	0.160517	27				
ADARB2	5.603375	0.215514	26				
SHANK2	4.911326	0.188897	26				
AGAP1	8.213638	0.328546	25				
CAMTA1	6.099428	0.243977	25				
SATB2	5.464538	0.227689	24				
RPTOR	10.66881	0.463861	23				
HOXB3	5.490551	0.23872	23				
NCOR2	4.956795	0.215513	23				
INPP5A	3.816948	0.165954	23				
PRKCZ	6.234103	0.283368	22				

TABLE 11:

SND1	4.597402	0.510823	9	RIMBP2	4.348611	0.18907	23
KCNH2	4.245815	0.471757	9	HOXB3	4.035728	0.175466	23
CACNA2D4	4.064338	0.451593	9	SKI	9.461609	0.450553	21
AXIN2	3.940874	0.437875	9	HOXA-AS3	3.253921	0.154949	21
ADAMTS2	3.932094	0.436899	9	SIM2	3.19159	0.15198	21
TSPAN9	3.817944	0.424216	9	FRMD4A	4.992572	0.249629	20
GPC6	3.730134	0.414459	9	ABR	4.973264	0.248663	20
LHX4	4.812097	0.601512	8	SDK1	4.302409	0.21512	20
LINC00311	3.881015	0.485127	8	MAD1L1	11.44015	0.602113	19
MSRA	3.742145	0.467768	8	ZNF423	7.98033	0.420017	19
AFF3	3.68184	0.46023	8	CASZ1	6.244159	0.32864	19
RORA	3.582455	0.447807	8	SMG1P2	6.101449	0.321129	19
RXRA	4.956798	0.708114	7	BOLA2	6.101449	0.321129	19
DUSP6	4.574231	0.653462	7	LOC613038	6.101449	0.321129	19
NAV1	4.421833	0.63169	7	KCNQ1	4.178427	0.219917	19
VPS13D	3.505702	0.500815	7	FOXK1	6.189604	0.343867	18
FMNL2	4.738833	0.789805	6	ANKRD11	4.543665	0.252426	18
FBXL18	4.621327	0.770221	6	MCF2L	3.783785	0.21021	18
ARHGEF7	4.827002	0.9654	5	SEPTIN9	3.743418	0.207968	18
TSNAX-DISC1	4.246502	0.8493	5	OPCML	6.010054	0.353533	17
TOLLIP	3.980093	0.796019	5	FOXP1	5.119723	0.319983	16
AP2A2	3.538338	0.707668	5	GLI2	8.505799	0.567053	15
RBMS3	5.039035	1.259759	4	DLX6-AS1	8.040784	0.536052	15
DTNA	3.667401	0.91685	4	BAIAP2	4.472712	0.298181	15
SLC25A22	3.735059	1.24502	3	COL23A1	3.569903	0.237994	15
SLC25A10	4.452157	2.226079	2	SLX1B-			
ANKLE2	4.048098	2.024049	2	SULT1A4	3.137898	0.209193	15
				SLX1A	3.137898	0.209193	15
				LOC606724	3.137898	0.209193	15
				RPS6KA2	6.920327	0.494309	14
				CUX1	5.050344	0.360739	14
				IQSEC1	4.966123	0.354723	14
				PRKAG2	4.891786	0.349413	14
				GNG7	3.327657	0.23769	14
				MSI2	6.349105	0.488393	13
				MYT1L	5.132238	0.394788	13
				MIRLET7BHG	4.702356	0.391863	12
				ADGRD1	4.548518	0.379043	12
				CMIP	4.280517	0.35671	12
				ZC3H3	3.399395	0.283283	12
				VGLL4	4.005113	0.364101	11
				GLUD1P2	3.982516	0.362047	11
				RAD51B	3.957538	0.359776	11
				CTBP2	3.237034	0.294276	11
				SH3RF3	5.121554	0.512155	10
				ACOT7	4.581365	0.458136	10
				ETS1	3.628299	0.36283	10
				NR2F1-AS1	3.550673	0.355067	10

TABLE 12: Cancer Type				CNS_NB_FOXR2			
Gene site	imp_sum	imp_mean	n				
PTPRN2	22.2855	0.271774	82				
PRDM16	8.402066	0.118339	71				
HDAC4	10.81953	0.29242	37				
RBFOX3	8.390319	0.239723	35				
PAX6	3.863507	0.110386	35				
DIP2C	9.245805	0.288931	32				
SOX2-OT	8.203317	0.282873	29				
GALNT9	3.830935	0.141886	27				
SHANK2	5.300173	0.203853	26				
ADARB2	5.192971	0.19973	26				
AGAP1	8.539411	0.341576	25				
CAMTA1	8.451029	0.338041	25				
PDGFRA	7.359602	0.294384	25				
SATB2	4.178537	0.174106	24				
RPTOR	8.841747	0.384424	23				
INPP5A	5.291318	0.230057	23				
NCOR2	4.690211	0.203922	23				

ATP11A	6.369748	0.70775	9	ADARB2	2.571709	0.098912	26					
SND1	6.008691	0.667632	9	SHANK2	2.41474	0.092875	26					
TRAPPC12	5.27194	0.585771	9	AGAP1	5.858976	0.234359	25					
TSPAN9	5.194926	0.577214	9	CAMTA1	3.003147	0.120126	25					
ADAMTS2	4.498595	0.499844	9	PDGFRA	2.160727	0.086429	25					
AXIN2	4.294901	0.477211	9	NCOR2	3.343412	0.145366	23					
CACNA2D4	3.895577	0.432842	9	RPTOR	3.27489	0.142387	23					
ASAP1	3.653458	0.40594	9	RIMBP2	2.615112	0.113701	23					
APBA2	3.36757	0.374174	9	HOXB3	1.836799	0.079861	23					
LINC00311	4.87739	0.609674	8	INPP5A	1.791248	0.07788	23					
DNMT3A	4.17539	0.521924	8	PRKCZ	4.651515	0.211433	22					
DLX5	3.590566	0.448821	8	SKI	4.121479	0.196261	21					
MSRA	3.448761	0.431095	8	SDK1	4.28274	0.214137	20					
ASPSR1	3.408459	0.426057	8	ABR	2.438093	0.121905	20					
NAV1	5.037875	0.719696	7	FRMD4A	2.286896	0.114345	20					
DUSP6	4.399055	0.628436	7	MAD1L1	10.02104	0.527423	19					
VPS13D	3.75286	0.536123	7	ZNF423	3.349011	0.176264	19					
LINC00461	3.67187	0.524553	7	CFAP46	2.950856	0.155308	19					
FBXL18	4.805531	0.800922	6	SMG1P2	2.053511	0.10808	19					
FAM181A	3.87676	0.646127	6	BOLA2	2.053511	0.10808	19					
RUNDC3A	5.224921	1.044984	5	LOC613038	2.053511	0.10808	19					
ARHGEF7	4.53184	0.906368	5	KCNQ1	1.872165	0.098535	19					
PRR5L	4.04784	0.809568	5	FOXK1	3.115821	0.173101	18					
TSNAX-DISC1	4.001967	0.800393	5	ANKRD11	2.45527	0.136404	18					
ASAP2	3.215839	0.643168	5	SEPTIN9	1.799112	0.099951	18					
DNAAF5	3.191462	0.638292	5	OPCML	3.581783	0.210693	17					
RBMS3	4.467137	1.116784	4	FOXP1	3.24319	0.202699	16					
STAP2	4.100788	1.025197	4	GLI2	6.248451	0.416563	15					
VOPPI	3.416731	0.854183	4	KNDC1	5.155305	0.343687	15					
DAGLB	3.791019	1.263673	3	BAIAP2	3.131474	0.208765	15					
GRIN2B	3.759161	1.253054	3	KIRREL3	2.629434	0.175296	15					
SOX10	4.869568	2.434784	2	LRMDA	1.991942	0.132796	15					
KIF21B	3.835147	1.917573	2	ZBTB20	1.813691	0.120913	15					
SLC25A10	3.765673	1.882836	2	RPS6KA2	6.042836	0.431631	14					
ANKLE2	3.723663	1.861831	2	IQSEC1	2.371576	0.169398	14					
CHTF18	3.366331	1.683166	2	CUX1	2.200599	0.157186	14					
TABLE 13:	Cancer Type CNS_SARC_DICER	imp_sum	imp_mean	n	MSI2	4.261561	0.327812	13				
					GSE1	2.42283	0.186372	13				
					RFX4	2.042377	0.157106	13				
					CLYBL	1.986742	0.152826	13				
					MYT1L	1.894854	0.145758	13				
					FBRSL1	2.967181	0.247265	12				
					MEGF6	2.13011	0.177509	12				
					ADGRD1	2.11279	0.176066	12				
					ZC3H3	2.061065	0.171755	12				
					MAML3	1.949386	0.162449	12				
					RASA3	1.929851	0.160821	12				
					COL4A1	2.574608	0.234055	11				
					Gene site							
					PTPRN2	11.53676	0.140692	82				
					PRDM16	6.861192	0.096637	71				
					HDAC4	8.635581	0.233394	37				
RBFOX3	5.971672	0.170619	35									
PAX6	3.621629	0.103475	35									
DIP2C	3.328282	0.104009	32									
SOX2-OT	2.161325	0.074528	29									
GALNT9	6.89057	0.255206	27									

ZC3H12D	1.892763	0.172069	11	PRDM16	17.72925	0.249708	71
ESR1	1.792318	0.162938	11	PCDHGA1	4.050169	0.068647	59
AKAP13	2.77468	0.277468	10	PCDHGA2	4.050169	0.071056	57
SH3RF3	2.737184	0.273718	10	PCDHGA3	3.749203	0.06943	54
TSPAN4	2.500322	0.250032	10	PCDHGB1	3.432817	0.06477	53
KLHL29	2.492991	0.249299	10	PCDHGA4	3.432817	0.06731	51
IGF1R	2.051063	0.205106	10	HDAC4	17.89076	0.483534	37
ACOT7	1.938008	0.193801	10	PAX6	7.824002	0.223543	35
SND1	2.848127	0.316459	9	RBFOX3	4.83382	0.138109	35
CACNA2D4	2.749816	0.305535	9	DIP2C	6.771467	0.211608	32
MGMT	2.501468	0.277941	9	SOX2-OT	8.34411	0.287728	29
KCNMA1	1.810327	0.201147	9	GALNT9	6.145555	0.227613	27
DLEU1	2.865375	0.358172	8	SHANK2	5.143475	0.197826	26
CRISPLD2	2.669829	0.333729	8	AGAP1	11.69691	0.467877	25
SYNJ2	2.371457	0.296432	8	PDGFRA	7.713638	0.308546	25
MACROD1	2.280948	0.285119	8	CAMTA1	7.140097	0.285604	25
TRAPPC9	2.117258	0.264657	8	SATB2	6.589201	0.27455	24
VRK2	2.064327	0.258041	8	RPTOR	12.02057	0.522634	23
AFF3	2.032248	0.254031	8	NXN	9.125426	0.396758	23
WWP2	2.029504	0.253688	8	INPP5A	7.926578	0.344634	23
CDH4	1.948911	0.243614	8	NCOR2	7.898032	0.343393	23
LINC00311	1.834155	0.229269	8	RIMBP2	5.93563	0.258071	23
CACHD1	1.801775	0.225222	8	PRKCZ	6.332177	0.287826	22
C19orf25	3.067579	0.438226	7	SKI	9.294558	0.442598	21
GAK	2.484219	0.354888	7	ZIC4	5.636609	0.26841	21
LINC01749	2.383224	0.340461	7	SDK1	6.150119	0.307506	20
FOXP4	1.929913	0.275702	7	FRMD4A	4.477427	0.223871	20
TRIM2	1.835568	0.262224	7	MAD1L1	11.13833	0.586228	19
FBXL18	3.350944	0.558491	6	ZNF423	6.304675	0.331825	19
ANKS1A	2.362196	0.393699	6	SMG1P2	4.879903	0.256837	19
STRA6	2.263036	0.377173	6	BOLA2	4.879903	0.256837	19
CRADD	2.148496	0.358083	6	LOC613038	4.879903	0.256837	19
RUNDC3A	4.048412	0.809682	5	CASZ1	4.189655	0.220508	19
BCAR1	2.566179	0.513236	5	KCNQ1	3.413829	0.179675	19
TSNAX-DISC1	2.53612	0.507224	5	FOKK1	6.901213	0.383401	18
VAV2	2.223338	0.444668	5	SEPTIN9	5.266403	0.292578	18
TK1	2.093538	0.418708	5	ANKRD11	3.946175	0.219232	18
ARHGEF7	2.014566	0.402913	5	PAX6-AS1	4.201016	0.247119	17
OLFM1	2.567071	0.641768	4	RCN1	4.201016	0.247119	17
DICER1	2.027828	0.675943	3	OPCML	3.583486	0.210793	17
KLHL26	1.803271	0.60109	3	HBG2	3.561709	0.209512	17
TBC1D7	1.799689	0.599896	3	EBF3	4.986091	0.311631	16
DISC1	2.624109	1.312055	2	SORBS2	4.218948	0.263684	16
RNF216	1.834681	0.917341	2	NAV2	4.216962	0.26356	16
				FOXP1	3.885851	0.242866	16
				SLX1B-			
				SULT1A4	4.717464	0.314498	15
				SLX1A	4.717464	0.314498	15
TABLE 14: Cancer Type CPC_A							
Gene site	imp_sum	imp_mean	n				
PTPRN2	16.00842	0.195225	82				

LOC606724	4.717464	0.314498	15	ARHGEF7	4.898215	0.979643	5
KIRREL3	4.545293	0.30302	15	RUNDC3A	4.211512	0.842302	5
LRMDA	4.192857	0.279524	15	NDRG4	3.330074	0.666015	5
GLI2	4.087578	0.272505	15	CHTF18	4.714201	2.3571	2
BAIAP2	3.473124	0.231542	15	TABLE 15: Cancer Type CPC_B			
IQSEC1	6.528853	0.466347	14				
MIR548F5	6.386218	0.456158	14	Gene site	imp_sum	imp_mean	n
RPS6KA2	5.41149	0.386535	14	PTPRN2	3.995573	0.048726	82
CUX1	5.263852	0.375989	14	PCDHGA1	4.32325	0.073275	59
C7orf50	4.43927	0.317091	14	PCDHGA2	4.32325	0.075846	57
ARHGEF10	4.314892	0.308207	14	PCDHGA3	4.006864	0.074201	54
PRKAG2	3.594082	0.25672	14	PCDHGB1	4.006864	0.075601	53
MSI2	5.326164	0.409705	13	PCDHGA4	4.006864	0.078566	51
RFX4	3.666617	0.282047	13	PCDHGB2	3.374092	0.068859	49
GSE1	3.615205	0.278093	13	PCDHGA5	3.374092	0.071789	47
GNA12	4.872908	0.406076	12	PCDHGB3	2.531088	0.058863	43
CMIP	4.719319	0.393277	12	PCDHGA6	2.531088	0.063277	40
ZC3H3	4.661378	0.388448	12	HDAC4	3.015967	0.081513	37
MAML3	4.122071	0.343506	12	PCDHGA7	2.531088	0.068408	37
TNS3	3.910643	0.325887	12	PCDHGB4	2.531088	0.072317	35
FBRSL1	3.519862	0.293322	12	PCDHGA8	2.531088	0.072317	35
CTBP2	4.266982	0.387907	11	RBFOX3	1.87321	0.05352	35
RAD51B	3.992868	0.362988	11	DIP2C	2.239472	0.069984	32
ANAPC16	3.804301	0.345846	11	PCDHGB5	1.898316	0.059322	32
VGLL4	3.651058	0.331914	11	PCDHGA9	1.898316	0.061236	31
NR5A2	4.686618	0.468662	10	PCDHGB6	1.58193	0.054549	29
AKAP13	4.170628	0.417063	10	PCDHGA10	1.58193	0.056498	28
NBEA	3.853657	0.385366	10	AGAP1	2.988213	0.119529	25
TSPAN4	3.472743	0.347274	10	CAMTA1	2.533234	0.101329	25
EBF1	3.38921	0.338921	10	RPTOR	3.283683	0.142769	23
ANKS1B	3.359524	0.335952	10	NXN	1.518958	0.066042	23
SND1	6.548215	0.727579	9	HOXB3	1.488788	0.06473	23
ADAMTS2	4.747935	0.527548	9	SIM2	1.812383	0.086304	21
TSPAN9	4.682856	0.520317	9	SKI	1.525215	0.072629	21
ATP11A	4.673193	0.519244	9	SDK1	1.998018	0.099901	20
TRAPPC12	3.411332	0.379037	9	MAD1L1	4.696756	0.247198	19
VRK2	6.497503	0.812188	8	SMG1P2	2.474409	0.130232	19
LINC00311	4.600767	0.575096	8	BOLA2	2.474409	0.130232	19
MSRA	4.151404	0.518926	8	LOC613038	2.474409	0.130232	19
SYNJ2	4.120538	0.515067	8	FO XK1	2.382865	0.132381	18
DLEU1	4.017219	0.502152	8	TBX15	2.255946	0.132703	17
MCIDAS	3.434927	0.429366	8	FOXP1	2.77394	0.173371	16
MIR548H4	4.040935	0.577276	7	SORBS2	1.712981	0.107061	16
NAV1	3.918137	0.559734	7	GLI2	1.673968	0.111598	15
RXRA	3.704701	0.529243	7	CUX1	3.02004	0.215717	14
GAK	3.380035	0.482862	7	C7orf50	1.96638	0.140456	14
CRADD	4.051051	0.675175	6	GSE1	2.337064	0.179774	13
ARHGAP18	3.476569	0.579428	6	MYT1L	2.080863	0.160066	13

MAML3	1.713439	0.142787	12	CAPG	1.412244	0.353061	4
ADGRD1	1.684387	0.140366	12	KCNIP1	1.712071	0.57069	3
CCDC140	2.964768	0.269524	11	DICER1	1.670578	0.556859	3
FGFR2	2.171443	0.197404	11	HOTTIP	1.55145	0.51715	3
RAD51B	1.737753	0.157978	11	SLC6A9	1.45193	0.483977	3
LBX1-AS1	2.690424	0.269042	10	BFSP2	1.441111	0.48037	3
TFAP2B	2.118207	0.211821	10	CHTF18	3.676269	1.838134	2
AKAP13	1.830847	0.183085	10	TRIM65	2.778116	1.389058	2
ACOT7	1.631082	0.163108	10	TSPAN14	1.626202	0.813101	2
WT1	1.593231	0.159323	10	SLC25A10	1.562957	0.781479	2
BCL11B	1.588108	0.158811	10	C6orf223	1.553416	1.553416	1
TSPAN4	1.538438	0.153844	10	TABLE 16: Cancer Type CPH_ADM			
SND1	3.245597	0.360622	9	Gene site	imp_sum	imp_mean	n
ZNF833P	3.156911	0.350768	9	PTPRN2	12.29209	0.149904	82
PAX3	2.274132	0.252681	9	PRDM16	11.69095	0.164661	71
ATP11A	2.166285	0.240698	9	PCDHGA1	4.493803	0.076166	59
KCNH2	2.02368	0.224853	9	PCDHGA2	4.177417	0.073288	57
CACNA2D4	1.837571	0.204175	9	PCDHGA3	3.544645	0.065642	54
TRAPPC12	1.681783	0.186865	9	PCDHGB1	3.544645	0.06688	53
TSPAN9	1.574946	0.174994	9	PCDHGA4	3.544645	0.069503	51
MSRA	2.697729	0.337216	8	HDAC4	14.58025	0.394061	37
MACROD1	2.641009	0.330126	8	RBFOX3	7.388665	0.211105	35
VRK2	2.342444	0.292806	8	PAX6	4.641956	0.132627	35
DNMT3A	2.147233	0.268404	8	DIP2C	8.478668	0.264958	32
SYNJ2	1.672535	0.209067	8	SOX2-OT	4.977386	0.171634	29
PPP2R2B	1.66247	0.207809	8	SHANK2	6.65119	0.255815	26
RORA	1.527647	0.190956	8	AGAP1	8.820289	0.352812	25
SHROOM3	1.407036	0.17588	8	CAMTA1	6.518146	0.260726	25
LINC00461	2.12156	0.30308	7	PDGFRA	4.49589	0.179836	25
HOTAIR	1.935889	0.276556	7	RPTOR	10.7314	0.466583	23
ITPK1	1.647546	0.235364	7	NCOR2	6.327405	0.275105	23
MIR548H4	1.469684	0.209955	7	NXN	5.500813	0.239166	23
RXRA	1.445779	0.20654	7	RIMBP2	4.098597	0.1782	23
PAX1	3.520315	0.586719	6	INPP5A	3.38079	0.146991	23
COLEC11	2.263679	0.37728	6	PRKCZ	5.020701	0.228214	22
SLC22A18AS	2.124858	0.354143	6	SKI	8.543431	0.40683	21
FBXL18	1.670225	0.278371	6	ABR	4.556746	0.227837	20
RUNDC3A	2.723196	0.544639	5	FRMD4A	4.506761	0.225338	20
TSNAX-DISC1	2.175881	0.435176	5	SDK1	3.860832	0.193042	20
CASP8	1.593029	0.318606	5	MAD1L1	14.50828	0.763594	19
MLC1	2.23873	0.559683	4	SMG1P2	5.448495	0.286763	19
GSG1	1.790305	0.447576	4	BOLA2	5.448495	0.286763	19
IGSF21	1.765871	0.441468	4	LOC613038	5.448495	0.286763	19
GRHL2	1.718594	0.429648	4	CASZ1	5.147721	0.270933	19
DTNA	1.632281	0.40807	4	ZNF423	4.71975	0.248408	19
FLJ12825	1.600283	0.400071	4	KCNQ1	3.549108	0.186795	19
TUBA1C	1.482734	0.370684	4	FO XK1	5.453911	0.302995	18
VOPPI	1.451522	0.36288	4				

SEPTIN9	4.703173	0.261287	18	C19orf25	4.178021	0.59686	7
TBC1D16	3.984165	0.221342	18	GAK	3.726453	0.53235	7
ANKRD11	3.756247	0.20868	18	VPS13D	3.699749	0.528536	7
OPCML	4.20818	0.24754	17	CRADD	3.663532	0.610589	6
HBG2	3.602584	0.211917	17	FBXL18	3.652621	0.60877	6
FOXP1	6.343187	0.396449	16	MYO16	3.51998	0.586663	6
NAV2	3.50163	0.218852	16	SLC22A18AS	3.508111	0.584685	6
GLI2	6.478656	0.43191	15	KDM4B	3.339818	0.556636	6
KIRREL3	4.649562	0.309971	15	RERE	3.31663	0.552772	6
NFIX	3.772506	0.2515	15	TSNAX-DISC1	4.961219	0.992244	5
BAIAP2	3.692668	0.246178	15	ARHGEF7	4.614511	0.922902	5
ZBTB20	3.549662	0.236644	15	RUNDC3A	4.443008	0.888602	5
RPS6KA2	7.461138	0.532938	14	NHSL1	3.883288	0.970822	4
IQSEC1	5.061474	0.361534	14	GSG1	3.562403	0.890601	4
CUX1	4.846724	0.346195	14	DAGLB	3.468613	1.156204	3
ARHGEF10	4.598722	0.32848	14	SLC25A10	3.744963	1.872481	2
C7orf50	3.766058	0.269004	14	ANKLE2	3.742803	1.871401	2
MOB2	3.730462	0.266462	14	CHTF18	3.59738	1.79869	2
MSI2	5.49049	0.422345	13	TABLE 17: Cancer Type CPH_PAP			
GSE1	4.094565	0.314967	13	Gene site	imp_sum	imp_mean	n
MYT1L	3.791384	0.291645	13	PTPRN2	15.76305	0.192232	82
RFX4	3.533487	0.271807	13	PRDM16	13.67823	0.192651	71
CMIP	5.387646	0.44897	12	PCDHGA1	5.703731	0.096673	59
ZC3H3	4.529418	0.377451	12	PCDHGA2	6.020117	0.105616	57
FBRSL1	4.508729	0.375727	12	PCDHGA3	5.703731	0.105625	54
GNA12	4.186371	0.348864	12	PCDHGB1	5.703731	0.107618	53
RASA3	3.47519	0.289599	12	PCDHGA4	5.387345	0.105634	51
VGLL4	4.800447	0.436404	11	PCDHGB2	5.387345	0.109946	49
TBCD	3.965128	0.360466	11	PCDHGA5	5.387345	0.114624	47
CTBP2	3.827094	0.347918	11	PCDHGB3	5.387345	0.125287	43
FGFR2	3.47253	0.315685	11	PCDHGA6	4.987145	0.124679	40
RAD51B	3.396735	0.308794	11	HDAC4	20.3413	0.549765	37
TSPAN4	3.432232	0.343223	10	PCDHGA7	4.54013	0.122706	37
KLHL29	3.36824	0.336824	10	PAX6	9.788933	0.279684	35
SND1	5.50511	0.611679	9	RBFOX3	5.926882	0.169339	35
ATP11A	5.258679	0.584298	9	PCDHGB4	4.54013	0.129718	35
TSPAN9	4.32151	0.480168	9	PCDHGA8	4.54013	0.129718	35
CACNA2D4	4.154955	0.461662	9	DIP2C	10.39729	0.324915	32
MGMT	3.560993	0.395666	9	PCDHGB5	4.54013	0.141879	32
AXIN2	3.380254	0.375584	9	PCDHGA9	4.54013	0.146456	31
NOTCH1	3.374999	0.375	9	SOX2-OT	6.276694	0.216438	29
LINC00311	5.384992	0.673124	8	PCDHGB6	4.093199	0.141145	29
VRK2	4.874748	0.609343	8	PCDHGA10	4.093199	0.146186	28
AFF3	3.800927	0.475116	8	SHANK2	6.600753	0.253875	26
DNMT3A	3.791412	0.473927	8	ADARB2	4.821925	0.185459	26
MSRA	3.519684	0.439961	8	AGAP1	12.15099	0.48604	25
NAV1	4.601684	0.657383	7	CAMTA1	7.096096	0.283844	25
MIR548H4	4.217779	0.60254	7				

PDGFRA	6.559998	0.2624	25	ZC3H3	5.118353	0.426529	12
RPTOR	13.67435	0.594537	23	RAD51B	5.26413	0.478557	11
NXN	8.651145	0.376137	23	TBCD	4.663455	0.42395	11
NCOR2	8.222368	0.357494	23	CTBP2	4.094029	0.372184	11
RIMBP2	4.835142	0.210224	23	CHST11	4.802943	0.480294	10
PRKCZ	5.785762	0.262989	22	AKAP13	4.651205	0.46512	10
SKI	7.781461	0.370546	21	ACOT7	4.501323	0.450132	10
FRMD4A	5.631758	0.281588	20	TSPAN4	4.229275	0.422928	10
SDK1	5.359402	0.26797	20	SND1	7.744689	0.860521	9
ABR	4.898258	0.244913	20	ATP11A	6.174457	0.686051	9
MAD1L1	12.41947	0.653656	19	TRAPPC12	5.034399	0.559378	9
ZNF423	5.52617	0.290851	19	ADAMTS2	4.879392	0.542155	9
SMG1P2	5.363616	0.282296	19	TSPAN9	4.564063	0.507118	9
BOLA2	5.363616	0.282296	19	LINC00311	5.309574	0.663697	8
LOC613038	5.363616	0.282296	19	MSRA	4.863272	0.607909	8
CASZ1	5.225511	0.275027	19	VRK2	4.291413	0.536427	8
KCNQ1	4.215948	0.221892	19	C19orf25	5.576676	0.796668	7
FO XK1	7.879019	0.437723	18	NAV1	4.89231	0.698901	7
TBC1D16	6.176091	0.343116	18	MIR548H4	4.148861	0.592694	7
MCF2L	5.990435	0.332802	18	STK10	4.361242	0.726874	6
PAX6-AS1	4.363491	0.256676	17	SLC22A18AS	4.298423	0.716404	6
RCN1	4.363491	0.256676	17	CRADD	4.076431	0.679405	6
OPCML	4.322223	0.254248	17	TSNAX-DISC1	5.131162	1.026232	5
FOXP1	7.606903	0.475431	16	KLHL25	4.900367	0.980073	5
NAV2	5.920485	0.37003	16	RUNDC3A	4.785457	0.957091	5
EBF3	4.823856	0.301491	16	NHSL1	4.953431	1.238358	4
SORBS2	4.427937	0.276746	16				
GLI2	6.928675	0.461912	15	TABLE 18: Cancer Type CPP_AD			
KIRREL3	5.898037	0.393202	15	Gene site	imp_sum	imp_mean	n
ZBTB20	5.401269	0.360085	15	PTPRN2	11.31281	0.137961	82
SLX1B-SULT1A4	4.904351	0.326957	15	PRDM16	13.74184	0.193547	71
SLX1A	4.904351	0.326957	15	PCDHGA1	3.610679	0.061198	59
LOC606724	4.904351	0.326957	15	PCDHGA2	3.294293	0.057795	57
BAIAP2	4.79365	0.319577	15	PCDHGA3	2.977907	0.055146	54
NFIX	4.373374	0.291558	15	PCDHGB1	2.977907	0.056187	53
RPS6KA2	6.634642	0.473903	14	PCDHGA4	2.977907	0.05839	51
C7orf50	6.268865	0.447776	14	PCDHGB2	2.977907	0.060774	49
CUX1	6.209467	0.443533	14	PCDHGA5	2.977907	0.06336	47
IQSEC1	5.122236	0.365874	14	PCDHGB3	3.294293	0.076611	43
PRKAG2	4.918648	0.351332	14	PCDHGA6	2.977907	0.074448	40
MSI2	7.371489	0.567038	13	HDAC4	12.8492	0.347276	37
MYT1L	4.530897	0.348531	13	PCDHGA7	2.977907	0.080484	37
GSE1	4.466342	0.343565	13	RBFOX3	5.853322	0.167238	35
RFX4	4.465521	0.343502	13	DIP2C	9.700563	0.303143	32
CMIP	7.333738	0.611145	12	SOX2-OT	3.208169	0.110627	29
FBRSL1	5.930377	0.494198	12	GALNT9	3.005051	0.111298	27
GNA12	5.617094	0.468091	12	SHANK2	5.434307	0.209012	26
				AGAP1	6.813914	0.272557	25

CAMTA1	3.302831	0.132113	25	VGLL4	3.177852	0.288896	11
MEIS1	5.0502	0.210425	24	FGFR2	3.173879	0.288534	11
RPTOR	11.01185	0.478776	23	TSPAN4	3.933783	0.393378	10
NXN	6.149227	0.267358	23	AKAP13	3.582406	0.358241	10
NCOR2	5.110155	0.222181	23	KLHL29	3.303085	0.330308	10
PRKCZ	5.866388	0.266654	22	AUTS2	2.990605	0.29906	10
SKI	10.44832	0.497539	21	SND1	6.386064	0.709563	9
ZIC4	3.92162	0.186744	21	ATP11A	4.668347	0.518705	9
FRMD4A	4.297019	0.214851	20	ADAMTS2	4.469375	0.496597	9
ABR	3.536087	0.176804	20	TSPAN9	4.339742	0.482194	9
MAD1L1	8.027724	0.422512	19	TRAPPC12	3.951345	0.439038	9
CASZ1	4.119798	0.216831	19	CACNA2D4	3.72499	0.413888	9
ZNF423	4.010193	0.211063	19	GPC6	3.711232	0.412359	9
SMG1P2	2.998275	0.157804	19	KCNH2	3.473724	0.385969	9
BOLA2	2.998275	0.157804	19	SSBP3	3.197893	0.355321	9
LOC613038	2.998275	0.157804	19	RUNX1	3.146465	0.349607	9
FOXK1	4.862215	0.270123	18	VRK2	4.205316	0.525664	8
TBC1D16	4.487671	0.249315	18	DLEU1	3.95583	0.494479	8
SEPTIN9	4.384937	0.243608	18	PPP2R2B	3.906005	0.488251	8
ANKRD11	3.167504	0.175972	18	MSRA	3.845906	0.480738	8
OPCML	5.13777	0.302222	17	NAV1	3.707811	0.529687	7
FOXP1	5.439543	0.339971	16	PITPNC1	3.328507	0.475501	7
EBF3	4.678157	0.292385	16	CXXC5	3.101939	0.443134	7
NAV2	4.315649	0.269728	16	LINC01140	3.012474	0.430353	7
SORBS2	3.006473	0.187905	16	SLC22A18AS	3.909045	0.651507	6
NFIX	4.173358	0.278224	15	CRADD	3.165654	0.527609	6
GLI2	3.837164	0.255811	15	RUNDC3A	4.433736	0.886747	5
BAIAP2	3.482668	0.232178	15	TSNAX-DISC1	3.732736	0.746547	5
KIRREL3	3.370273	0.224685	15	ARHGEF7	3.234689	0.646938	5
NFATC1	3.068066	0.204538	15	EXT1	3.532838	0.88321	4
RPS6KA2	5.846022	0.417573	14	CRB2	3.04556	0.76139	4
CUX1	4.552806	0.3252	14	KCNIP1	2.970068	0.990023	3
PRKAG2	4.5192	0.3228	14	TRIM65	3.537311	1.768656	2
MIR548F5	3.732932	0.266638	14	TABLE 19: Cancer Type CPP_INF			
TBX5	3.406149	0.243296	14	Gene site	imp_sum	imp_mean	n
C7orf50	3.159648	0.225689	14	PTPRN2	15.19001	0.185244	82
GNG7	3.099068	0.221362	14	PRDM16	14.43299	0.203282	71
MYT1L	3.688104	0.2837	13	PCDHGA1	3.724804	0.063132	59
GSE1	3.54579	0.272753	13	PCDHGA2	3.408418	0.059797	57
MSI2	3.162515	0.24327	13	PCDHGA3	3.092032	0.05726	54
CMIP	3.815283	0.31794	12	PCDHGB1	3.092032	0.05834	53
GNA12	3.335193	0.277933	12	PCDHGB2	3.092032	0.063103	49
TNS3	3.209968	0.267497	12	HDAC4	10.31392	0.278755	37
ADGRD1	3.129744	0.260812	12	RBFOX3	6.644166	0.189833	35
MIRLET7BHG	3.055175	0.254598	12	PAX6	3.977644	0.113647	35
ZC3H12D	3.93079	0.357345	11	DIP2C	5.98807	0.187127	32
RAD51B	3.279301	0.298118	11	SOX2-OT	4.371246	0.150733	29
SPON2	3.277534	0.297958	11				

GALNT9	4.601184	0.170414	27	MEGF6	3.341803	0.278484	12
SHANK2	4.820486	0.185403	26	TNS3	3.257131	0.271428	12
AGAP1	7.010968	0.280439	25	MAML3	2.939116	0.244926	12
CAMTA1	5.642138	0.225686	25	RAD51B	4.043203	0.367564	11
RPTOR	11.11451	0.48324	23	CTBP2	3.630376	0.330034	11
NXN	6.525128	0.283701	23	VGLL4	3.285303	0.298664	11
RIMBP2	4.030315	0.175231	23	TBCD	3.162087	0.287462	11
NCOR2	3.582323	0.155753	23	SPON2	3.057463	0.277951	11
PRKCZ	6.332197	0.287827	22	TSPAN4	4.814937	0.481494	10
SKI	7.47976	0.356179	21	AKAP13	3.798065	0.379806	10
ZIC4	4.477112	0.213196	21	ACOT7	3.29048	0.329048	10
SDK1	4.570761	0.228538	20	KLHL29	3.284723	0.328472	10
FRMD4A	3.647532	0.182377	20	AUTS2	2.927169	0.292717	10
ABR	3.602999	0.18015	20	SND1	6.036166	0.670685	9
MAD1L1	7.775015	0.409211	19	ATP11A	4.604429	0.511603	9
ZNF423	5.623971	0.295998	19	TSPAN9	3.7764	0.4196	9
SMG1P2	4.520349	0.237913	19	ADAMTS2	3.507534	0.389726	9
BOLA2	4.520349	0.237913	19	KCNH2	3.472232	0.385804	9
LOC613038	4.520349	0.237913	19	AXIN2	3.263217	0.36258	9
CASZ1	4.385646	0.230823	19	CACNA2D4	3.066299	0.3407	9
KCNQ1	3.410898	0.179521	19	NOTCH1	2.973379	0.330375	9
FOKK1	4.972638	0.276258	18	PPP2R2B	4.877357	0.60967	8
SEPTIN9	4.438428	0.246579	18	VRK2	4.873352	0.609169	8
OPCML	3.528898	0.207582	17	LINC00311	3.42386	0.427983	8
TBX15	3.24008	0.190593	17	GAK	3.4657	0.4951	7
NAV2	6.568887	0.410555	16	MIR548H4	3.216472	0.459496	7
FOXP1	5.218166	0.326135	16	RXRA	3.162505	0.451786	7
EBF3	3.681068	0.230067	16	NAV1	3.044468	0.434924	7
GLI2	5.955313	0.397021	15	PACRG	3.023698	0.431957	7
KIRREL3	3.935595	0.262373	15	SLC22A18AS	3.344646	0.557441	6
ZBTB20	3.197168	0.213145	15	COLEC11	2.917414	0.486236	6
BAIAP2	3.103791	0.206919	15	RUNDC3A	4.628337	0.925667	5
RPS6KA2	5.853346	0.418096	14	TSNAX-DISC1	3.530465	0.706093	5
CUX1	5.323808	0.380272	14	PRR5L	3.35567	0.671134	5
IQSEC1	3.75573	0.268266	14	ARHGEF7	3.14822	0.629644	5
PRKAG2	3.191906	0.227993	14	EXT1	3.444927	0.861232	4
C7orf50	3.078872	0.219919	14	DAGLB	3.089325	1.029775	3
CACNA1H	2.971891	0.212278	14	TRIM65	3.467956	1.733978	2
MSI2	5.777816	0.444447	13	SLC25A10	2.9975	1.49875	2
MYT1L	3.567409	0.274416	13	ANKLE2	2.970224	1.485112	2
RFX4	3.279066	0.252236	13	TABLE 20: Cancer Type CRINET			
SPTBN4	3.22895	0.248381	13				
GSE1	3.121687	0.24013	13	Gene site	imp_sum	imp_mean	n
KIF26B	2.894191	0.22263	13	PTPRN2	10.96688	0.133742	82
ADGRD1	4.78956	0.39913	12	PRDM16	3.231634	0.045516	71
ZC3H3	4.638332	0.386528	12	HDAC4	9.014051	0.243623	37
CMIP	3.69183	0.307652	12	RBFOX3	2.723093	0.077803	35
MIRLET7BHG	3.548295	0.295691	12	DIP2C	5.186759	0.162086	32

SOX2-OT	2.214702	0.076369	29	TSPAN4	2.775921	0.277592	10
SHANK2	3.170026	0.121924	26	ACOT7	2.749893	0.274989	10
AGAP1	6.532723	0.261309	25	SH3RF3	2.591023	0.259102	10
PDGFRA	2.020678	0.080827	25	RGS12	2.235544	0.223554	10
CAMTA1	1.94058	0.077623	25	ASIC2	1.994926	0.199493	10
MEIS1	2.337064	0.097378	24	ADAMTS2	3.822137	0.424682	9
RPTOR	5.3942	0.23453	23	SND1	3.643114	0.40479	9
NXN	3.022357	0.131407	23	KCNH2	3.47615	0.386239	9
PRKCZ	2.86389	0.130177	22	ATP11A	3.127011	0.347446	9
SKI	5.215756	0.248369	21	RUNX1	2.356786	0.261865	9
FRMD4A	3.17079	0.158539	20	TRAPPC12	2.069967	0.229996	9
ABR	2.662139	0.133107	20	CACNA2D4	2.067426	0.229714	9
MAD1L1	4.844803	0.25499	19	ASAP1	1.936216	0.215135	9
KCNQ1	2.893974	0.152314	19	DLEU1	3.183968	0.397996	8
SMG1P2	2.681757	0.141145	19	SYNJ2	2.551492	0.318936	8
BOLA2	2.681757	0.141145	19	LINC00311	2.02507	0.253134	8
LOC613038	2.681757	0.141145	19	MIR548H4	2.87209	0.410299	7
ZNF423	2.506076	0.131899	19	NAV1	2.631564	0.375938	7
CASZ1	2.414157	0.127061	19	VPS13D	2.378957	0.339851	7
RBFOX1	4.229047	0.234947	18	TRIM2	2.313096	0.330442	7
FO XK1	3.165101	0.175839	18	RXRA	2.205592	0.315085	7
MCF2L	2.018677	0.112149	18	CXXC5	2.127757	0.303965	7
SEPTIN9	1.986037	0.110335	18	FBXL18	3.631538	0.605256	6
OPCML	2.287588	0.134564	17	CRADD	2.401529	0.400255	6
FOXP1	2.606269	0.162892	16	ANKS1A	2.142732	0.357122	6
NAV2	2.149384	0.134336	16	FMNL2	1.920409	0.320068	6
GLI2	4.099938	0.273329	15	PRKCH	1.886246	0.314374	6
KIRREL3	3.891284	0.259419	15	RUNDC3A	3.235876	0.647175	5
ZBTB20	3.184826	0.212322	15	ARHGEF7	3.176019	0.635204	5
SLX1B-				ATXN7L1	2.714337	0.542867	5
SULT1A4	2.560456	0.170697	15	TSNAX-DISC1	2.582524	0.516505	5
SLX1A	2.560456	0.170697	15	BACH2	2.486198	0.49724	5
LOC606724	2.560456	0.170697	15	ATP2B4	2.417072	0.483414	5
BAIAP2	2.554968	0.170331	15	DNM3	2.151421	0.430284	5
LRMDA	2.029367	0.135291	15	RAPGEF4	2.05881	0.411762	5
RPS6KA2	4.199917	0.299994	14	TMEM132C	1.994235	0.398847	5
C7orf50	2.496931	0.178352	14	PRR5L	1.891281	0.378256	5
CUX1	2.305252	0.164661	14	NHSL1	3.397888	0.849472	4
IQSEC1	2.012079	0.14372	14	IGSF21	2.815659	0.703915	4
MYT1L	2.987968	0.229844	13	RBMS3	2.310324	0.577581	4
MSI2	2.073547	0.159504	13	DTNA	2.266953	0.566738	4
CMIP	4.596826	0.383069	12	SLC6A9	2.544667	0.848222	3
ADGRD1	2.993272	0.249439	12	SPATA13	2.438531	0.812844	3
ZC3H3	2.864994	0.23875	12	DICER1	2.094806	0.698269	3
FBRSL1	2.627979	0.218998	12	RALGAPA2	3.044181	1.52209	2
RAD51B	2.654735	0.24134	11	CACNA1D	2.116989	1.058494	2
CTBP2	2.1824	0.1984	11	SLC25A10	2.067739	1.033869	2
AKAP13	2.799577	0.279958	10	RUBCN	1.946876	1.946876	1

TABLE 21: Cancer Type DGONC

Gene site	imp_sum	imp_mean	n
PTPRN2	13.13503	0.160183	82
PRDM16	10.3477	0.145742	71
HDAC4	11.05626	0.298818	37
RBFOX3	8.461747	0.241764	35
PAX6	6.129446	0.175127	35
DIP2C	6.563504	0.205109	32
SOX2-OT	6.35483	0.219132	29
GALNT9	2.974276	0.110158	27
SHANK2	4.935714	0.189835	26
CAMTA1	6.542261	0.26169	25
AGAP1	6.192129	0.247685	25
PDGFRA	5.486155	0.219446	25
MEIS1	3.384971	0.14104	24
RPTOR	6.534565	0.284112	23
HOXB3	3.613134	0.157093	23
RIMBP2	3.415794	0.148513	23
NXN	2.923121	0.127092	23
PRKCZ	4.393011	0.199682	22
SKI	9.18904	0.437573	21
FRMD4A	5.480103	0.274005	20
ABR	3.264658	0.163233	20
MAD1L1	10.47917	0.551535	19
SMG1P2	7.187217	0.378275	19
BOLA2	7.187217	0.378275	19
LOC613038	7.187217	0.378275	19
ZNF423	7.024963	0.369735	19
CASZ1	4.495115	0.236585	19
ANKRD11	4.490421	0.249468	18
SEPTIN9	4.125948	0.229219	18
FOKK1	4.076412	0.226467	18
RBFOX1	3.121084	0.173394	18
OPCML	5.364502	0.315559	17
FOXP1	5.925927	0.37037	16
NAV2	3.796292	0.237268	16
GLI2	9.47517	0.631678	15
BAIAP2	3.763679	0.250912	15
ZBTB20	3.758867	0.250591	15
LRMDA	3.368728	0.224582	15
RPS6KA2	6.19269	0.442335	14
PRKAG2	3.71711	0.265508	14
C7orf50	3.299165	0.235655	14
IQSEC1	3.229465	0.230676	14
ARHGEF10	2.978949	0.212782	14
MSI2	4.797151	0.369012	13

MYT1L	3.091459	0.237805	13
CMIP	5.628687	0.469057	12
MEGF6	4.733266	0.394439	12
ZC3H3	4.539162	0.378264	12
MIRLET7BHG	4.231054	0.352588	12
FBRSL1	4.164398	0.347033	12
CTNNA2	3.999547	0.333296	12
TNS3	3.194033	0.266169	12
ADGRD1	3.077153	0.256429	12
RAD51B	4.43364	0.403058	11
VGLL4	3.615133	0.328648	11
CTBP2	3.204323	0.291302	11
FGFR2	2.960961	0.269178	11
ACOT7	4.589562	0.458956	10
ATP11A	6.140285	0.682254	9
SND1	5.557866	0.617541	9
ASAP1	4.317153	0.479684	9
AXIN2	4.179311	0.464368	9
ADGRB1	3.586638	0.398515	9
ADAMTS2	3.585293	0.398366	9
TSPAN9	3.570083	0.396676	9
TRAPPC12	3.478144	0.38646	9
PACS2	3.445642	0.382849	9
RUNX1	3.322449	0.369161	9
CACNA2D4	3.235785	0.359532	9
LINC00311	4.871942	0.608993	8
GRIK2	3.741669	0.467709	8
MSRA	3.510317	0.43879	8
RORA	3.03757	0.379696	8
DLEU1	3.024723	0.37809	8
NAV1	4.171854	0.595979	7
LINC00461	3.869468	0.552781	7
DUSP6	3.7407	0.534386	7
LINC01140	3.17112	0.453017	7
CXXC5	3.156982	0.450997	7
FBXL18	4.736061	0.789343	6
KDM4B	3.908086	0.651348	6
MYO16	3.643539	0.607256	6
CRADD	3.620798	0.603466	6
FAM181A	3.100463	0.516744	6
COQ8A	2.955684	0.492614	6
FMNL2	2.906814	0.484469	6
RUNDC3A	4.876724	0.975345	5
TSNAX-DISC1	3.841281	0.768256	5
ARHGEF7	3.637038	0.727408	5
SLC8A2	3.142738	0.628548	5
TEAD1	3.001606	0.600321	5
RBMS3	4.49997	1.124992	4

STAP2	3.308779	0.827195	4	SLX1B-			
GRIN2B	3.874143	1.291381	3	SULT1A4	2.486581	0.165772	15
SRRM3	3.759727	1.253242	3	SLX1A	2.486581	0.165772	15
TTC12	3.117951	1.039317	3	LOC606724	2.486581	0.165772	15
DAGLB	2.897008	0.965669	3	CUX1	3.773402	0.269529	14
SOX10	4.815607	2.407804	2	IQSEC1	3.532998	0.252357	14
SLC25A10	3.451075	1.725538	2	RPS6KA2	3.149474	0.224962	14
ANKLE2	3.363035	1.681517	2	ARHGEF10	2.925318	0.208951	14
TABLE 22: Cancer Type DLBCL				PPP2R2A	2.730323	0.195023	14
				TBX5	2.275259	0.162518	14
Gene site	imp_sum	imp_mean	n	SYCP2L	2.187062	0.156219	14
PTPRN2	7.35736	0.089724	82	RFX4	3.210626	0.246971	13
PRDM16	5.048598	0.071107	71	MSI2	2.979907	0.229224	13
PCDHGA1	2.529679	0.042876	59	HOXA10-			
PCDHGA2	2.529679	0.04438	57	HOXA9	2.337064	0.179774	13
PCDHGA3	2.529679	0.046846	54	CMIP	4.129253	0.344104	12
PCDHGB1	2.529679	0.04773	53	FBRSL1	3.906961	0.32558	12
PCDHGA4	2.213293	0.043398	51	CTNNA2	3.079083	0.25659	12
HDAC4	10.21894	0.276188	37	ISLR2	2.956629	0.246386	12
PAX6	6.266407	0.17904	35	ZC3H3	2.838728	0.236561	12
RBFOX3	3.511339	0.100324	35	GNA12	2.558761	0.21323	12
DIP2C	3.718857	0.116214	32	ADGRD1	2.332938	0.194411	12
SOX2-OT	4.25213	0.146625	29	MAML3	2.121208	0.176767	12
SHANK2	2.849971	0.109614	26	ZC3H12D	3.371605	0.30651	11
AGAP1	4.49937	0.179975	25	RAD51B	3.168855	0.288078	11
PDGFRA	2.749791	0.109992	25	GLUD1P2	2.92937	0.266306	11
SATB2	3.286222	0.136926	24	VGLL4	2.276061	0.206915	11
MEIS1	3.073452	0.128061	24	ACOT7	4.342496	0.43425	10
INPP5A	2.628684	0.114291	23	SKOR1	2.667111	0.266711	10
NCOR2	2.577036	0.112045	23	AKAP13	2.526244	0.252624	10
SKI	5.349457	0.254736	21	JUP	2.2755	0.22755	10
HOXA-AS3	3.448386	0.164209	21	NR2F1-AS1	2.098752	0.209875	10
SIM2	2.978525	0.141835	21	ATP11A	4.725982	0.525109	9
SDK1	2.685795	0.13429	20	SND1	3.979144	0.442127	9
ABR	2.520912	0.126046	20	ADAMTS2	3.896946	0.432994	9
MAD1L1	7.437988	0.391473	19	MGMT	2.34924	0.261027	9
ZNF423	3.677587	0.193557	19	RUNX1	2.314993	0.257221	9
CASZ1	3.599919	0.189469	19	VAX1	2.125157	0.236129	9
SMG1P2	2.65989	0.139994	19	LHX4	3.689458	0.461182	8
BOLA2	2.65989	0.139994	19	MSRA	3.232702	0.404088	8
LOC613038	2.65989	0.139994	19	LMX1B	2.456416	0.307052	8
SEPTIN9	3.787837	0.210435	18	TRAPPC9	2.186304	0.273288	8
FO XK1	3.702087	0.205671	18	CXXC5	3.199163	0.457023	7
TBC1D16	2.563787	0.142433	18	WWOX	2.715789	0.38797	7
HOXA3	2.37731	0.132073	18	ITPK1	2.388983	0.341283	7
TBX15	2.44435	0.143785	17	IQCE	2.341671	0.334524	7
EBF3	4.650985	0.290687	16	LINC01140	2.282949	0.326136	7
FOXP1	2.433564	0.152098	16	LDLRAD4	2.247761	0.321109	7

VPS13D	2.207715	0.315388	7	SKI	8.889427	0.423306	21
CLDN10	2.124797	0.303542	7	FRMD4A	5.673992	0.2837	20
FBXL18	3.068542	0.511424	6	ABR	4.382257	0.219113	20
FMNL2	2.730825	0.455137	6	MAD1L1	8.172234	0.430118	19
LRRFIP1	2.390845	0.398474	6	ZNF423	7.770215	0.408959	19
MIR548G	2.275784	0.379297	6	SMG1P2	4.301612	0.226401	19
LYPD1	2.127456	0.354576	6	BOLA2	4.301612	0.226401	19
ARHGEF7	3.512343	0.702469	5	LOC613038	4.301612	0.226401	19
CCR6	2.624993	0.524999	5	FOXK1	5.49026	0.305014	18
AP2A2	2.257238	0.451448	5	ANKRD11	4.019946	0.22333	18
NHSL1	2.697164	0.674291	4	MCF2L	3.058393	0.169911	18
SPTBN1	2.676614	0.669154	4	OPCML	6.360814	0.374166	17
DTNA	2.447217	0.611804	4	NAV2	3.273524	0.204595	16
TBC1D7	2.617603	0.872534	3	GLI2	9.264765	0.617651	15
DICER1	2.396974	0.798991	3	BAIAP2	4.361371	0.290758	15
CDC42BPB	2.22176	0.740587	3	EMX2OS	2.952614	0.196841	15
DAGLB	2.118044	0.706015	3	CACNA1H	3.460287	0.247163	14
TABLE 23: Cancer Type DLGNT_1				C7orf50	3.304953	0.236068	14
				RPS6KA2	3.05343	0.218102	14
Gene site	imp_sum	imp_mean	n	CUX1	2.937762	0.20984	14
PTPRN2	17.73156	0.216239	82	MSI2	4.465639	0.343511	13
PRDM16	8.961345	0.126216	71	GSE1	3.69265	0.28405	13
PCDHGA1	3.540457	0.060008	59	KIF26B	3.240362	0.249259	13
PCDHGA2	3.540457	0.062113	57	MYT1L	2.91326	0.224097	13
PCDHGA3	3.115981	0.057703	54	CMIP	5.886653	0.490554	12
PCDHGB1	3.115981	0.058792	53	ZC3H3	3.878974	0.323248	12
PCDHGA4	3.432367	0.067301	51	MIRLET7BHG	3.866699	0.322225	12
PCDHGB2	3.432367	0.070048	49	ADGRD1	3.850417	0.320868	12
PCDHGA5	3.432367	0.073029	47	MAML3	3.735777	0.311315	12
HDAC4	10.20179	0.275724	37	FGFR2	4.667649	0.424332	11
PAX6	7.077885	0.202225	35	RAD51B	4.545562	0.413233	11
RBFOX3	4.135104	0.118146	35	GLUD1P2	3.061923	0.278357	11
DIP2C	7.384183	0.230756	32	ZC3H12D	3.043476	0.27668	11
SOX2-OT	6.020509	0.207604	29	AKAP13	4.186819	0.418682	10
GALNT9	3.126337	0.11579	27	KLHL29	4.089224	0.408922	10
ADARB2	4.454864	0.171341	26	TSPAN4	3.372985	0.337299	10
SHANK2	3.51474	0.135182	26	GRID1	3.178463	0.317846	10
AGAP1	8.824816	0.352993	25	SND1	5.409044	0.601005	9
PDGFRA	4.565095	0.182604	25	ATP11A	4.057139	0.450793	9
CAMTA1	3.907532	0.156301	25	TRAPPC12	3.789579	0.421064	9
MEIS1	6.510303	0.271263	24	ASAP1	3.622777	0.402531	9
SATB2	4.395429	0.183143	24	TSPAN9	3.493469	0.388163	9
HOXB3	10.90119	0.473965	23	AXIN2	3.097557	0.344173	9
RPTOR	7.373151	0.320572	23	PACS2	2.99983	0.333314	9
NCOR2	5.682337	0.247058	23	ADGRB1	2.994008	0.332668	9
INPP5A	4.658587	0.202547	23	SLC22A18	2.950168	0.327796	9
NXN	4.158511	0.180805	23	SSBP3	2.93931	0.32659	9
RIMBP2	3.499651	0.152159	23	NOTCH1	2.92436	0.324929	9

ADAMTS2	2.919976	0.324442	9	AGAP1	6.999717	0.279989	25
LINC00311	4.667601	0.58345	8	PDGFRA	4.465416	0.178617	25
GRIK2	3.593081	0.449135	8	SATB2	5.084407	0.21185	24
MSRA	3.52281	0.440351	8	MEIS1	3.433495	0.143062	24
DPP6	2.871326	0.358916	8	NXN	4.316404	0.18767	23
DUSP6	5.050046	0.721435	7	RPTOR	3.892675	0.169247	23
LINC00461	4.063855	0.580551	7	PRKCZ	3.490803	0.158673	22
NAV1	3.68482	0.526403	7	SKI	5.236229	0.249344	21
HOXB-AS3	3.328612	0.475516	7	FRMD4A	4.39425	0.219713	20
FHIT	3.055776	0.436539	7	ABR	2.5481	0.127405	20
C19orf25	2.863584	0.409083	7	MAD1L1	6.792536	0.357502	19
FAM181A	3.778152	0.629692	6	CASZ1	3.666051	0.19295	19
COQ8A	3.077893	0.512982	6	SMG1P2	3.356343	0.17665	19
CRADD	2.969012	0.494835	6	BOLA2	3.356343	0.17665	19
RUNDC3A	4.806159	0.961232	5	LOC613038	3.356343	0.17665	19
ARHGEF7	3.251554	0.650311	5	ZNF423	2.657667	0.139877	19
PRR5L	3.176393	0.635279	5	ANKRD11	4.535455	0.25197	18
TSNAX-DISC1	2.850348	0.57007	5	MCF2L	4.054608	0.225256	18
RBMS3	3.900037	0.975009	4	FOXK1	3.405545	0.189197	18
CRB2	3.186812	0.796703	4	OPCML	5.077194	0.298658	17
LINC00856	3.068772	0.767193	4	FOXP1	4.235477	0.264717	16
GRIN2B	3.258367	1.086122	3	SORBS2	2.589215	0.161826	16
LOXL3	2.79616	0.932053	3	GLI2	4.691495	0.312766	15
SOX10	4.490155	2.245078	2	RPS6KA2	3.790283	0.270734	14
TABLE 24: Cancer Type DLGNT_2				CUX1	2.480754	0.177197	14
				IQSEC1	2.470793	0.176485	14
Gene site	imp_sum	imp_mean	n	MSI2	3.922805	0.301754	13
PTPRN2	7.060492	0.086104	82	MYT1L	3.569878	0.274606	13
PRDM16	6.311401	0.088893	71	MIR9-3HG	2.559278	0.196868	13
PCDHGA1	4.401863	0.074608	59	KIF26B	2.340501	0.180039	13
PCDHGA2	4.401863	0.077226	57	GSE1	2.253312	0.173332	13
PCDHGA3	5.097912	0.094406	54	ADGRD1	3.133694	0.261141	12
PCDHGB1	5.097912	0.096187	53	FBRSL1	2.796324	0.233027	12
PCDHGA4	5.414298	0.106163	51	CMIP	2.782287	0.231857	12
PCDHGB2	5.414298	0.110496	49	TNS3	2.531411	0.210951	12
PCDHGA5	5.414298	0.115198	47	MIRLET7BHG	2.453634	0.20447	12
PCDHGB3	4.336825	0.100856	43	RAD51B	2.998745	0.272613	11
PCDHGA6	3.279577	0.081989	40	SLC9A3	2.70451	0.245865	11
HDAC4	5.169197	0.139708	37	SPON2	2.249612	0.20451	11
PCDHGA7	2.431053	0.065704	37	LBX1-AS1	3.804831	0.380483	10
PAX6	6.464383	0.184697	35	GRID1	3.744038	0.374404	10
PCDHGB4	2.431053	0.069459	35	AKAP13	3.081928	0.308193	10
PCDHGA8	2.431053	0.069459	35	ACOT7	2.348144	0.234814	10
RBFOX3	2.376116	0.067889	35	SH3RF3	2.321484	0.232148	10
DIP2C	5.085695	0.158928	32	NR2F1-AS1	2.227467	0.222747	10
SOX2-OT	3.01975	0.104129	29	SND1	4.69145	0.521272	9
GALNT9	3.107066	0.115077	27	ATP11A	4.206191	0.467355	9
SHANK2	3.110309	0.119627	26	NOTCH1	3.06654	0.340727	9

ASAP1	2.962156	0.329128	9	RBFOX3	4.758746	0.135964	35
TSPAN9	2.632807	0.292534	9	PCDHGB4	4.085106	0.116717	35
ADAMTS2	2.358105	0.262012	9	PCDHGA8	4.085106	0.116717	35
KCNMA1	2.311715	0.256857	9	DIP2C	4.051875	0.126621	32
CACNA2D4	2.278375	0.253153	9	PCDHGB5	3.76872	0.117772	32
MSRA	3.321819	0.415227	8	PCDHGA9	3.452334	0.111366	31
ESRRG	2.820181	0.352523	8	SOX2-OT	6.608075	0.227865	29
HMG2	2.564935	0.320617	8	GALNT9	3.416686	0.126544	27
LINC00311	2.477684	0.309711	8	ADARB2	6.029704	0.231912	26
DUSP6	3.322224	0.474603	7	SHANK2	5.422076	0.208541	26
NAV1	3.275629	0.467947	7	AGAP1	6.047859	0.241914	25
CDYL	2.77406	0.396294	7	CAMTA1	5.252322	0.210093	25
TACC2	2.509948	0.358564	7	PDGFRA	4.033234	0.161329	25
VPS13D	2.346989	0.335284	7	SATB2	8.554768	0.356449	24
TOX2	2.226045	0.318006	7	MEIS1	3.819655	0.159152	24
FAM181A	2.772031	0.462005	6	RPTOR	8.828935	0.383867	23
SLC22A18AS	2.612686	0.435448	6	INPP5A	5.385072	0.234134	23
FMNL2	2.316991	0.386165	6	NCOR2	5.028779	0.218643	23
WFIKN2	2.263369	0.377228	6	NXN	3.427883	0.149038	23
RUNDC3A	3.855633	0.771127	5	SKI	5.322244	0.25344	21
TSNAX-DISC1	3.171449	0.63429	5	FRMD4A	3.658609	0.18293	20
ARHGEF7	2.9695	0.5939	5	ABR	3.419208	0.17096	20
STARD13	2.39862	0.479724	5	MAD1L1	8.348755	0.439408	19
RBMS3	2.645573	0.661393	4	CASZ1	5.312578	0.279609	19
LINC00856	2.427806	0.606951	4	ZNF423	4.896747	0.257724	19
VOPPI	2.323359	0.58084	4	SMG1P2	4.675455	0.246077	19
GRIN2B	3.269344	1.089781	3	BOLA2	4.675455	0.246077	19
DICER1	2.681425	0.893808	3	LOC613038	4.675455	0.246077	19
TTC12	2.289017	0.763006	3	KCNQ1	3.153024	0.165949	19
SOX10	4.151197	2.075598	2	FOXK1	7.009082	0.389393	18
SLC25A10	2.504357	1.252178	2	SEPTIN9	4.708469	0.261582	18
TABLE 25: Cancer Type DMG_EGFR				OPCML	4.150794	0.244164	17
				PAX6-AS1	3.578693	0.210511	17
Gene site	imp_sum	imp_mean	n	RCN1	3.578693	0.210511	17
PTPRN2	15.85834	0.193394	82	FOXP1	4.90985	0.306866	16
PRDM16	12.21921	0.172102	71	GLI2	9.248652	0.616577	15
PCDHGA1	6.245608	0.105858	59	ZBTB20	3.101754	0.206784	15
PCDHGA2	6.561994	0.115123	57	CUX1	3.980969	0.284355	14
PCDHGA3	5.929222	0.1098	54	RPS6KA2	3.593044	0.256646	14
PCDHGB1	5.929222	0.111872	53	SYCP2L	3.104278	0.221734	14
PCDHGA4	5.612836	0.110056	51	MSI2	4.747729	0.36521	13
PCDHGB2	5.612836	0.114548	49	RFX4	4.046308	0.311254	13
PCDHGA5	5.29645	0.11269	47	MYT1L	3.388034	0.260618	13
PCDHGB3	4.663678	0.108458	43	GSE1	3.351157	0.257781	13
PCDHGA6	4.085106	0.102128	40	CLYBL	3.188773	0.24529	13
HDAC4	9.855461	0.266364	37	ISLR2	4.716973	0.393081	12
PCDHGA7	4.085106	0.110408	37	TNS3	4.219632	0.351636	12
PAX6	8.05116	0.230033	35	CMIP	3.56734	0.297278	12

ZC3H3	3.444859	0.287072	12	PCDHGB2	4.143029	0.084552	49
ADGRD1	3.195367	0.266281	12	PCDHGA5	4.065802	0.086506	47
ZC3H12D	4.377418	0.397947	11	HDAC4	10.96991	0.296484	37
VGLL4	3.693413	0.335765	11	PAX6	10.49824	0.29995	35
ACOT7	4.221232	0.422123	10	RBFOX3	9.787693	0.279648	35
NR2F1-AS1	3.314474	0.331447	10	PCDHGB4	4.075303	0.116437	35
GAS7	3.254024	0.325402	10	PCDHGA8	4.075303	0.116437	35
IGF1R	3.193725	0.319373	10	DIP2C	8.807282	0.275228	32
SH3RF3	3.144937	0.314494	10	SOX2-OT	9.756366	0.336426	29
OTX1	3.111864	0.311186	10	GALNT9	5.452091	0.201929	27
NTM	3.077721	0.307772	10	SHANK2	7.383968	0.283999	26
ATP11A	5.154603	0.572734	9	ADARB2	6.762464	0.260095	26
SND1	4.57076	0.507862	9	AGAP1	8.206947	0.328278	25
TSPAN9	4.039484	0.448832	9	PDGFRA	8.082227	0.323289	25
GPC6	3.707782	0.411976	9	CAMTA1	6.751014	0.270041	25
ADAMTS2	3.279404	0.364378	9	SATB2	8.80167	0.366736	24
APBA2	3.119427	0.346603	9	MEIS1	6.106283	0.254428	24
ASAP1	3.082338	0.342482	9	RPTOR	10.21494	0.444128	23
ESRRG	4.257093	0.532137	8	INPP5A	5.743264	0.249707	23
DLEU1	3.977631	0.497204	8	RIMBP2	4.992673	0.217073	23
LINC00311	3.497257	0.437157	8	PRKCZ	5.61555	0.255252	22
SHROOM3	3.441927	0.430241	8	SKI	8.819106	0.419957	21
CACHD1	3.393871	0.424234	8	SIM2	5.705069	0.27167	21
NR2E1	3.173751	0.396719	8	FRMD4A	6.527279	0.326364	20
LRRC61	3.162027	0.395253	8	ABR	5.269892	0.263495	20
MBP	3.081164	0.385145	8	SDK1	3.978181	0.198909	20
RBM20	5.516208	0.78803	7	MAD1L1	11.64079	0.612673	19
DUSP6	4.582044	0.654578	7	ZNF423	8.071874	0.424835	19
CDYL	4.232254	0.604608	7	SMG1P2	6.846055	0.360319	19
SATB2-AS1	4.553871	0.758978	6	BOLA2	6.846055	0.360319	19
LYPD1	3.684283	0.614047	6	LOC613038	6.846055	0.360319	19
FAM181A	3.570674	0.595112	6	CASZ1	6.291507	0.331132	19
FBXL18	3.354561	0.559094	6	KCNQ1	4.355987	0.229262	19
ARHGEF7	3.328795	0.665759	5	MCF2L	5.979139	0.332174	18
TSNAX-DISC1	3.270572	0.654114	5	FO XK1	5.014289	0.278572	18
SOX10	3.962391	1.981196	2	SEPTIN9	4.42487	0.245826	18
SLC25A10	3.492986	1.746493	2	OPCML	6.324302	0.372018	17
PITX3	3.419494	1.709747	2	FOXP1	6.538128	0.408633	16
TABLE 26: Cancer Type DMG_K27				SORBS2	4.894695	0.305918	16
				NAV2	4.071884	0.254493	16
				GLI2	9.212083	0.614139	15
				BAIAP2	6.044562	0.402971	15
				ZBTB20	5.38983	0.359322	15
				LRMDA	4.689959	0.312664	15
				SLX1B-			
				SULT1A4	4.034964	0.268998	15
				SLX1A	4.034964	0.268998	15
				LOC606724	4.034964	0.268998	15
Gene site	imp_sum	imp_mean	n				
PTPRN2	27.0199	0.329511	82				
PRDM16	16.37316	0.230608	71				
PCDHGA1	5.539625	0.093892	59				
PCDHGA2	5.223239	0.091636	57				
PCDHGA3	4.143029	0.076723	54				
PCDHGB1	4.143029	0.07817	53				
PCDHGA4	4.143029	0.081236	51				

RPS6KA2	7.032418	0.502316	14
PRKAG2	5.203722	0.371694	14
CACNA1H	4.995215	0.356801	14
CUX1	4.433446	0.316675	14
ARHGEF10	4.264465	0.304605	14
MSI2	6.463358	0.497181	13
MYT1L	5.756885	0.442837	13
GSE1	4.627927	0.355994	13
MIRLET7BHG	4.998906	0.416576	12
CMIP	4.933786	0.411149	12
ZC3H3	4.313245	0.359437	12
FBRSL1	4.041739	0.336812	12
ZC3H12D	6.425285	0.584117	11
VGLL4	5.302111	0.48201	11
GLUD1P2	5.213483	0.473953	11
RAD51B	4.828441	0.438949	11
LBX1-AS1	6.635166	0.663517	10
TFAP2A	6.403444	0.640344	10
NTM	4.444618	0.444462	10
ACOT7	4.423884	0.442388	10
ATP11A	6.416854	0.712984	9
SND1	5.460144	0.606683	9
ADGRB1	5.015126	0.557236	9
TSPAN9	4.762758	0.529195	9
TRAPPC12	4.673668	0.519296	9
ASAP1	4.649147	0.516572	9
ADAMTS2	4.59228	0.510253	9
AXIN2	4.006386	0.445154	9
LINC00311	4.851372	0.606421	8
GRIK2	4.699392	0.587424	8
MSRA	4.565799	0.570725	8
ESRRG	4.179633	0.522454	8
NXPH1	3.939175	0.492397	8
RBM20	4.642311	0.663187	7
LINC00461	4.476811	0.639544	7
SOX6	4.441231	0.634462	7
DUSP6	4.180105	0.597158	7
FBXL18	4.11915	0.686525	6
RUNDC3A	5.093146	1.018629	5
TSNAX-DISC1	4.796075	0.959215	5
HHEX	4.600647	0.920129	5
LOC100132215	4.562513	0.912503	5
STAP2	4.697057	1.174264	4
RBMS3	4.522479	1.13062	4
GRIN2B	4.179322	1.393107	3
SOX10	5.183544	2.591772	2

TABLE 27:

Cancer Type

DMT_SMARCB1

Gene site	imp_sum	imp_mean	n
PTPRN2	5.17006	0.06305	82
PRDM16	6.362014	0.089606	71
PCDHGA1	5.844879	0.099066	59
PCDHGA2	5.528493	0.096991	57
PCDHGA3	5.528493	0.102379	54
PCDHGB1	5.528493	0.104311	53
PCDHGA4	5.528493	0.108402	51
PCDHGB2	5.844879	0.119283	49
PCDHGA5	5.528493	0.117628	47
PCDHGB3	5.528493	0.12857	43
PCDHGA6	4.773358	0.119334	40
HDAC4	12.66161	0.342206	37
PCDHGA7	5.089744	0.137561	37
PCDHGB4	5.089744	0.145421	35
PCDHGA8	5.089744	0.145421	35
PAX6	4.859457	0.138842	35
DIP2C	7.547304	0.235853	32
PCDHGB5	4.327758	0.135242	32
PCDHGA9	4.327758	0.139605	31
PCDHGB6	4.011372	0.138323	29
SOX2-OT	3.122386	0.107668	29
PCDHGA10	4.011372	0.143263	28
SHANK2	2.884832	0.110955	26
AGAP1	9.038532	0.361541	25
CAMTA1	4.948669	0.197947	25
PDGFRA	2.775512	0.111102	25
PCDHGB7	3.694986	0.153958	24
RPTOR	7.462939	0.324476	23
NCOR2	4.665983	0.202869	23
INPP5A	4.39195	0.190954	23
PCDHGA11	3.694986	0.160652	23
NXN	2.795014	0.121522	23
SKI	7.436983	0.354142	21
FRMD4A	3.768225	0.188411	20
SDK1	2.96255	0.148127	20
ABR	2.65345	0.132673	20
MAD1L1	6.562907	0.345416	19
ZNF423	4.355779	0.229252	19
CASZ1	3.440739	0.181092	19
KCNQ1	3.203313	0.168595	19
SMG1P2	2.831309	0.149016	19
BOLA2	2.831309	0.149016	19
LOC613038	2.831309	0.149016	19
FOXK1	7.395893	0.410883	18
TBC1D16	3.543282	0.196849	18

SEPTIN9	2.916372	0.162021	18	ATXN7L1	3.259591	0.651918	5
ANKRD11	2.809903	0.156106	18	BCAR1	2.875345	0.575069	5
EBF3	3.501225	0.218827	16	NPHP4	2.611543	0.522309	5
BAIAP2	3.977481	0.265165	15	NHSL1	3.377846	0.844462	4
GLI2	3.757937	0.250529	15	ABAT	3.052387	0.763097	4
KIRREL3	2.516101	0.16774	15	SPATA13	2.604406	0.868135	3
RPS6KA2	4.560523	0.325752	14	RALGAPA2	4.200075	2.100037	2
CUX1	3.824346	0.273168	14				
IQSEC1	3.614146	0.258153	14	TABLE 28:	Cancer Type DNET		
ARHGEF10	3.410766	0.243626	14	Gene site	imp_sum	imp_mean	n
PCDHGA12	3.3786	0.241329	14	PTPRN2	26.04532	0.317626	82
PRKAG2	2.733286	0.195235	14	PRDM16	17.79369	0.250615	71
MSI2	2.809603	0.216123	13	PCDHGA1	6.699804	0.113556	59
CMIP	4.493421	0.374452	12	PCDHGA2	6.383418	0.11199	57
ZC3H3	3.334721	0.277893	12	PCDHGA3	7.332576	0.135788	54
FBRSL1	3.011552	0.250963	12	PCDHGB1	7.332576	0.13835	53
GNA12	2.547348	0.212279	12	PCDHGA4	7.648962	0.14998	51
RAD51B	3.828061	0.348006	11	PCDHGB2	7.648962	0.156101	49
FGFR2	3.088996	0.280818	11	PCDHGA5	7.01619	0.149281	47
PCDHGC3	2.604336	0.236758	11	PCDHGB3	6.699804	0.155809	43
TSPAN4	3.397272	0.339727	10	PCDHGA6	6.075185	0.15188	40
CHST11	3.113301	0.31133	10	HDAC4	14.4597	0.390803	37
FMN1	2.877649	0.287765	10	PCDHGA7	5.710249	0.154331	37
MAML2	2.793081	0.279308	10	PAX6	10.60999	0.303143	35
AKAP13	2.737725	0.273772	10	RBFOX3	10.5905	0.302586	35
ATP11A	5.858672	0.650964	9	PCDHGB4	5.435549	0.155301	35
SND1	5.645283	0.627254	9	PCDHGA8	5.435549	0.155301	35
TRAPPC12	3.39871	0.377634	9	DIP2C	12.4335	0.388547	32
MGMT	3.231188	0.359021	9	SOX2-OT	13.19713	0.455073	29
KCNH2	2.502517	0.278057	9	SHANK2	6.302076	0.242388	26
DNMT3A	3.015792	0.376974	8	AGAP1	11.54586	0.461835	25
VEPH1	2.685126	0.335641	8	CAMTA1	9.288115	0.371525	25
SMAD3	2.591666	0.323958	8	PDGFRA	8.112691	0.324508	25
RORA	2.493642	0.311705	8	MEIS1	8.001583	0.333399	24
GAK	3.52123	0.503033	7	SATB2	6.968141	0.290339	24
C19orf25	3.213252	0.459036	7	RPTOR	12.74644	0.554193	23
ITPKB	3.073253	0.439036	7	NCOR2	8.19049	0.356108	23
NAV1	2.840115	0.405731	7	INPP5A	6.71395	0.291911	23
VPS13D	2.710978	0.387283	7	HOXB3	5.973479	0.259716	23
GLT8D2	3.456794	0.576132	6	NXN	5.910295	0.256969	23
FBXL18	3.165773	0.527629	6	PRKCZ	8.038706	0.365396	22
CRADD	2.900562	0.483427	6	SKI	13.61224	0.648202	21
ANKS1A	2.847804	0.474634	6	SIM2	7.657535	0.364645	21
SH3BP4	2.516224	0.419371	6	ZIC4	5.477019	0.26081	21
COQ8A	2.506326	0.417721	6	FRMD4A	9.657993	0.4829	20
RUNDC3A	4.169424	0.833885	5	ABR	7.607979	0.380399	20
ARHGEF7	3.675151	0.73503	5	SDK1	6.329743	0.316487	20
TSNAX-DISC1	3.532458	0.706492	5	MAD1L1	13.60926	0.716277	19

ZNF423	11.35844	0.597813	19	ASAP1	5.147062	0.571896	9
SMG1P2	9.201404	0.484284	19	RUNX1	5.012481	0.556942	9
BOLA2	9.201404	0.484284	19	ADAMTS2	5.011711	0.556857	9
LOC613038	9.201404	0.484284	19	LINC00311	5.629979	0.703747	8
FOXK1	8.735914	0.485329	18	MSRA	5.060013	0.632502	8
SEPTIN9	6.772426	0.376246	18	DLEU1	5.004066	0.625508	8
MCF2L	6.663531	0.370196	18	BAHCC1	4.914394	0.614299	8
TBC1D16	5.385253	0.299181	18	DUSP6	7.849487	1.121355	7
OPCML	8.057438	0.473967	17	LINC00461	6.097674	0.871096	7
TBX15	5.724624	0.336743	17	FBXL18	5.180878	0.86348	6
PAX6-AS1	5.605127	0.329713	17	RUNDC3A	5.74448	1.148896	5
RCN1	5.605127	0.329713	17	TSNAX-DISC1	5.218257	1.043651	5
FOXP1	6.955576	0.434724	16	RBMS3	5.248101	1.312025	4
SORBS2	5.457054	0.341066	16	SOX10	5.594431	2.797216	2
NAV2	5.057675	0.316105	16				
GLI2	12.35834	0.82389	15	TABLE 29: Cancer Type EFT_CIC			
ZBTB20	6.868129	0.457875	15	Gene site	imp_sum	imp_mean	n
LRMDA	5.440614	0.362708	15	PTPRN2	15.69893	0.19145	82
KIRREL3	5.046605	0.33644	15	PRDM16	10.37322	0.146102	71
EMX2OS	4.94183	0.329455	15	PCDHGA1	3.849692	0.065249	59
IQSEC1	8.156287	0.582592	14	PCDHGA2	3.849692	0.067538	57
RPS6KA2	6.561333	0.468667	14	PCDHGA3	4.296947	0.079573	54
CUX1	6.051219	0.43223	14	PCDHGB1	4.296947	0.081074	53
PRKAG2	4.96462	0.354616	14	PCDHGA4	4.296947	0.084254	51
MSI2	8.776704	0.675131	13	PCDHGB2	4.296947	0.087693	49
RFX4	6.597553	0.507504	13	PCDHGA5	4.296947	0.091424	47
MYT1L	5.581442	0.429342	13	PCDHGB3	3.542328	0.08238	43
CMIP	7.341354	0.61178	12	HDAC4	20.06051	0.542176	37
ADGRD1	6.359399	0.52995	12	RBFOX3	7.234492	0.2067	35
ZC3H3	6.332313	0.527693	12	DIP2C	9.369931	0.29281	32
MIRLET7BHG	5.644003	0.470334	12	GALNT9	3.307723	0.122508	27
CTNNA2	5.265326	0.438777	12	AGAP1	11.98824	0.47953	25
RAD51B	6.834098	0.621282	11	CAMTA1	6.759721	0.270389	25
VGLL4	5.941739	0.540158	11	PDGFRA	4.565291	0.182612	25
FGFR2	5.805118	0.527738	11	MEIS1	3.306195	0.137758	24
CCDC140	5.399858	0.490896	11	RPTOR	14.38339	0.625365	23
LBX1-AS1	6.466089	0.646609	10	NCOR2	8.787906	0.382083	23
ACOT7	5.880168	0.588017	10	RIMBP2	5.939037	0.258219	23
SH3RF3	5.368831	0.536883	10	INPP5A	5.394275	0.234534	23
AKAP13	5.073876	0.507388	10	NXN	3.774468	0.164107	23
CHST11	4.895963	0.489596	10	PRKCZ	4.532974	0.206044	22
ATP11A	6.921049	0.769005	9	SKI	9.570696	0.455747	21
SND1	6.468896	0.718766	9	ZIC4	4.057271	0.193203	21
KCNMA1	5.922196	0.658022	9	FRMD4A	6.351301	0.317565	20
NOTCH1	5.900979	0.655664	9	SDK1	3.556188	0.177809	20
ADGRB1	5.876715	0.652968	9	ABR	3.35357	0.167679	20
TSPAN9	5.852712	0.650301	9	MAD1L1	11.30899	0.59521	19
TRAPPC12	5.310382	0.590042	9	CASZ1	4.205329	0.221333	19

KCNQ1	4.153197	0.218589	19	MACROD1	3.917303	0.489663	8
SMG1P2	3.946729	0.207723	19	VRK2	3.883965	0.485496	8
BOLA2	3.946729	0.207723	19	SMAD3	3.497736	0.437217	8
LOC613038	3.946729	0.207723	19	DNMT3A	3.26916	0.408645	8
FO XK1	9.052327	0.502907	18	NAV1	5.350086	0.764298	7
TBC1D16	7.005745	0.389208	18	C19orf25	4.618985	0.659855	7
ANKRD11	4.84078	0.268932	18	GAK	4.613203	0.659029	7
SEPTIN9	4.804021	0.26689	18	VPS13D	4.405545	0.629364	7
OPCML	4.784635	0.281449	17	CXXC5	4.085912	0.583702	7
HBG2	3.396259	0.19978	17	RXRA	3.73027	0.532896	7
FOXP1	5.207881	0.325493	16	FBXL18	4.445815	0.740969	6
EBF3	3.74803	0.234252	16	RADIL	3.640124	0.606687	6
NAV2	3.705764	0.23161	16	SLC22A18AS	3.310195	0.551699	6
GLI2	5.479074	0.365272	15	RUNDC3A	4.686968	0.937394	5
ZBTB20	5.327162	0.355144	15	IDI2	4.480619	0.896124	5
NFIX	3.577441	0.238496	15	ARHGEF7	4.161226	0.832245	5
RPS6KA2	8.859121	0.632794	14	TSNAX-DISC1	3.98883	0.797766	5
CUX1	5.914514	0.422465	14	TEAD1	3.752391	0.750478	5
IQSEC1	5.317055	0.37979	14	BACH2	3.39684	0.679368	5
PRKAG2	3.27492	0.233923	14	BCAR1	3.264798	0.65296	5
MYT1L	4.496364	0.345874	13	LPCAT1	3.317234	0.829308	4
MSI2	4.48584	0.345065	13				
GSE1	4.053829	0.311833	13	TABLE 30: Cancer Type EMB_ND_A			
GNA12	8.060213	0.671684	12	Gene site	imp_sum	imp_mean	n
ZC3H3	4.269692	0.355808	12	PTPRN2	6.81907	0.083159	82
CMIP	3.859055	0.321588	12	PRDM16	6.657308	0.093765	71
FBRSL1	3.514157	0.292846	12	HDAC4	2.10005	0.056758	37
RASA3	3.397433	0.283119	12	RBFOX3	2.716649	0.077619	35
ISLR2	3.288839	0.27407	12	DIP2C	2.712477	0.084765	32
VGLL4	4.146115	0.37692	11	SOX2-OT	1.898316	0.065459	29
ZC3H12D	4.014933	0.364994	11	GALNT9	2.996064	0.110965	27
CTBP2	3.450046	0.313641	11	SHANK2	1.976531	0.07602	26
TBCD	3.342356	0.303851	11	ADARB2	1.947008	0.074885	26
TSPAN4	5.379919	0.537992	10	CAMTA1	7.662871	0.306515	25
AKAP13	4.374475	0.437448	10	AGAP1	3.756501	0.15026	25
ACOT7	4.174203	0.41742	10	PDGFRA	1.823498	0.07294	25
SH3RF3	3.868139	0.386814	10	SATB2	1.712981	0.071374	24
CHST11	3.349543	0.334954	10	NCOR2	3.21767	0.139899	23
FMN1	3.297768	0.329777	10	INPP5A	2.483872	0.107994	23
ETS1	3.294779	0.329478	10	RIMBP2	1.898316	0.082535	23
SND1	7.89485	0.877206	9	RPTOR	1.837491	0.079891	23
ATP11A	7.543381	0.838153	9	PRKCZ	3.665876	0.166631	22
TSPAN9	4.661157	0.517906	9	FRMD4A	2.923035	0.146152	20
ADAMTS2	4.265749	0.473972	9	SDK1	2.866507	0.143325	20
PACS2	4.158122	0.462014	9	ABR	2.14641	0.107321	20
AXIN2	3.966172	0.440686	9	MAD1L1	10.86609	0.571899	19
CACNA2D4	3.653871	0.405986	9	CASZ1	3.960455	0.208445	19
DLEU1	4.601812	0.575227	8	SMG1P2	2.340821	0.123201	19

BOLA2	2.340821	0.123201	19	NAV1	1.662738	0.237534	7
LOC613038	2.340821	0.123201	19	IQCE	1.633709	0.233387	7
KCNQ1	1.712981	0.090157	19	LHX2	1.622807	0.23183	7
CFAP46	1.704292	0.0897	19	KDM4B	2.039913	0.339986	6
MCF2L	2.826414	0.157023	18	TSNAX-DISC1	3.035165	0.607033	5
ANKRD11	2.77096	0.153942	18	SNX29	2.269418	0.453884	5
RBFOX1	2.604038	0.144669	18	ARHGEF7	2.229606	0.445921	5
FOXK1	2.189679	0.121649	18	CHN2	1.950905	0.390181	5
TBC1D16	1.699622	0.094423	18	TK1	1.933623	0.386725	5
BAIAP2	2.568393	0.171226	15	PRR5L	1.854182	0.370836	5
NFIX	2.442774	0.162852	15	CCDC88C	1.76954	0.353908	5
KIRREL3	1.630378	0.108692	15	SDK2	1.745977	0.349195	5
ARHGEF10	2.854761	0.203912	14	GSG1	3.227564	0.806891	4
IQSEC1	2.333749	0.166696	14	TUBA1C	3.217455	0.804364	4
PRKAG2	1.783804	0.127415	14	CPE	1.630466	0.407616	4
MSI2	5.218074	0.40139	13	PARD3B	1.625209	0.406302	4
CLYBL	1.712981	0.131768	13	DICER1	2.028776	0.676259	3
FBRSL1	3.203264	0.266939	12	RASGRP3	1.741203	0.580401	3
ZC3H3	2.935532	0.244628	12	ANKLE2	3.330966	1.665483	2
CMIP	2.058885	0.171574	12	KIF21B	2.313804	1.156902	2
MEGF6	1.704495	0.142041	12	CHTF18	2.289967	1.144983	2
RAD51B	2.142947	0.194813	11	DISC1	1.885237	0.942618	2
ZC3H12D	1.801775	0.163798	11	SLC7A5	1.810281	0.90514	2
AKAP13	2.707485	0.270749	10	SLC25A10	1.742511	0.871255	2
AUTS2	2.447964	0.244796	10	ERI3	1.687948	0.843974	2
SPPL2B	1.898316	0.189832	10	DNAJC27	1.831026	1.831026	1
LMF1	1.699622	0.169962	10	ARL6IP6	1.658743	1.658743	1
ADAMTS2	4.204788	0.467199	9	GTF2E2	1.613845	1.613845	1
SSBP3	2.535213	0.28169	9				
TRAPPC12	2.528214	0.280913	9				
ATP11A	2.339968	0.259996	9	TABLE 31:	Cancer Type ENB		
GPC6	2.309533	0.256615	9	Gene site	imp_sum	imp_mean	n
TSPAN9	2.27613	0.252903	9	PTPRN2	15.29415	0.186514	82
CPNE4	1.626078	0.180675	9	PRDM16	15.30242	0.215527	71
PPP2R2B	2.901208	0.362651	8	HDAC4	17.79599	0.480973	37
VRK2	2.560103	0.320013	8	RBFOX3	10.28258	0.293788	35
MSRA	2.175092	0.271887	8	PAX6	4.405568	0.125873	35
MACROD1	2.015901	0.251988	8	DIP2C	8.96023	0.280007	32
POU6F2	1.898316	0.237289	8	GALNT9	4.383891	0.162366	27
DNMT3A	1.853521	0.23169	8	SHANK2	7.017624	0.269909	26
LINC00311	1.747994	0.218499	8	AGAP1	10.51418	0.420567	25
ESRRG	1.676804	0.2096	8	CAMTA1	7.082051	0.283282	25
PRKCA	2.295029	0.327861	7	SATB2	5.011261	0.208803	24
PACRG	2.279764	0.325681	7	MEIS1	4.017727	0.167405	24
RXRA	2.098188	0.299741	7	RPTOR	8.723779	0.379295	23
TBR1	2.028354	0.289765	7	NXN	7.212264	0.313577	23
PITPNC1	1.86804	0.266863	7	INPP5A	6.465217	0.281096	23
MIR548H4	1.663976	0.237711	7	NCOR2	5.465209	0.237618	23

RIMBP2	4.603744	0.200163	23	ZC3H3	5.709299	0.475775	12
PRKCZ	5.805332	0.263879	22	GNA12	4.857636	0.404803	12
SKI	8.012568	0.381551	21	TNS3	4.451887	0.370991	12
ZIC4	4.212597	0.2006	21	FBRSL1	4.206857	0.350571	12
HOXA-AS3	3.507593	0.167028	21	ADGRD1	4.040292	0.336691	12
ABR	3.548115	0.177406	20	MEGF6	3.908699	0.325725	12
FRMD4A	3.209784	0.160489	20	CTBP2	4.783155	0.434832	11
MAD1L1	7.124601	0.374979	19	FGFR2	3.28003	0.298185	11
SMG1P2	6.130362	0.322651	19	TSPAN4	4.591197	0.45912	10
BOLA2	6.130362	0.322651	19	AKAP13	4.440316	0.444032	10
LOC613038	6.130362	0.322651	19	ACOT7	3.995017	0.399502	10
CASZ1	5.65431	0.297595	19	BCL11B	3.458283	0.345828	10
KCNQ1	5.43857	0.286241	19	CHST11	3.347793	0.334779	10
ZNF423	4.858426	0.255707	19	IGF1R	3.325429	0.332543	10
FO XK1	6.753271	0.375182	18	AUTS2	3.281351	0.328135	10
MCF2L	5.352531	0.297363	18	SND1	7.441603	0.826845	9
ANKRD11	5.20414	0.289119	18	ATP11A	6.169478	0.685498	9
HOXA3	4.506994	0.250389	18	ADAMTS2	4.343738	0.482638	9
TBC1D16	4.213596	0.234089	18	VRK2	4.873592	0.609199	8
SEPTIN9	3.215852	0.178658	18	TRAPPC9	4.102197	0.512775	8
RBFOX1	3.208115	0.178229	18	LINC00311	3.840759	0.480095	8
OPCML	4.373813	0.257283	17	DLEU1	3.8326	0.479075	8
PAX6-AS1	3.665276	0.215604	17	PPP2R2B	3.383298	0.422912	8
RCN1	3.665276	0.215604	17	RORA	3.341857	0.417732	8
SORBS2	3.618661	0.226166	16	DNMT3A	3.198196	0.399774	8
FOXP1	3.471364	0.21696	16	MIR548H4	3.907537	0.55822	7
NAV2	3.225146	0.201572	16	NAV1	3.394831	0.484976	7
GLI2	5.610039	0.374003	15	C19orf25	3.289949	0.469993	7
ZBTB20	4.909148	0.327277	15	TSNAX-DISC1	4.775104	0.955021	5
SLX1B-				ARHGEF7	3.753903	0.750781	5
SULT1A4	4.84874	0.323249	15	RUNDC3A	3.589411	0.717882	5
SLX1A	4.84874	0.323249	15	PRR5L	3.44163	0.688326	5
LOC606724	4.84874	0.323249	15	AP2A2	3.376591	0.675318	5
BAIAP2	4.556419	0.303761	15	LIPE-AS1	3.656927	0.914232	4
DLX6-AS1	4.249325	0.283288	15	DAGLB	3.708907	1.236302	3
KIRREL3	3.858567	0.257238	15	DICER1	3.585845	1.195282	3
LRMDA	3.23644	0.215763	15	TRIO	3.300107	1.100036	3
RPS6KA2	5.007312	0.357665	14				
MOB2	4.504779	0.32177	14				
IQSEC1	4.409895	0.314993	14				
CUX1	4.066748	0.290482	14				
CACNA1H	4.052721	0.28948	14				
MIR548F5	3.380989	0.241499	14				
GNG7	3.198749	0.228482	14				
GSE1	5.068009	0.389847	13				
MSI2	4.956654	0.381281	13				
RFX4	3.670637	0.282357	13				
CMIP	7.143086	0.595257	12				

TABLE 32: Cancer Type EPN_MPE			
Gene site	imp_sum	imp_mean	n
PTPRN2	14.32221	0.174661	82
PRDM16	16.92066	0.238319	71
PCDHGA1	6.198403	0.105058	59
PCDHGA2	5.882017	0.103193	57
PCDHGA3	5.565631	0.103067	54
PCDHGB1	5.565631	0.105012	53
PCDHGA4	5.565631	0.10913	51
PCDHGB2	5.249245	0.107127	49

PCDHGA5	5.565631	0.118418	47	RFX4	5.185562	0.398889	13
PCDHGB3	5.249245	0.122075	43	MYT1L	4.949706	0.380747	13
PCDHGA6	4.932859	0.123321	40	KIF26B	4.137998	0.318308	13
HDAC4	10.4859	0.283403	37	CLYBL	3.641455	0.280112	13
PCDHGA7	4.886933	0.132079	37	MIRLET7BHG	6.049958	0.504163	12
RBFOX3	7.484427	0.213841	35	ADGRD1	4.478436	0.373203	12
PCDHGB4	4.886933	0.139627	35	ZC3H3	3.849677	0.320806	12
PCDHGA8	4.886933	0.139627	35	TNS3	3.798714	0.31656	12
DIP2C	11.24452	0.351391	32	CMIP	3.686039	0.30717	12
PCDHGB5	4.570547	0.14283	32	MEGF6	3.541811	0.295151	12
PCDHGA9	4.254161	0.137231	31	ZC3H12D	5.475938	0.497813	11
SOX2-OT	4.810056	0.165864	29	VGLL4	4.601871	0.418352	11
PCDHGB6	3.86752	0.133363	29	CTBP2	4.487393	0.407945	11
SHANK2	4.851686	0.186603	26	RAD51B	3.608856	0.328078	11
ADARB2	4.570843	0.175802	26	ACOT7	4.626879	0.462688	10
AGAP1	7.877983	0.315119	25	AKAP13	4.587557	0.458756	10
CAMTA1	5.644876	0.225795	25	KLHL29	4.04698	0.404698	10
SATB2	3.821489	0.159229	24	FMN1	3.83224	0.383224	10
RPTOR	10.40549	0.452412	23	TSPAN4	3.7268	0.37268	10
HOXB3	6.248789	0.271686	23	SND1	5.70032	0.633369	9
NCOR2	5.752322	0.250101	23	ATP11A	5.41207	0.601341	9
INPP5A	3.534761	0.153685	23	ADAMTS2	5.056659	0.561851	9
SKI	8.303878	0.395423	21	ASAP1	4.247257	0.471917	9
SIM2	3.533503	0.168262	21	AXIN2	4.138498	0.459833	9
FRMD4A	4.183428	0.209171	20	TSPAN9	4.122258	0.458029	9
ABR	3.920332	0.196017	20	TRAPPC12	3.624908	0.402768	9
SDK1	3.803673	0.190184	20	RUNX1	3.610029	0.401114	9
MAD1L1	11.24071	0.591616	19	LINC00311	4.495447	0.561931	8
ZNF423	8.169802	0.42999	19	LHX4	4.416192	0.552024	8
CASZ1	5.379156	0.283113	19	DLEU1	3.893139	0.486642	8
CFAP46	4.035361	0.212387	19	MACROD1	3.759084	0.469885	8
FO XK1	4.71225	0.261792	18	MCC	3.698126	0.462266	8
TBC1D16	4.476315	0.248684	18	WWP2	3.540691	0.442586	8
RBFOX1	3.56034	0.197797	18	SYNJ2	3.510006	0.438751	8
OPCML	7.709194	0.453482	17	NAV1	5.25118	0.750169	7
FOXP1	5.359968	0.334998	16	RXRA	4.033838	0.576263	7
NAV2	4.168476	0.26053	16	FBXL18	3.917171	0.652862	6
GLI2	6.447499	0.429833	15	LRRFIP1	3.740917	0.623486	6
ZBTB20	4.319508	0.287967	15	SLC22A18AS	3.641649	0.606941	6
LRMDA	3.985014	0.265668	15	RUNDC3A	4.523264	0.904653	5
NFIX	3.73468	0.248979	15	TSNAX-DISC1	4.43698	0.887396	5
CUX1	6.207969	0.443426	14	PRR5L	3.555141	0.711028	5
RPS6KA2	5.815656	0.415404	14	SLC25A10	4.694753	2.347376	2
PRKAG2	4.811351	0.343668	14	ANKLE2	3.867527	1.933764	2
ARHGEF10	3.644336	0.26031	14				
C7orf50	3.528157	0.252011	14				
HOXC4	6.713735	0.516441	13				
MSI2	6.683626	0.514125	13				

TABLE 33:	Cancer Type	EPN_PF_SE	
Gene site	imp_sum	imp_mean	n
PTPRN2	16.74131	0.204162	82

PRDM16	18.68393	0.263154	71	SORBS2	5.478021	0.342376	16
PCDHGA1	5.212948	0.088355	59	NAV2	4.87996	0.304997	16
PCDHGA2	5.212948	0.091455	57	FOXP1	4.849099	0.303069	16
PCDHGA3	5.212948	0.096536	54	GLI2	9.889871	0.659325	15
PCDHGB1	5.212948	0.098358	53	BAIAP2	5.307801	0.353853	15
PCDHGA4	5.212948	0.102215	51	NFIX	4.855866	0.323724	15
PCDHGB2	5.212948	0.106387	49	KIRREL3	4.673915	0.311594	15
PCDHGA5	5.212948	0.110914	47	ZBTB20	4.470387	0.298026	15
PCDHGB3	4.580176	0.106516	43	RPS6KA2	7.145132	0.510367	14
HDAC4	13.05699	0.352892	37	CUX1	6.958483	0.497035	14
PAX6	14.08594	0.402455	35	PRKAG2	6.515057	0.465361	14
RBFOX3	9.531626	0.272332	35	C7orf50	5.629425	0.402102	14
DIP2C	11.05853	0.345579	32	IQSEC1	4.598494	0.328464	14
SOX2-OT	10.77132	0.371425	29	MSI2	7.252988	0.557922	13
GALNT9	6.548071	0.242521	27	CLYBL	6.49018	0.499245	13
SHANK2	7.222144	0.277775	26	GSE1	5.760461	0.443112	13
ADARB2	7.06597	0.271768	26	KIF26B	4.998393	0.384492	13
AGAP1	9.531944	0.381278	25	RFX4	4.463465	0.343343	13
CAMTA1	6.908462	0.276338	25	MYT1L	4.411582	0.339352	13
SATB2	4.923948	0.205165	24	ZC3H3	6.609641	0.550803	12
NCOR2	9.16504	0.39848	23	MIRLET7BHG	5.018458	0.418205	12
RPTOR	9.035759	0.392859	23	CMIP	4.987616	0.415635	12
INPP5A	6.803703	0.295813	23	RASA3	4.825289	0.402107	12
RIMBP2	6.063599	0.263635	23	TNS3	4.58364	0.38197	12
HOXB3	6.055053	0.263263	23	FBRSL1	4.523777	0.376981	12
NXN	5.033246	0.218837	23	ZC3H12D	7.527348	0.684304	11
PRKCZ	7.013904	0.318814	22	RAD51B	4.527513	0.411592	11
SKI	12.7486	0.607076	21	VGLL4	4.423538	0.40214	11
ZIC4	6.09695	0.290331	21	ACOT7	5.239658	0.523966	10
SDK1	6.579672	0.328984	20	SND1	6.341657	0.704629	9
ABR	5.743593	0.28718	20	RUNX1	5.143644	0.571516	9
FRMD4A	5.402081	0.270104	20	ATP11A	4.991781	0.554642	9
MAD1L1	11.98565	0.630824	19	ADAMTS2	4.778374	0.53093	9
ZNF423	8.825708	0.464511	19	SPECC1	4.748781	0.527642	9
CASZ1	6.786586	0.357189	19	SLC22A18	4.568763	0.50764	9
SMG1P2	6.215715	0.327143	19	TSPAN9	4.535394	0.503933	9
BOLA2	6.215715	0.327143	19	CACNA2D4	4.441201	0.493467	9
LOC613038	6.215715	0.327143	19	GPC6	4.370579	0.48562	9
KCNQ1	5.03099	0.264789	19	MSRA	5.033826	0.629228	8
SEPTIN9	7.707187	0.428177	18	PRDM6	4.968878	0.62111	8
FOXK1	6.449852	0.358325	18	LHX4	4.742436	0.592804	8
TBC1D16	6.066392	0.337022	18	DLEU1	4.542607	0.567826	8
MCF2L	5.143681	0.28576	18	LINC00311	4.450046	0.556256	8
ANKRD11	4.599412	0.255523	18	RXRA	4.631648	0.661664	7
OPCML	7.137084	0.419828	17	FBXL18	4.514288	0.752381	6
SIM1	4.796091	0.282123	17	PRR5L	5.238089	1.047618	5
PAX6-AS1	4.465569	0.262681	17	TSNAX-DISC1	4.697662	0.939532	5
RCN1	4.465569	0.262681	17	ARHGEF7	4.366168	0.873234	5

RBMS3	5.452308	1.363077	4	SIM1	4.539674	0.26704	17
VOPPI	4.361184	1.090296	4	FOXP1	6.034973	0.377186	16
SLC25A10	4.633583	2.316791	2	EBF3	5.740264	0.358766	16
TABLE 34:	Cancer Type	EPN_PFA_1a		NAV2	5.648016	0.353001	16
				GLI2	8.575904	0.571727	15
Gene site	imp_sum	imp_mean	n	LRMDA	5.238657	0.349244	15
PTPRN2	15.52606	0.189342	82	KIRREL3	5.157525	0.343835	15
PRDM16	23.29599	0.328113	71	SLX1B-			
HDAC4	15.59615	0.421518	37	SULT1A4	4.672051	0.31147	15
PAX6	14.80671	0.423049	35	SLX1A	4.672051	0.31147	15
RBFOX3	9.838801	0.281109	35	LOC606724	4.672051	0.31147	15
DIP2C	11.85036	0.370324	32	KNDC1	4.538057	0.302537	15
SOX2-OT	10.03478	0.346027	29	RPS6KA2	7.648904	0.54635	14
GALNT9	9.558407	0.354015	27	CUX1	6.492923	0.46378	14
ADARB2	8.950612	0.344254	26	PRKAG2	5.487928	0.391995	14
SHANK2	8.436808	0.324493	26	IQSEC1	5.464688	0.390335	14
CAMTA1	8.475074	0.339003	25	MSI2	6.180107	0.475393	13
AGAP1	7.717198	0.308688	25	MYT1L	5.996413	0.461263	13
SATB2	12.39102	0.516293	24	KIF26B	5.857538	0.45058	13
MEIS1	4.193362	0.174723	24	GSE1	5.745502	0.441962	13
RPTOR	11.60107	0.504395	23	CLYBL	5.378406	0.413724	13
HOXB3	8.611445	0.374411	23	ADGRD1	6.913338	0.576112	12
INPP5A	8.234079	0.358003	23	ZC3H3	5.485077	0.45709	12
NCOR2	6.356224	0.276358	23	TNS3	5.08837	0.424031	12
RIMBP2	6.032696	0.262291	23	MAML3	4.984269	0.415356	12
PRKCZ	8.289756	0.376807	22	FBRSL1	4.978429	0.414869	12
SKI	10.89492	0.518806	21	CMIP	4.842426	0.403536	12
ZIC4	5.134383	0.244494	21	RASA3	4.540034	0.378336	12
SIM2	4.512566	0.214884	21	ZC3H12D	7.228159	0.657105	11
SDK1	9.202593	0.46013	20	VGLL4	5.184496	0.471318	11
FRMD4A	5.773121	0.288656	20	FGFR2	4.752801	0.432073	11
ABR	5.746127	0.287306	20	RAD51B	4.447319	0.404302	11
MAD1L1	11.8922	0.625905	19	PITX2	4.928226	0.492823	10
ZNF423	7.763591	0.40861	19	CBFA2T3	4.784692	0.478469	10
CASZ1	7.479987	0.393684	19	ACOT7	4.758271	0.475827	10
SMG1P2	6.572637	0.345928	19	EBF1	4.337505	0.43375	10
BOLA2	6.572637	0.345928	19	RUNX1	6.471203	0.719023	9
LOC613038	6.572637	0.345928	19	ATP11A	6.196063	0.688451	9
CFAP46	5.974489	0.314447	19	TSPAN9	5.199594	0.577733	9
FOKK1	6.754044	0.375225	18	SND1	4.946798	0.549644	9
SEPTIN9	6.590998	0.366167	18	ADAMTS2	4.843958	0.538218	9
TBC1D16	4.678671	0.259926	18	ZNF833P	4.638324	0.515369	9
ANKRD11	4.397949	0.244331	18	CACNA2D4	4.584298	0.509366	9
OPCML	6.527074	0.383946	17	GPC6	4.331115	0.481235	9
PAX6-AS1	4.713084	0.27724	17	PRDM6	6.419268	0.802409	8
RCN1	4.713084	0.27724	17	KIF26A	4.365822	0.545728	8
TBX15	4.574999	0.269118	17	MSRA	4.191841	0.52398	8
				NAV1	5.777994	0.825428	7

LHX2	4.853107	0.693301	7	CASZ1	7.203368	0.379125	19
TBR1	4.581182	0.654455	7	CFAP46	6.658374	0.350441	19
SATB2-AS1	6.181148	1.030191	6	SMG1P2	5.094956	0.268156	19
FBXL18	4.744899	0.790816	6	BOLA2	5.094956	0.268156	19
ROR1	4.257896	0.709649	6	LOC613038	5.094956	0.268156	19
TSNAX-DISC1	5.005668	1.001134	5	KCNQ1	4.523578	0.238083	19
CNPY1	4.858208	0.971642	5	SEPTIN9	8.631588	0.479533	18
LOC100132215	4.781487	0.956297	5	FOXK1	7.603187	0.422399	18
PRR5L	4.594552	0.91891	5	TBC1D16	5.568902	0.309383	18
RUNDC3A	4.378322	0.875664	5	ANKRD11	4.94688	0.274827	18
RBMS3	5.481089	1.370272	4	PAX6-AS1	9.044886	0.532052	17
SLC25A10	4.564369	2.282184	2	RCN1	9.044886	0.532052	17
TABLE 35:	Cancer Type	EPN_PFA_1b		OPCML	6.926837	0.407461	17
				SIM1	5.133736	0.301984	17
Gene site	imp_sum	imp_mean	n	EBF3	5.860246	0.366265	16
PTPRN2	17.00674	0.207399	82	NAV2	5.259041	0.32869	16
PRDM16	21.39185	0.301294	71	FOXP1	4.87325	0.304578	16
PCDHGA1	4.956857	0.084015	59	SORBS2	4.74376	0.296485	16
PCDHGA2	4.956857	0.086962	57	GLI2	8.270372	0.551358	15
PCDHGA3	4.640471	0.085935	54	SLX1B-			
PCDHGB1	4.640471	0.087556	53	SULT1A4	4.890562	0.326037	15
PCDHGA4	4.324085	0.084786	51	SLX1A	4.890562	0.326037	15
HDAC4	14.23228	0.384656	37	LOC606724	4.890562	0.326037	15
PAX6	13.98822	0.399663	35	KNDC1	4.76532	0.317688	15
RBFOX3	10.43696	0.298199	35	LRMDA	4.502978	0.300199	15
DIP2C	11.68025	0.365008	32	KIRREL3	4.162307	0.277487	15
SOX2-OT	7.988427	0.275463	29	RPS6KA2	7.531504	0.537965	14
GALNT9	9.278607	0.343652	27	CUX1	7.522806	0.537343	14
ADARB2	9.419679	0.362295	26	C7orf50	5.249022	0.37493	14
SHANK2	7.951411	0.305823	26	IQSEC1	4.812408	0.343743	14
AGAP1	11.28464	0.451385	25	SYCP2L	4.425098	0.316078	14
CAMTA1	8.537349	0.341494	25	PRKAG2	4.204794	0.300342	14
PDGFRA	6.872677	0.274907	25	MSI2	6.955762	0.535059	13
SATB2	13.52923	0.563718	24	CLYBL	5.60432	0.431102	13
HOXB3	11.84852	0.515153	23	KIF26B	5.154783	0.396522	13
RPTOR	8.046414	0.349844	23	MYT1L	4.795307	0.36887	13
NCOR2	7.069104	0.307352	23	ADGRD1	5.906996	0.49225	12
INPP5A	6.100277	0.265229	23	MAML3	5.269018	0.439085	12
PRKCZ	8.355116	0.379778	22	RASA3	5.263297	0.438608	12
HOXA-AS3	10.37138	0.493875	21	ZC3H12D	7.595957	0.690542	11
SKI	9.906447	0.471736	21	FGFR2	6.744716	0.613156	11
ZIC4	5.046113	0.240291	21	VGLL4	4.938567	0.448961	11
SIM2	4.694236	0.223535	21	SKOR1	4.541739	0.454174	10
SDK1	8.716676	0.435834	20	ACOT7	4.528174	0.452817	10
ABR	6.204368	0.310218	20	EBF1	4.477643	0.447764	10
MAD1L1	11.81708	0.621951	19	SND1	6.236707	0.692967	9
ZNF423	8.031473	0.422709	19	ATP11A	6.137343	0.681927	9
				RUNX1	5.965829	0.66287	9

AXIN2	4.774154	0.530462	9	ZIC4	6.534315	0.311158	21
CACNA2D4	4.638878	0.515431	9	HOXA-AS3	6.528584	0.310885	21
ADAMTS2	4.438726	0.493192	9	SIM2	4.095009	0.195	21
TSPAN9	4.426164	0.491796	9	SDK1	8.876261	0.443813	20
PRDM6	6.398119	0.799765	8	ABR	5.934879	0.296744	20
MSRA	5.256958	0.65712	8	FRMD4A	5.02878	0.251439	20
DLEU1	5.203452	0.650431	8	MAD1L1	11.62792	0.611996	19
LINC00311	4.698301	0.587288	8	ZNF423	8.003832	0.421254	19
AFF3	4.215017	0.526877	8	CASZ1	7.87127	0.414277	19
BAHCC1	4.160761	0.520095	8	SMG1P2	6.37962	0.335769	19
RORA	4.078508	0.509814	8	BOLA2	6.37962	0.335769	19
NAV1	6.307546	0.901078	7	LOC613038	6.37962	0.335769	19
HOXB-AS1	5.440172	0.777167	7	CFAP46	6.180987	0.325315	19
SATB2-AS1	5.309555	0.884926	6	KCNQ1	4.248304	0.223595	19
ROR1	4.858985	0.809831	6	FO XK1	7.751933	0.430663	18
FBXL18	4.25365	0.708942	6	SEPTIN9	7.626152	0.423675	18
CNPY1	5.842525	1.168505	5	TBC1D16	4.759312	0.264406	18
LOC100132215	4.750425	0.950085	5	PAX6-AS1	7.680562	0.451798	17
TSNAX-DISC1	4.549935	0.909987	5	RCN1	7.680562	0.451798	17
RBMS3	5.307114	1.326778	4	OPCML	6.246465	0.367439	17
SLC25A10	4.466961	2.233481	2	SIM1	5.766294	0.339194	17
TABLE 36:	Cancer Type	EPN_PFA_1c		EBF3	5.762216	0.360138	16
				NAV2	5.017001	0.313563	16
Gene site	imp_sum	imp_mean	n	FOXP1	4.656013	0.291001	16
PTPRN2	11.73423	0.1431	82	GLI2	7.572671	0.504845	15
PRDM16	21.7832	0.306806	71	LRMDA	5.232108	0.348807	15
HDAC4	11.65731	0.315062	37	KNDC1	4.497326	0.299822	15
PAX6	11.46737	0.327639	35	BAIAP2	4.222307	0.281487	15
RBFOX3	8.085018	0.231001	35	SLX1B-			
DIP2C	10.63225	0.332258	32	SULT1A4	4.148554	0.27657	15
SOX2-OT	9.704987	0.334655	29	SLX1A	4.148554	0.27657	15
GALNT9	7.860133	0.291116	27	LOC606724	4.148554	0.27657	15
ADARB2	8.467804	0.325685	26	RPS6KA2	7.479873	0.534277	14
SHANK2	8.274469	0.318249	26	CUX1	6.16701	0.440501	14
AGAP1	8.253203	0.330128	25	IQSEC1	4.72887	0.337776	14
CAMTA1	6.683582	0.267343	25	SYCP2L	4.00661	0.286186	14
PDGFRA	6.467133	0.258685	25	MSI2	6.405085	0.492699	13
SATB2	13.66347	0.569311	24	KIF26B	5.629066	0.433005	13
MEIS1	4.600093	0.191671	24	MYT1L	4.50348	0.346422	13
HOXB3	13.57523	0.590227	23	GSE1	4.000032	0.307695	13
RPTOR	10.26378	0.446251	23	ADGRD1	6.29846	0.524872	12
NXN	6.038699	0.262552	23	RASA3	4.932304	0.411025	12
NCOR2	5.781112	0.251353	23	CMIP	4.764815	0.397068	12
RIMBP2	5.121475	0.222673	23	ZC3H3	4.64397	0.386997	12
INPP5A	4.056281	0.17636	23	MAML3	4.500624	0.375052	12
PRKCZ	6.347057	0.288503	22	TNS3	4.451974	0.370998	12
SKI	10.71367	0.510175	21	FBRSL1	3.987885	0.332324	12
				ZC3H12D	7.076528	0.643321	11

CCDC140	5.695759	0.517796	11	RBFOX3	7.481977	0.213771	35
TBCD	4.563491	0.414863	11	DIP2C	10.57351	0.330422	32
ACOT7	4.484055	0.448406	10	SOX2-OT	8.581972	0.29593	29
TFAP2B	4.443817	0.444382	10	GALNT9	7.811737	0.289324	27
AKAP13	4.031576	0.403158	10	SHANK2	9.067266	0.348741	26
ATP11A	5.629712	0.625524	9	ADARB2	7.012347	0.269706	26
RUNX1	4.768155	0.529795	9	AGAP1	9.67105	0.386842	25
ADAMTS2	4.381118	0.486791	9	PDGFRA	7.736738	0.30947	25
TSPAN9	4.358179	0.484242	9	CAMTA1	6.544932	0.261797	25
AXIN2	4.28654	0.476282	9	SATB2	8.389307	0.349554	24
IGF2BP1	3.951526	0.439058	9	HOXB3	10.88869	0.473421	23
MSRA	5.028607	0.628576	8	RPTOR	10.71092	0.465692	23
DLEU1	4.521561	0.565195	8	NCOR2	6.734153	0.292789	23
PRDM6	4.441132	0.555142	8	RIMBP2	4.764066	0.207133	23
AFF3	4.261966	0.532746	8	INPP5A	4.069466	0.176933	23
HOXB-AS3	5.999753	0.857108	7	PRKCZ	4.627069	0.210321	22
NAV1	5.943536	0.849077	7	SKI	9.279129	0.441863	21
HOXD3	5.14118	0.734454	7	ZIC4	5.871497	0.279595	21
HOXB-AS1	4.638274	0.662611	7	SDK1	9.318171	0.465909	20
LHX2	4.013036	0.573291	7	ABR	5.91374	0.295687	20
SATB2-AS1	5.34783	0.891305	6	FRMD4A	5.159279	0.257964	20
ROR1	4.741215	0.790203	6	MAD1L1	11.62279	0.611726	19
FBXL18	3.922361	0.653727	6	ZNF423	7.81374	0.411249	19
TSNAX-DISC1	4.656461	0.931292	5	SMG1P2	6.691693	0.352194	19
CNPY1	4.581687	0.916337	5	BOLA2	6.691693	0.352194	19
PRR5L	4.463218	0.892644	5	LOC613038	6.691693	0.352194	19
ARHGEF7	4.278868	0.855774	5	CASZ1	5.736559	0.301924	19
RUNDC3A	4.013063	0.802613	5	CFAP46	5.597067	0.294582	19
RBMS3	5.434225	1.358556	4	SEPTIN9	8.140972	0.452276	18
SLC25A10	4.49209	2.246045	2	FO XK1	6.739737	0.37443	18
				TBC1D16	5.201468	0.28897	18
				MCF2L	4.169744	0.231652	18
				PAX6-AS1	7.221093	0.42477	17
				RCN1	7.221093	0.42477	17
				OPCML	5.635106	0.331477	17
				SIM1	4.81768	0.283393	17
				EBF3	4.791317	0.299457	16
				NAV2	4.475462	0.279716	16
				FOXP1	4.401058	0.275066	16
				SORBS2	4.070503	0.254406	16
				GLI2	8.844511	0.589634	15
				LRMDA	5.609227	0.373948	15
				KNDC1	5.573397	0.37156	15
				SLX1B-			
				SULT1A4	5.061652	0.337443	15
				SLX1A	5.061652	0.337443	15
				LOC606724	5.061652	0.337443	15
				BAIAP2	4.715108	0.314341	15

TABLE 37: Cancer Type EPN_PFA_1d							
Gene site	imp_sum	imp_mean	n				
PTPRN2	14.16403	0.172732	82				
PRDM16	20.32788	0.286308	71				
PCDHGA1	4.457227	0.075546	59				
PCDHGA2	4.773613	0.083748	57				
PCDHGA3	4.773613	0.0884	54				
PCDHGB1	4.773613	0.090068	53				
PCDHGA4	4.773613	0.0936	51				
PCDHGB2	4.773613	0.097421	49				
PCDHGA5	4.773613	0.101566	47				
PCDHGB3	4.773613	0.111014	43				
PCDHGA6	4.140841	0.103521	40				
HDAC4	15.46144	0.417877	37				
PCDHGA7	4.140841	0.111915	37				
PAX6	12.5182	0.357663	35				

CUX1	7.899281	0.564234	14	PCDHGB1	6.249149	0.117908	53	
RPS6KA2	5.501559	0.392969	14	PCDHGA4	6.249149	0.122532	51	
PRKAG2	5.237114	0.37408	14	PCDHGB2	6.249149	0.127534	49	
C7orf50	4.527671	0.323405	14	PCDHGA5	6.249149	0.132961	47	
MSI2	5.354662	0.411897	13	PCDHGB3	6.249149	0.145329	43	
MIR9-3HG	4.517006	0.347462	13	PCDHGA6	5.616377	0.140409	40	
MYT1L	4.500654	0.346204	13	HDAC4	13.72711	0.371003	37	
CLYBL	4.143654	0.318743	13	PCDHGA7	5.616377	0.151794	37	
ADGRD1	5.40329	0.450274	12	PAX6	11.95651	0.341615	35	
CMIP	4.791817	0.399318	12	RBFOX3	6.248808	0.178537	35	
FBRSL1	4.247617	0.353968	12	PCDHGB4	4.983605	0.142389	35	
FGFR2	7.174125	0.652193	11	PCDHGA8	4.983605	0.142389	35	
ZC3H12D	6.5122	0.592018	11	DIP2C	12.07684	0.377401	32	
VGLL4	4.940937	0.449176	11	PCDHGB5	4.983605	0.155738	32	
PITX2	4.521435	0.452143	10	PCDHGA9	4.983605	0.160761	31	
SKOR1	4.258637	0.425864	10	SOX2-OT	8.488804	0.292717	29	
RUNX1	6.700412	0.74449	9	PCDHGB6	4.462174	0.153868	29	
ATP11A	5.674704	0.630523	9	PCDHGA10	4.462174	0.159363	28	
SND1	5.065513	0.562835	9	GALNT9	7.836874	0.290255	27	
IGF2BP1	4.389758	0.487751	9	ADARB2	9.084362	0.349399	26	
AXIN2	4.329011	0.481001	9	SHANK2	7.663285	0.294742	26	
DLEU1	5.261077	0.657635	8	AGAP1	10.63693	0.425477	25	
PRDM6	4.880923	0.610115	8	PDGFRA	7.632836	0.305313	25	
LINC00311	4.240971	0.530121	8	CAMTA1	7.157302	0.286292	25	
AFF3	4.069896	0.508737	8	SATB2	12.85457	0.535607	24	
NAV1	5.018063	0.716866	7	MEIS1	6.554545	0.273106	24	
HOXB-AS1	4.986665	0.712381	7	PCDHGB7	4.437355	0.18489	24	
HOXB-AS3	4.934192	0.704885	7	RPTOR	10.07816	0.438181	23	
HOXD3	4.268153	0.609736	7	HOXB3	8.867335	0.385536	23	
SATB2-AS1	4.635977	0.772663	6	RIMBP2	6.878422	0.299062	23	
ROR1	4.372884	0.728814	6	NCOR2	6.285882	0.273299	23	
CNPY1	5.582239	1.116448	5	INPP5A	5.269959	0.229129	23	
TSNAX-DISC1	4.78141	0.956282	5	PRKCZ	8.630716	0.392305	22	
LOC100132215	4.543738	0.908748	5	SKI	9.400294	0.447633	21	
PRR5L	4.167306	0.833461	5	ZIC4	5.787979	0.275618	21	
YJEFN3	4.125815	0.825163	5	HOXA-AS3	5.32864	0.253745	21	
NDUFA13	4.125815	0.825163	5	SDK1	8.473301	0.423665	20	
RBMS3	5.532971	1.383243	4	ABR	5.397539	0.269877	20	
SLC25A10	4.494503	2.247252	2	MAD1L1	12.29839	0.647284	19	
TABLE 38:	Cancer Type EPN_PFA_1e	imp_sum	imp_mean	n	ZNF423	7.872681	0.414352	19
					SMG1P2	6.494341	0.341807	19
					BOLA2	6.494341	0.341807	19
					LOC613038	6.494341	0.341807	19
					CFAP46	5.689287	0.299436	19
					CASZ1	4.609441	0.242602	19
					SEPTIN9	8.178796	0.454378	18
					FOXK1	7.898339	0.438797	18
					TBC1D16	5.470113	0.303895	18
Gene site	imp_sum	imp_mean	n					
PTPRN2	18.00181	0.219534	82					
PRDM16	21.74627	0.306286	71					
PCDHGA1	6.881921	0.116643	59					
PCDHGA2	6.565535	0.115185	57					
PCDHGA3	6.565535	0.121584	54					

OPCML	6.190017	0.364119	17
TBX15	5.706091	0.335652	17
SIM1	5.192404	0.305436	17
EBF3	5.90028	0.368768	16
NAV2	5.221878	0.326367	16
FOXP1	5.181933	0.323871	16
GLI2	9.065835	0.604389	15
SLX1B-			
SULT1A4	5.499113	0.366608	15
SLX1A	5.499113	0.366608	15
LOC606724	5.499113	0.366608	15
ZBTB20	5.387733	0.359182	15
KIRREL3	4.942907	0.329527	15
LRMDA	4.930817	0.328721	15
BAIAP2	4.662475	0.310832	15
EMX2OS	4.429826	0.295322	15
RPS6KA2	6.445326	0.46038	14
CUX1	6.293085	0.449506	14
PRKAG2	5.440297	0.388593	14
MSI2	7.114332	0.547256	13
KIF26B	5.683044	0.437157	13
CLYBL	5.449649	0.419204	13
MYT1L	4.83363	0.371818	13
ADGRD1	5.371757	0.447646	12
ZC3H3	4.983983	0.415332	12
RASA3	4.983927	0.415327	12
FBRSL1	4.769712	0.397476	12
CMIP	4.637998	0.3865	12
ZC3H12D	6.775582	0.615962	11
FGFR2	6.004602	0.545873	11
VGLL4	5.254372	0.47767	11
RUNX1	6.920844	0.768983	9
SND1	6.114865	0.679429	9
ATP11A	5.509849	0.612205	9
AXIN2	4.969639	0.552182	9
ZNF833P	4.887175	0.543019	9
ADAMTS2	4.738917	0.526546	9
TSPAN9	4.542104	0.504678	9
PRDM6	6.947315	0.868414	8
AFF3	4.755751	0.594469	8
LHX4	4.538205	0.567276	8
NAV1	5.378917	0.768417	7
HOXB-AS1	5.110234	0.730033	7
SATB2-AS1	6.250726	1.041788	6
TSNAX-DISC1	5.009414	1.001883	5
CNPY1	4.547343	0.909469	5
RBMS3	5.281652	1.320413	4
SLC25A10	4.677629	2.338814	2

TABLE 39:

Cancer Type
EPN_PFA_1f

Gene site	imp_sum	imp_mean	n
PTPRN2	13.09278	0.159668	82
PRDM16	20.14761	0.283769	71
PCDHGA1	4.014954	0.06805	59
HDAC4	15.21987	0.411348	37
PAX6	12.20129	0.348608	35
RBFOX3	9.580381	0.273725	35
DIP2C	10.53293	0.329154	32
SOX2-OT	6.568508	0.2265	29
GALNT9	8.901503	0.329685	27
ADARB2	8.342014	0.320847	26
SHANK2	5.925792	0.227915	26
AGAP1	8.423821	0.336953	25
CAMTA1	6.335015	0.253401	25
SATB2	7.790586	0.324608	24
MEIS1	4.099364	0.170807	24
RPTOR	10.86983	0.472601	23
NCOR2	7.09586	0.308516	23
HOXB3	5.862146	0.254876	23
RIMBP2	5.378929	0.233866	23
INPP5A	4.380518	0.190457	23
NXN	4.04771	0.175987	23
PRKCZ	6.916562	0.314389	22
SKI	9.348199	0.445152	21
ZIC4	6.393505	0.304453	21
SIM2	5.109225	0.243296	21
SDK1	5.862156	0.293108	20
FRMD4A	5.766686	0.288334	20
ABR	4.713662	0.235683	20
MAD1L1	11.80233	0.621175	19
ZNF423	8.685542	0.457134	19
SMG1P2	6.149274	0.323646	19
BOLA2	6.149274	0.323646	19
LOC613038	6.149274	0.323646	19
CFAP46	5.760275	0.303172	19
CASZ1	4.40723	0.231959	19
SEPTIN9	6.327048	0.351503	18
FO XK1	6.211907	0.345106	18
ANKRD11	4.557418	0.25319	18
RBFOX1	4.215856	0.234214	18
TBC1D16	4.160834	0.231157	18
OPCML	5.509342	0.324079	17
SIM1	5.074315	0.298489	17
PAX6-AS1	4.557005	0.268059	17
RCN1	4.557005	0.268059	17

TBX15	4.011994	0.236	17	SATB2-AS1	4.803834	0.800639	6
FOXP1	5.473053	0.342066	16	FBXL18	4.26291	0.710485	6
EBF3	5.279453	0.329966	16	TSNAX-DISC1	5.572732	1.114546	5
NAV2	5.163328	0.322708	16	ARHGEF7	4.651486	0.930297	5
GLI2	8.377429	0.558495	15	PRR5L	4.485171	0.897034	5
KIRREL3	5.753279	0.383552	15	RBMS3	5.367267	1.341817	4
KNDC1	5.392565	0.359504	15	VOPP1	4.143062	1.035765	4
BAIAP2	4.27612	0.285075	15	SLC25A10	4.685335	2.342668	2
SLX1B-SULT1A4	4.264888	0.284326	15	ANKLE2	4.116607	2.058304	2
SLX1A	4.264888	0.284326	15	TABLE 40: Cancer Type EPN_PFA_2a			
LOC606724	4.264888	0.284326	15				
RPS6KA2	5.911852	0.422275	14	Gene site	imp_sum	imp_mean	n
CUX1	5.504203	0.393157	14	PTPRN2	15.91598	0.194097	82
MSI2	7.326236	0.563557	13	PRDM16	23.91302	0.336803	71
MYT1L	5.63385	0.433373	13	PCDHGA3	4.395619	0.0814	54
KIF26B	5.058706	0.389131	13	PCDHGB1	4.395619	0.082936	53
GSE1	4.889862	0.376143	13	PCDHGA4	4.395619	0.086189	51
CLYBL	4.867994	0.374461	13	PCDHGB2	4.395619	0.089707	49
ZC3H3	5.537883	0.46149	12	PCDHGA5	4.395619	0.093524	47
ADGRD1	5.301199	0.441767	12	HDAC4	14.58312	0.394138	37
TNS3	5.192588	0.432716	12	PAX6	12.40615	0.354462	35
CMIP	4.83491	0.402909	12	RBFOX3	9.246467	0.264185	35
MIRLET7BHG	4.293505	0.357792	12	DIP2C	11.2906	0.352831	32
MAML3	4.005847	0.333821	12	SOX2-OT	8.738627	0.301332	29
ZC3H12D	7.258058	0.659823	11	GALNT9	6.750716	0.250027	27
TBCD	4.863163	0.442106	11	ADARB2	8.387141	0.322582	26
GLUD1P2	4.329645	0.393604	11	SHANK2	7.117336	0.273744	26
ACOT7	4.973412	0.497341	10	AGAP1	9.061107	0.362444	25
PITX2	4.414111	0.441411	10	PDGFRA	6.28606	0.251442	25
ADGRA1	4.322472	0.432247	10	CAMTA1	6.048119	0.241925	25
SND1	5.8504	0.650044	9	SATB2	11.72	0.488333	24
ATP11A	5.752276	0.639142	9	MEIS1	5.705858	0.237744	24
ADAMTS2	4.993887	0.554876	9	RPTOR	10.21814	0.444267	23
CACNA2D4	4.607028	0.511892	9	NCOR2	7.929984	0.344782	23
ZNF833P	4.412196	0.490244	9	HOXB3	6.116576	0.265938	23
AXIN2	4.31999	0.479999	9	RIMBP2	5.100058	0.221742	23
RUNX1	4.309572	0.478841	9	INPP5A	4.733123	0.205788	23
SLC22A18	4.285245	0.476138	9	PRKCZ	8.624156	0.392007	22
MSRA	4.847284	0.60591	8	SKI	9.70777	0.462275	21
PRDM6	4.456104	0.557013	8	ZIC4	6.670683	0.317652	21
LINC00311	4.311468	0.538934	8	HOXA-AS3	6.511321	0.310063	21
DLEU1	4.263023	0.532878	8	ABR	7.33488	0.366744	20
AFF3	4.025175	0.503147	8	SDK1	6.881182	0.344059	20
NAV1	5.601169	0.800167	7	FRMD4A	5.001019	0.250051	20
DUSP6	4.205483	0.600783	7	MAD1L1	10.76549	0.566605	19
TBR1	4.175176	0.596454	7	ZNF423	8.242158	0.433798	19
LHX2	4.10337	0.586196	7	CASZ1	6.766843	0.35615	19

CFAP46	5.636312	0.296648	19	PITX2	5.128856	0.512886	10
SMG1P2	5.570027	0.293159	19	ACOT7	4.918146	0.491815	10
BOLA2	5.570027	0.293159	19	SPPL2B	4.624696	0.46247	10
LOC613038	5.570027	0.293159	19	SND1	6.477967	0.719774	9
SEPTIN9	8.545258	0.474737	18	ATP11A	6.136883	0.681876	9
FO XK1	7.476101	0.415339	18	ADAMTS2	4.85214	0.539127	9
TBC1D16	5.022636	0.279035	18	AXIN2	4.512541	0.501393	9
PAX6-AS1	7.162201	0.421306	17	MSRA	5.754357	0.719295	8
RCN1	7.162201	0.421306	17	LINC00311	4.716263	0.589533	8
OPCML	7.013243	0.412544	17	SOX6	5.215185	0.745026	7
SIM1	5.849929	0.344113	17	ROR1	4.798833	0.799805	6
TBX15	5.613326	0.330196	17	SATB2-AS1	4.516259	0.75271	6
EBF3	6.450012	0.403126	16	CNPY1	5.6611	1.13222	5
NAV2	5.462722	0.34142	16	YJEFN3	5.459693	1.091939	5
FOXP1	4.794453	0.299653	16	NDUFA13	5.459693	1.091939	5
GLI2	8.084175	0.538945	15	TSNAX-DISC1	5.227233	1.045447	5
EMX2OS	5.703506	0.380234	15	RBMS3	4.524161	1.13104	4
KNDC1	5.68967	0.379311	15	SLC25A10	4.544005	2.272002	2
KIRREL3	5.202305	0.34682	15				
DLX6-AS1	5.125709	0.341714	15				
SLX1B-							
SULT1A4	5.009364	0.333958	15				
SLX1A	5.009364	0.333958	15				
LOC606724	5.009364	0.333958	15				
LRMDA	4.712534	0.314169	15				
NFATC1	4.691042	0.312736	15				
NFIX	4.567902	0.304527	15				
COL23A1	4.555395	0.303693	15				
BAIAP2	4.490191	0.299346	15				
RPS6KA2	7.827096	0.559078	14				
C7orf50	5.63246	0.402319	14				
PRKAG2	5.5359	0.395421	14				
CUX1	4.998438	0.357031	14				
MSI2	6.849053	0.52685	13				
CLYBL	6.024401	0.463415	13				
KIF26B	4.922835	0.37868	13				
MYT1L	4.757005	0.365923	13				
MIR9-3HG	4.576315	0.352024	13				
TBX4	5.54634	0.462195	12				
ZC3H3	5.30363	0.441969	12				
MIRLET7BHG	4.931953	0.410996	12				
FBRSL1	4.927912	0.410659	12				
CMIP	4.902181	0.408515	12				
TNS3	4.855115	0.404593	12				
RASA3	4.712357	0.392696	12				
ADGRD1	4.583055	0.381921	12				
ZC3H12D	7.345878	0.667807	11				
CCDC140	4.570185	0.415471	11				

TABLE 41:				Cancer Type			
				EPN_PFA_2b			
Gene site	imp_sum	imp_mean	n				
PTPRN2	16.4127	0.200155	82				
PRDM16	22.36941	0.315062	71				
PCDHGA1	6.212905	0.105303	59				
PCDHGA2	6.212905	0.108998	57				
PCDHGA3	6.212905	0.115054	54				
PCDHGB1	5.896519	0.111255	53				
PCDHGA4	5.896519	0.115618	51				
PCDHGB2	5.472043	0.111674	49				
PCDHGA5	5.155657	0.109695	47				
PCDHGB3	4.839271	0.112541	43				
HDAC4	14.80896	0.400242	37				
PAX6	13.46938	0.384839	35				
RBFOX3	9.79059	0.279731	35				
DIP2C	10.95171	0.342241	32				
SOX2-OT	6.22414	0.214626	29				
GALNT9	6.534668	0.242025	27				
ADARB2	9.127855	0.351071	26				
SHANK2	7.648487	0.294173	26				
AGAP1	10.27307	0.410923	25				
CAMTA1	5.472853	0.218914	25				
PDGFRA	5.468118	0.218725	25				
SATB2	11.96168	0.498403	24				
RPTOR	10.96186	0.476603	23				
NCOR2	7.371677	0.320508	23				
NXN	5.650817	0.245688	23				

RIMBP2	5.223607	0.227113	23	OTX1	5.952922	0.595292	10
INPP5A	5.095016	0.221522	23	SPPL2B	5.368011	0.536801	10
PRKCZ	7.415118	0.337051	22	IGF1R	4.426751	0.442675	10
SKI	9.66072	0.460034	21	SND1	5.88217	0.653574	9
HOXA-AS3	5.713977	0.272094	21	ATP11A	5.318731	0.59097	9
ZIC4	5.294912	0.252139	21	ADAMTS2	4.829158	0.536573	9
SDK1	7.395307	0.369765	20	RUNX1	4.626345	0.514038	9
ABR	6.916678	0.345834	20	IGF2BP1	4.45	0.494444	9
FRMD4A	5.148597	0.25743	20	PRDM6	5.608682	0.701085	8
MAD1L1	11.11146	0.584814	19	DLEU1	5.328889	0.666111	8
ZNF423	8.81835	0.464124	19	KIF26A	4.561173	0.570147	8
CFAP46	6.346435	0.334023	19	LHX4	4.421062	0.552633	8
SMG1P2	6.214699	0.327089	19	LINC00311	4.418239	0.55228	8
BOLA2	6.214699	0.327089	19	MSRA	4.328181	0.541023	8
LOC613038	6.214699	0.327089	19	DUSP6	5.270804	0.752972	7
CASZ1	5.447154	0.286692	19	NAV1	4.987175	0.712454	7
KCNQ1	5.41355	0.284924	19	SOX6	4.593669	0.656238	7
SEPTIN9	7.560517	0.420029	18	SATB2-AS1	5.56202	0.927003	6
FO XK1	7.422858	0.412381	18	ROR1	4.56876	0.76146	6
TBC1D16	5.337114	0.296506	18	YJEFN3	6.354918	1.270984	5
PAX6-AS1	7.879274	0.463487	17	NDUFA13	6.354918	1.270984	5
RCN1	7.879274	0.463487	17	CNPY1	4.812447	0.962489	5
SIM1	6.533671	0.384334	17	LOC100132215	4.778136	0.955627	5
OPCML	6.023777	0.35434	17	TSNAX-DISC1	4.722043	0.944409	5
FOXP1	4.801912	0.300119	16	ARHGEF7	4.42906	0.885812	5
NAV2	4.439677	0.27748	16	PRR5L	4.349745	0.869949	5
GLI2	8.675359	0.578357	15	RBMS3	5.220141	1.305035	4
KIRREL3	5.848906	0.389927	15	SLC25A10	4.703802	2.351901	2
KNDC1	5.36737	0.357825	15				
BAIAP2	4.920026	0.328002	15				
SLX1B-							
SULT1A4	4.849583	0.323306	15				
SLX1A	4.849583	0.323306	15				
LOC606724	4.849583	0.323306	15				
LRMDA	4.515397	0.301026	15				
RPS6KA2	7.297086	0.52122	14				
PRKAG2	5.45784	0.389846	14				
CUX1	5.375193	0.383942	14				
MSI2	7.013927	0.539533	13				
GSE1	4.576023	0.352002	13				
ADGRD1	5.774253	0.481188	12				
ZC3H3	5.25217	0.437681	12				
TBX4	5.04624	0.42052	12				
FBRSL1	4.714604	0.392884	12				
RASA3	4.589192	0.382433	12				
CMIP	4.508705	0.375725	12				
ZC3H12D	8.257341	0.750667	11				
FGFR2	7.598239	0.690749	11				

TABLE 15.

Cancer Type
EPN_PFA_2c

Gene site	imp_sum	imp_mean	n
PTPRN2	11.6565	0.142152	82
PRDM16	23.70492	0.333872	71
PCDHGA1	4.37733	0.074192	59
PCDHGA2	4.37733	0.076795	57
PCDHGA3	4.37733	0.081062	54
PCDHGB1	4.37733	0.082591	53
PCDHGA4	4.37733	0.08583	51
PCDHGB2	4.060944	0.082876	49
PCDHGA5	4.060944	0.086403	47
HDAC4	13.29829	0.359413	37
PAX6	14.48402	0.413829	35
RBFOX3	6.241908	0.17834	35
DIP2C	8.787136	0.274598	32
SOX2-OT	7.319255	0.252388	29
GALNT9	6.266872	0.232106	27
ADARB2	8.089442	0.311132	26

SHANK2	6.05991	0.233073	26	CLYBL	5.510349	0.423873	13
AGAP1	8.374534	0.334981	25	MYT1L	5.126763	0.394366	13
PDGFRA	5.01173	0.200469	25	ZC3H3	4.978083	0.41484	12
CAMTA1	4.487403	0.179496	25	ADGRD1	4.926207	0.410517	12
SATB2	8.753201	0.364717	24	CMIP	4.886292	0.407191	12
MEIS1	4.083446	0.170144	24	TNS3	4.622121	0.385177	12
RPTOR	9.988587	0.434286	23	FBRSL1	4.094101	0.341175	12
NCOR2	6.55577	0.285033	23	ZC3H12D	7.253406	0.659401	11
HOXB3	5.776906	0.25117	23	CCDC140	5.226762	0.47516	11
RIMBP2	5.376796	0.233774	23	VGLL4	4.634901	0.421355	11
NXN	4.613719	0.200596	23	ACOT7	5.075241	0.507524	10
PRKCZ	7.616692	0.346213	22	ATP11A	6.340161	0.704462	9
SKI	9.345082	0.445004	21	SND1	6.218579	0.690953	9
ZIC4	5.183042	0.246812	21	RUNX1	4.884786	0.542754	9
SDK1	7.884654	0.394233	20	SLC22A18	4.190517	0.465613	9
FRMD4A	6.143578	0.307179	20	ADAMTS2	4.018914	0.446546	9
ABR	5.536943	0.276847	20	CACNA2D4	3.999655	0.444406	9
MAD1L1	11.41524	0.600802	19	MSRA	4.921088	0.615136	8
ZNF423	8.664317	0.456017	19	LMX1B	4.536467	0.567058	8
CFAP46	5.304846	0.279202	19	PRDM6	4.518116	0.564764	8
SMG1P2	4.825948	0.253997	19	DLEU1	4.483962	0.560495	8
BOLA2	4.825948	0.253997	19	LINC00311	4.213928	0.526741	8
LOC613038	4.825948	0.253997	19	KIF26A	4.10704	0.51338	8
CASZ1	4.66076	0.245303	19	TENM3-AS1	4.767356	0.681051	7
KCNQ1	4.603715	0.242301	19	C1orf94	4.572866	0.653267	7
SEPTIN9	8.788187	0.488233	18	HOXB-AS3	4.288964	0.612709	7
FO XK1	6.147356	0.34152	18	NAV1	4.213013	0.601859	7
TBC1D16	5.28406	0.293559	18	DUSP6	4.100914	0.585845	7
PAX6-AS1	5.994998	0.352647	17	SATB2-AS1	4.979445	0.829907	6
RCN1	5.994998	0.352647	17	CNPY1	5.302207	1.060441	5
OPCML	5.742541	0.337797	17	TSNAX-DISC1	4.636077	0.927215	5
NAV2	5.608379	0.350524	16	PRR5L	4.341445	0.868289	5
EBF3	5.075295	0.317206	16	RUNDC3A	4.159525	0.831905	5
FOXP1	4.729745	0.295609	16	RBMS3	4.617734	1.154433	4
GLI2	7.42542	0.495028	15	SLC25A10	4.631508	2.315754	2
BAIAP2	4.950271	0.330018	15	ANKLE2	4.023139	2.01157	2
LRMDA	4.691617	0.312774	15	TABLE 43: Cancer Type EPN_PFB_1			
NFATC1	4.682222	0.312148	15				
KNDC1	4.580988	0.305399	15	Gene site	imp_sum	imp_mean	n
NFIX	4.565442	0.304363	15	PTPRN2	14.34232	0.174906	82
EMX2OS	4.433473	0.295565	15	PRDM16	19.15675	0.269813	71
RPS6KA2	8.526582	0.609042	14	PCDHGB1	3.436915	0.064847	53
CUX1	6.091662	0.435119	14	PCDHGB2	3.436915	0.070141	49
PRKAG2	5.14939	0.367814	14	PCDHGA5	3.436915	0.073126	47
C7orf50	5.013166	0.358083	14	PCDHGB3	3.436915	0.079928	43
ARHGEF10	4.177837	0.298417	14	PCDHGA6	3.553808	0.088845	40
MSI2	6.653697	0.511823	13	HDAC4	9.949331	0.268901	37
KIF26B	5.568032	0.42831	13	PCDHGA7	3.870194	0.1046	37

PAX6	14.36937	0.410553	35	MIR548F5	3.520189	0.251442	14
RBFOX3	7.486781	0.213908	35	GSE1	5.18713	0.39901	13
PCDHGB4	3.870194	0.110577	35	MYT1L	4.935413	0.379647	13
PCDHGA8	3.870194	0.110577	35	MSI2	4.665388	0.358876	13
DIP2C	10.83914	0.338723	32	RFX4	4.204038	0.323388	13
SOX2-OT	8.596926	0.296446	29	KIF26B	4.056407	0.312031	13
GALNT9	6.171874	0.228588	27	CLYBL	3.462787	0.266368	13
SHANK2	7.985448	0.307133	26	ZC3H3	5.412723	0.45106	12
ADARB2	4.97106	0.191195	26	MIRLET7BHG	4.697784	0.391482	12
AGAP1	7.294908	0.291796	25	TNS3	4.627592	0.385633	12
CAMTA1	5.086112	0.203444	25	CMIP	4.384051	0.365338	12
SATB2	6.296275	0.262345	24	MAML3	3.565524	0.297127	12
RPTOR	8.152366	0.354451	23	RASA3	3.47917	0.289931	12
HOXB3	5.319994	0.231304	23	VGLL4	3.684002	0.334909	11
RIMBP2	4.533346	0.197102	23	ZC3H12D	3.516208	0.319655	11
INPP5A	4.21213	0.183136	23	ACOT7	4.804751	0.480475	10
NCOR2	3.666971	0.159434	23	SH3RF3	3.992997	0.3993	10
PRKCZ	4.701794	0.213718	22	NR2F1-AS1	3.661456	0.366146	10
SKI	7.691187	0.366247	21	AKAP13	3.469122	0.346912	10
ZIC4	6.763892	0.32209	21	SND1	6.320565	0.702285	9
SDK1	5.929341	0.296467	20	ATP11A	5.097164	0.566352	9
FRMD4A	5.310431	0.265522	20	ADAMTS2	4.443487	0.493721	9
MAD1L1	9.899326	0.521017	19	KAZN	3.745411	0.416157	9
ZNF423	8.938096	0.470426	19	IGF2BP1	3.449928	0.383325	9
CASZ1	5.802896	0.305416	19	RORA	5.794622	0.724328	8
SMG1P2	4.4044	0.231811	19	AFF3	4.712983	0.589123	8
BOLA2	4.4044	0.231811	19	LHX4	4.609795	0.576224	8
LOC613038	4.4044	0.231811	19	DLEU1	4.327767	0.540971	8
FO XK1	7.895185	0.438621	18	LINC00311	4.047595	0.505949	8
SEPTIN9	6.791985	0.377333	18	MSRA	4.01467	0.501834	8
ANKRD11	5.579274	0.30996	18	DUSP6	4.033287	0.576184	7
TBC1D16	5.542428	0.307913	18	RXRA	3.800895	0.542985	7
OPCML	5.939946	0.349409	17	SLC22A18AS	3.913593	0.652265	6
PAX6-AS1	5.00947	0.294675	17	MIR100HG	3.468902	0.57815	6
RCN1	5.00947	0.294675	17	TSNAX-DISC1	4.330247	0.866049	5
SIM1	3.834599	0.225565	17	RUNDC3A	4.179604	0.835921	5
FOXP1	5.652189	0.353262	16	PRR5L	3.888385	0.777677	5
NAV2	4.151343	0.259459	16	HOXB6	3.711412	0.742282	5
GLI2	10.6818	0.71212	15	BCAR1	3.496141	0.699228	5
BAIAP2	4.41495	0.29433	15	VOPP1	3.945338	0.986334	4
KNDC1	4.348924	0.289928	15	DTNA	3.457698	0.864424	4
ZBTB20	3.707767	0.247184	15	SLC25A10	4.417827	2.208914	2
RPS6KA2	6.415394	0.458242	14	ANKLE2	3.597331	1.798665	2
PRKAG2	5.699687	0.40712	14				
CUX1	5.448411	0.389172	14				
IQSEC1	4.576315	0.32688	14				
C7orf50	4.191569	0.299398	14				
TBX5	3.814253	0.272447	14				

TABLE 44: Cancer Type EPN_PFB_2

Gene site	imp_sum	imp_mean	n
PTPRN2	10.64422	0.129808	82
PRDM16	20.94126	0.294947	71

PCDHGA1	4.625461	0.078398	59	FOXP1	4.178346	0.261147	16
PCDHGA2	4.309075	0.075598	57	GLI2	9.179313	0.611954	15
PCDHGA3	4.309075	0.079798	54	BAIAP2	4.301727	0.286782	15
PCDHGB1	4.309075	0.081303	53	KIRREL3	3.88947	0.259298	15
PCDHGA4	4.309075	0.084492	51	KNDC1	3.806155	0.253744	15
PCDHGB2	4.309075	0.08794	49	CUX1	5.473789	0.390985	14
PCDHGA5	4.309075	0.091682	47	RPS6KA2	4.773826	0.340988	14
PCDHGB3	4.309075	0.100211	43	IQSEC1	4.576661	0.326904	14
HDAC4	9.160366	0.247577	37	PRKAG2	4.566589	0.326185	14
PAX6	12.17926	0.347979	35	MSI2	6.194145	0.476473	13
RBFOX3	8.260381	0.236011	35	HOXC4	5.120243	0.393865	13
DIP2C	9.945545	0.310798	32	GSE1	4.956749	0.381288	13
SOX2-OT	7.444734	0.256715	29	CLYBL	4.880451	0.375419	13
GALNT9	3.714889	0.137588	27	RFX4	4.176726	0.321287	13
ADARB2	7.560911	0.290804	26	KIF26B	3.550082	0.273083	13
SHANK2	7.534784	0.289799	26	TNS3	4.732704	0.394392	12
AGAP1	6.452711	0.258108	25	ZC3H3	4.458258	0.371522	12
CAMTA1	6.356277	0.254251	25	MIRLET7BHG	3.820327	0.318361	12
SATB2	5.476687	0.228195	24	ADGRD1	3.795001	0.31625	12
MEIS1	3.786328	0.157764	24	MEIS2	3.703953	0.308663	12
RPTOR	10.50927	0.456925	23	CMIP	3.662126	0.305177	12
NCOR2	5.665408	0.246322	23	ZC3H12D	6.308579	0.573507	11
HOXB3	5.333976	0.231912	23	VGLL4	4.51024	0.410022	11
INPP5A	4.486591	0.195069	23	FGFR2	4.33965	0.394514	11
PRKCZ	4.776667	0.217121	22	ACOT7	5.294485	0.529449	10
SKI	7.723905	0.367805	21	SH3RF3	3.765773	0.376577	10
ZIC4	5.592501	0.26631	21	SND1	6.409491	0.712166	9
HOXA-AS3	3.813032	0.181573	21	ATP11A	5.546325	0.616258	9
SIM2	3.689477	0.175689	21	ADAMTS2	5.51799	0.61311	9
ABR	5.02434	0.251217	20	RUNX1	4.372101	0.485789	9
SDK1	4.985671	0.249284	20	GPC6	4.279437	0.475493	9
FRMD4A	3.900745	0.195037	20	SLC22A18	4.057507	0.450834	9
MAD1L1	10.37438	0.54602	19	TSPAN9	3.972817	0.441424	9
ZNF423	7.72118	0.406378	19	DLEU1	5.051633	0.631454	8
CASZ1	6.641635	0.34956	19	LINC00311	3.977828	0.497228	8
SMG1P2	4.909237	0.258381	19	TRAPPC9	3.716779	0.464597	8
BOLA2	4.909237	0.258381	19	LHX4	3.668568	0.458571	8
LOC613038	4.909237	0.258381	19	NAV1	5.538133	0.791162	7
CFAP46	3.84721	0.202485	19	RXRA	4.146925	0.592418	7
FO XK1	6.551795	0.363989	18	CXXC5	3.870947	0.552992	7
TBC1D16	5.057483	0.280971	18	HOXB-AS3	3.664901	0.523557	7
SEPTIN9	4.458712	0.247706	18	PRR5L	4.522524	0.904505	5
HOXA3	4.091188	0.227288	18	RUNDC3A	4.510368	0.902074	5
OPCML	6.375074	0.375004	17	HOXB6	3.934206	0.786841	5
PAX6-AS1	4.454477	0.262028	17	BCAR1	3.763479	0.752696	5
RCN1	4.454477	0.262028	17	RBMS3	5.001333	1.250333	4
EBF3	4.717717	0.294857	16	VOPP1	3.885374	0.971344	4
NAV2	4.486574	0.280411	16	DTNA	3.583953	0.895988	4

SLC25A10	4.433538	2.216769	2	OPCML	4.277913	0.251642	17
ANKLE2	3.768291	1.884146	2	NAV2	3.630784	0.226924	16
TABLE 45: Cancer Type EPN_PFB_3				FOXP1	3.541174	0.221323	16
				GLI2	8.564224	0.570948	15
Gene site	imp_sum	imp_mean	n	BAIAP2	6.205878	0.413725	15
PTPRN2	11.25944	0.13731	82	NFIX	4.487322	0.299155	15
PRDM16	10.83668	0.152629	71	SLX1B-			
PCDHGA1	4.725174	0.080088	59	SULT1A4	3.45221	0.230147	15
PCDHGA2	4.725174	0.082898	57	SLX1A	3.45221	0.230147	15
PCDHGA3	4.725174	0.087503	54	LOC606724	3.45221	0.230147	15
PCDHGB1	4.725174	0.089154	53	COL23A1	3.392095	0.22614	15
PCDHGA4	4.725174	0.09265	51	RPS6KA2	5.650107	0.403579	14
PCDHGB2	4.725174	0.096432	49	CUX1	4.699737	0.335695	14
PCDHGA5	4.725174	0.100536	47	PRKAG2	4.307095	0.30765	14
PCDHGB3	4.420877	0.102811	43	IQSEC1	3.413923	0.243852	14
HDAC4	10.7486	0.290503	37	CACNA1H	3.359408	0.239958	14
RBFOX3	7.590022	0.216858	35	MSI2	4.910911	0.377762	13
PAX6	3.458426	0.098812	35	GSE1	4.885898	0.375838	13
DIP2C	10.01905	0.313095	32	MYT1L	4.069793	0.313061	13
SOX2-OT	3.796971	0.13093	29	KIF26B	3.833933	0.294918	13
GALNT9	5.113729	0.189397	27	MIRLET7BHG	4.778635	0.39822	12
SHANK2	7.883804	0.303223	26	ZC3H3	4.647555	0.387296	12
ADARB2	3.627241	0.139509	26	CMIP	4.240018	0.353335	12
AGAP1	7.079758	0.28319	25	ADGRD1	3.971306	0.330942	12
CAMTA1	6.428511	0.25714	25	MAML3	3.603578	0.300298	12
PDGFRA	4.221835	0.168873	25	RASA3	3.385833	0.282153	12
RPTOR	9.645559	0.419372	23	CTNNA2	3.281086	0.273424	12
NCOR2	6.617263	0.287707	23	VGLL4	4.388228	0.39893	11
HOXB3	3.617653	0.157289	23	TBCD	3.611524	0.32832	11
PRKCZ	3.516451	0.159839	22	SPON2	3.420958	0.310996	11
SKI	8.472504	0.403453	21	CTBP2	3.387802	0.307982	11
ZIC4	4.417608	0.210362	21	RAD51B	3.273957	0.297632	11
ABR	6.032617	0.301631	20	AUTS2	4.1794	0.41794	10
FRMD4A	5.405346	0.270267	20	ACOT7	3.657825	0.365783	10
SDK1	4.210196	0.21051	20	ATP11A	5.797338	0.644149	9
MAD1L1	9.027777	0.475146	19	SND1	5.407752	0.600861	9
ZNF423	8.819575	0.464188	19	RUNX1	4.813294	0.53481	9
CASZ1	7.223512	0.380185	19	TSPAN9	3.624113	0.402679	9
SMG1P2	4.699263	0.24733	19	CACNA2D4	3.508756	0.389862	9
BOLA2	4.699263	0.24733	19	KAZN	3.459391	0.384377	9
LOC613038	4.699263	0.24733	19	ADAMTS2	3.387526	0.376392	9
KCNQ1	3.721046	0.195845	19	DLEU1	5.128955	0.641119	8
FO XK1	6.592575	0.366254	18	RORA	4.728827	0.591103	8
TBC1D16	5.752235	0.319569	18	LHX4	4.710325	0.588791	8
SEPTIN9	5.262248	0.292347	18	AFF3	4.070909	0.508864	8
MCF2L	3.453333	0.191852	18	MSRA	3.470129	0.433766	8
PAX6-AS1	4.768791	0.280517	17	RXRA	4.622069	0.660296	7
RCN1	4.768791	0.280517	17	NAV1	3.295544	0.470792	7

LHX2	3.277039	0.468148	7	TBX15	2.864971	0.168528	17
RUNDC3A	4.323891	0.864778	5	HBG2	2.761104	0.162418	17
TSNAX-DISC1	3.718752	0.74375	5	FOXP1	4.56657	0.285411	16
IFT80	3.555972	0.711194	5	EBF3	3.552658	0.222041	16
BCAR1	3.455726	0.691145	5	NAV2	3.185503	0.199094	16
PRR5L	3.445009	0.689002	5	SORBS2	3.165694	0.197856	16
VOPPI	3.63351	0.908377	4	GLI2	7.900942	0.526729	15
RBMS3	3.507961	0.87699	4	BAIAP2	4.598937	0.306596	15
SLC25A10	4.224294	2.112147	2	NFIX	4.032807	0.268854	15
ANKLE2	3.376797	1.688399	2	SLX1B-SULT1A4	3.487957	0.23253	15
TABLE 46: Cancer Type EPN_PFB_4				SLX1A	3.487957	0.23253	15
Gene site	imp_sum	imp_mean	n	LOC606724	3.487957	0.23253	15
PTPRN2	9.754981	0.118963	82	KIRREL3	3.232994	0.215533	15
PRDM16	13.42466	0.18908	71	LRMDA	3.152952	0.210197	15
HDAC4	9.67948	0.261608	37	RPS6KA2	5.767982	0.411999	14
RBFOX3	5.7616	0.164617	35	CUX1	4.361508	0.311536	14
PAX6	4.761217	0.136035	35	C7orf50	3.691524	0.26368	14
DIP2C	8.308398	0.259637	32	ARHGEF10	3.185612	0.227544	14
SOX2-OT	3.781182	0.130386	29	PRKAG2	3.118083	0.22272	14
GALNT9	3.659274	0.135529	27	MSI2	5.350692	0.411592	13
SHANK2	4.397145	0.169121	26	GSE1	4.20783	0.323679	13
AGAP1	7.614459	0.304578	25	HOXC4	4.020625	0.309279	13
CAMTA1	4.517669	0.180707	25	RFX4	3.932162	0.302474	13
PDGFRA	3.958665	0.158347	25	KIF26B	3.425524	0.263502	13
RPTOR	9.507141	0.413354	23	CLYBL	3.13253	0.240964	13
NCOR2	7.694682	0.334551	23	ADGRD1	3.799622	0.316635	12
HOXB3	4.353924	0.189301	23	ZC3H3	3.778042	0.314837	12
NXN	3.725682	0.161986	23	TNS3	3.47612	0.289677	12
RIMBP2	2.932044	0.12748	23	RASA3	3.461626	0.288469	12
PRKCZ	4.460639	0.202756	22	MIRLET7BHG	3.280793	0.273399	12
SKI	7.174851	0.34166	21	CMIP	3.237477	0.26979	12
ABR	3.173557	0.158678	20	MEGF6	3.108194	0.259016	12
MAD1L1	8.136349	0.428229	19	LRBA	2.98263	0.248553	12
ZNF423	7.654871	0.402888	19	RAD51B	4.407876	0.400716	11
CASZ1	5.117286	0.269331	19	VGLL4	3.312149	0.301104	11
SMG1P2	3.870562	0.203714	19	SPON2	3.021012	0.274637	11
BOLA2	3.870562	0.203714	19	ACOT7	4.363092	0.436309	10
LOC613038	3.870562	0.203714	19	ADGRA1	3.005443	0.300544	10
KCNQ1	2.770132	0.145796	19	ANKS1B	2.745824	0.274582	10
SEPTIN9	5.085943	0.282552	18	SND1	6.445786	0.716198	9
FOXK1	3.982923	0.221274	18	ATP11A	3.993485	0.443721	9
ANKRD11	3.179216	0.176623	18	RUNX1	3.668851	0.40765	9
RBFOX1	2.833921	0.15744	18	ADAMTS2	3.344618	0.371624	9
PAX6-AS1	6.991442	0.411261	17	TSPAN9	3.203848	0.355983	9
RCN1	6.991442	0.411261	17	DLEU1	4.281097	0.535137	8
OPCML	5.525355	0.325021	17	MSRA	4.095142	0.511893	8
SIM1	3.239462	0.190557	17	LHX4	3.732792	0.466599	8

LINC00311	3.48934	0.436167	8	GLI2	3.249755	0.21665	15
AFF3	3.192509	0.399064	8	BAIAP2	2.020019	0.134668	15
MACROD1	3.049246	0.381156	8	CUX1	2.880317	0.205737	14
ESRRG	2.782387	0.347798	8	RPS6KA2	2.432854	0.173775	14
RXRA	3.991019	0.570146	7	MIR548F5	1.87059	0.133614	14
PRKCA	2.732046	0.390292	7	KIF26B	2.463411	0.189493	13
SLC22A18AS	3.21655	0.536092	6	RFX4	2.459586	0.189199	13
FAM181A	3.132089	0.522015	6	MSI2	1.943557	0.149504	13
CRADD	2.986429	0.497738	6	MYT1L	1.687426	0.129802	13
PRR5L	4.220856	0.844171	5	ADGRD1	2.522095	0.210175	12
RUNDC3A	3.896503	0.779301	5	FBRSL1	2.208379	0.184032	12
TSNAX-DISC1	3.804691	0.760938	5	ZC3H3	2.008673	0.167389	12
IFT80	2.761688	0.552338	5	MIRLET7BHG	1.691575	0.140965	12
CRB2	3.298683	0.824671	4	MAML3	1.58193	0.131827	12
VOPPI	2.967116	0.741779	4	ZC3H12D	2.923161	0.265742	11
GRIN2B	2.872451	0.957484	3	CTBP2	2.005876	0.182352	11
DAGLB	2.752212	0.917404	3	SH3RF3	2.498859	0.249886	10
SLC25A10	4.463499	2.23175	2	ACOT7	2.319072	0.231907	10
TABLE 47:	Cancer Type EPN_PFB_5			WT1	2.219465	0.221947	10
				BCL11B	2.138854	0.213885	10
Gene site	imp_sum	imp_mean	n	AKAP13	1.704292	0.170429	10
PTPRN2	4.46851	0.054494	82	SLC22A18	3.499743	0.38886	9
PRDM16	6.483381	0.091315	71	SND1	3.135897	0.348433	9
HDAC4	9.176118	0.248003	37	ATP11A	3.070559	0.341173	9
PAX6	4.84465	0.138419	35	TSPAN9	2.635775	0.292864	9
RBFOX3	3.097536	0.088501	35	ADAMTS2	1.980199	0.220022	9
DIP2C	2.944686	0.092021	32	AXIN2	1.953341	0.217038	9
SOX2-OT	2.029367	0.069978	29	CACNA2D4	1.774977	0.19722	9
ADARB2	3.327972	0.127999	26	RORA	2.616519	0.327065	8
AGAP1	3.839349	0.153574	25	MECOM	2.340984	0.292623	8
CAMTA1	2.746112	0.109844	25	DLEU1	1.911684	0.23896	8
PDGFRA	2.255211	0.090208	25	NAV1	3.138964	0.448423	7
MEIS1	1.598138	0.066589	24	ITPK1	1.998211	0.285459	7
INPP5A	2.40014	0.104354	23	PITPNC1	1.855749	0.265107	7
RPTOR	2.183762	0.094946	23	TACC2	1.700116	0.242874	7
RIMBP2	1.61115	0.07005	23	LHX2	1.65945	0.237064	7
PRKCZ	2.212583	0.100572	22	TAF4A	1.624949	0.232136	7
SKI	5.060951	0.240998	21	C1orf94	1.615256	0.230751	7
ZIC4	1.665744	0.079321	21	FBXL18	2.981045	0.496841	6
SDK1	4.455208	0.22276	20	LRRFIP1	2.215662	0.369277	6
FRMD4A	2.685163	0.134258	20	SLC22A18AS	1.734773	0.289129	6
MAD1L1	5.054423	0.266022	19	DENND3	1.704292	0.284049	6
ZNF423	3.168039	0.166739	19	FAM181A	1.650962	0.27516	6
FOXK1	3.297041	0.183169	18	PTPRG	1.649666	0.274944	6
RBFOX1	2.862815	0.159045	18	PRR5L	2.98927	0.597854	5
SEPTIN9	2.798426	0.155468	18	RUNDC3A	2.945389	0.589078	5
OPCML	2.522854	0.148403	17	AP2A2	2.327598	0.46552	5
NAV2	3.636725	0.227295	16	TSNAX-DISC1	2.19047	0.438094	5

NRCAM	1.974293	0.394859	5	AGAP1	9.977599	0.399104	25
VAV2	1.700459	0.340092	5	CAMTA1	7.307139	0.292286	25
TENM4	3.56457	0.891143	4	PDGFRA	5.039539	0.201582	25
CRB2	2.560978	0.640245	4	SATB2	6.869827	0.286243	24
VOPP1	2.342273	0.585568	4	MEIS1	4.057547	0.169064	24
HK1	1.730885	0.432721	4	RPTOR	10.63516	0.462398	23
GCK	3.08857	1.029523	3	NCOR2	8.031995	0.349217	23
PLXNC1	2.249994	0.749998	3	RIMBP2	6.227338	0.270754	23
LRP2	2.090608	0.696869	3	INPP5A	4.07289	0.177082	23
SLC6A9	1.844057	0.614686	3	PRKCZ	6.578606	0.299028	22
ZNF536	1.688754	0.562918	3	SKI	12.54878	0.597561	21
GRIN2B	1.622195	0.540732	3	FRMD4A	6.162069	0.308103	20
DAGLB	1.612261	0.53742	3	ABR	5.331761	0.266588	20
SLC25A10	3.804738	1.902369	2	CASZ1	12.44942	0.655233	19
CHTF18	1.796626	0.898313	2	ZNF423	10.80291	0.568574	19
ANKLE2	1.796345	0.898173	2	MAD1L1	10.12687	0.532993	19
PDE4D	1.670607	0.835304	2	SMG1P2	5.095489	0.268184	19
MLLT1	1.607184	0.803592	2	BOLA2	5.095489	0.268184	19
ZIC5	1.603097	0.801548	2	LOC613038	5.095489	0.268184	19
RABGAP1L	2.233425	2.233425	1	FOXK1	5.739273	0.318849	18
RNF4	2.181539	2.181539	1	SEPTIN9	5.347458	0.297081	18
ACAD10	2.071929	2.071929	1	ANKRD11	4.533038	0.251835	18
C10orf105	1.897344	1.897344	1	TBC1D16	4.319345	0.239964	18
GRTPI	1.739101	1.739101	1	OPCML	7.479851	0.439991	17
DPY19L1P1	1.654306	1.654306	1	PAX6-AS1	4.50606	0.265062	17
TABLE 48:	Cancer Type EPN_RELN_Like_A			RCN1	4.50606	0.265062	17
				FOXP1	5.290618	0.330664	16
Gene site	imp_sum	imp_mean	n	EBF3	4.42745	0.276716	16
PTPRN2	18.96264	0.231252	82	GLI2	8.995217	0.599681	15
PRDM16	17.17107	0.241846	71	BAIAP2	5.866399	0.391093	15
PCDHGA1	5.310824	0.090014	59	KIRREL3	5.358859	0.357257	15
PCDHGA2	5.310824	0.093172	57	NFIX	5.357149	0.357143	15
PCDHGA3	5.310824	0.098349	54	ZBTB20	4.91273	0.327515	15
PCDHGB1	5.310824	0.100204	53	CUX1	5.73646	0.409747	14
PCDHGA4	5.310824	0.104134	51	RPS6KA2	5.57806	0.398433	14
PCDHGB2	5.30142	0.108192	49	C7orf50	4.361648	0.311546	14
PCDHGA5	4.567029	0.097171	47	MSI2	6.655446	0.511957	13
PCDHGB3	4.250643	0.098852	43	MYT1L	4.804576	0.369583	13
HDAC4	10.24476	0.276885	37	KIF26B	4.424066	0.340313	13
PAX6	11.80595	0.337313	35	CLYBL	4.212438	0.324034	13
RBFOX3	6.523044	0.186373	35	GSE1	3.963453	0.304881	13
DIP2C	8.912799	0.278525	32	ZC3H3	6.297857	0.524821	12
PCDHGA9	4.120281	0.132912	31	CMIP	5.610394	0.467533	12
SOX2-OT	6.262955	0.215964	29	TNS3	5.516677	0.459723	12
GALNT9	4.782744	0.177139	27	MIRLET7BHG	5.302931	0.441911	12
ADARB2	6.83138	0.262745	26	MAML3	4.779313	0.398276	12
SHANK2	5.402521	0.207789	26	ZC3H12D	5.434465	0.494042	11
				SPON2	4.314227	0.392202	11

CTBP2	4.268214	0.388019	11	DIP2C	8.212701	0.256647	32
ACOT7	5.073081	0.507308	10	SHANK2	3.83591	0.147535	26
AKAP13	4.530778	0.453078	10	AGAP1	5.482431	0.219297	25
IGF1R	3.911352	0.391135	10	PDGFRA	3.144052	0.125762	25
SND1	5.767781	0.640865	9	CAMTA1	2.660756	0.10643	25
ATP11A	5.572346	0.61915	9	RPTOR	7.607041	0.330741	23
ASAP1	5.194917	0.577213	9	NXN	4.617392	0.200756	23
KCNH2	5.12592	0.569547	9	NCOR2	4.450173	0.193486	23
ADAMTS2	4.690699	0.521189	9	RIMBP2	3.898763	0.169511	23
KAZN	4.625799	0.513978	9	INPP5A	2.501373	0.108755	23
GPC6	4.588583	0.509843	9	SKI	6.831676	0.325318	21
SLC22A18	4.576435	0.508493	9	FRMD4A	4.473011	0.223651	20
TSPAN9	4.438942	0.493216	9	MAD1L1	7.081564	0.372714	19
NOTCH1	4.239227	0.471025	9	ZNF423	3.653806	0.192306	19
PACS2	4.130017	0.458891	9	SMG1P2	3.167207	0.166695	19
TRAPPC12	4.122235	0.458026	9	BOLA2	3.167207	0.166695	19
LHX4	5.440953	0.680119	8	LOC613038	3.167207	0.166695	19
DLEU1	5.334289	0.666786	8	CASZ1	2.518759	0.132566	19
MSRA	4.729411	0.591176	8	ANKRD11	3.711528	0.206196	18
LINC00311	4.337721	0.542215	8	FOXK1	3.303989	0.183555	18
NRXN1	3.917334	0.489667	8	SEPTIN9	2.365648	0.131425	18
PPP2R2B	3.884981	0.485623	8	TBX15	3.629988	0.213529	17
KDM4B	4.077813	0.679636	6	OPCML	2.793909	0.164348	17
SLC22A18AS	3.993219	0.665537	6	FOXP1	3.316318	0.20727	16
RUNDC3A	4.824861	0.964972	5	SORBS2	3.060689	0.191293	16
KLHL25	4.759709	0.951942	5	NAV2	2.448398	0.153025	16
ARHGEF7	4.23351	0.846702	5	BAIAP2	6.727984	0.448532	15
TSNAX-DISC1	4.134782	0.826956	5	GLI2	5.852392	0.390159	15
CACNA1I	4.067336	0.813467	5	LRMDA	4.396956	0.29313	15
RAPGEF4	3.934423	0.786885	5	SLX1B-			
NDST1	4.171788	1.042947	4	SULT1A4	2.601392	0.173426	15
RBMS3	4.018327	1.004582	4	SLX1A	2.601392	0.173426	15
ANKLE2	3.901795	1.950898	2	LOC606724	2.601392	0.173426	15
				RPS6KA2	4.913033	0.350931	14
				C7orf50	3.631155	0.259368	14
				PRKAG2	3.252456	0.232318	14
				IQSEC1	3.004048	0.214575	14
				MOB2	2.55029	0.182164	14
				ARHGEF10	2.468803	0.176343	14
				MYT1L	3.298473	0.253729	13
				MSI2	3.141991	0.241692	13
				MIR9-3HG	2.575378	0.198106	13
				GSE1	2.523138	0.194088	13
				MIRLET7BHG	4.024739	0.335395	12
				ZC3H3	3.214761	0.267897	12
				GNA12	3.054646	0.254554	12
				CTNNA2	2.852575	0.237715	12
				RAD51B	3.708749	0.337159	11

TABLE 49: Cancer Type EPN_RELN_Like_B							
Gene site	imp_sum	imp_mean	n				
PTPRN2	8.75796	0.106804	82				
PRDM16	7.915152	0.111481	71				
PCDHGA1	3.231128	0.054765	59				
PCDHGA2	2.914742	0.051136	57				
PCDHGA3	2.598356	0.048118	54				
PCDHGB1	2.598356	0.049026	53				
PCDHGB2	2.598356	0.053028	49				
PCDHGA5	2.598356	0.055284	47				
HDAC4	7.807278	0.211008	37				
PAX6	4.474432	0.127841	35				
RBFOX3	3.785148	0.108147	35				

FGFR2	3.340094	0.303645	11	HDAC4	9.792911	0.264673	37
COL4A1	2.802232	0.254748	11	RBFOX3	6.142056	0.175487	35
ZC3H12D	2.63323	0.239385	11	PAX6	3.959655	0.113133	35
VGLL4	2.392066	0.217461	11	DIP2C	4.684374	0.146387	32
TSPAN4	3.385127	0.338513	10	ADARB2	4.939766	0.189991	26
NR2F1-AS1	3.342812	0.334281	10	SHANK2	4.853133	0.186659	26
FMN1	2.947547	0.294755	10	AGAP1	6.329685	0.253187	25
MAML2	2.479743	0.247974	10	CAMTA1	4.983153	0.199326	25
BCL11B	2.467026	0.246703	10	PDGFRA	2.555145	0.102206	25
CHST11	2.421051	0.242105	10	SATB2	3.113167	0.129715	24
AXIN2	4.265368	0.47393	9	MEIS1	3.111077	0.129628	24
SND1	3.882986	0.431443	9	NXN	5.39116	0.234398	23
ADAMTS2	3.725764	0.413974	9	NCOR2	5.355784	0.23286	23
TSPAN9	3.365121	0.373902	9	RPTOR	5.185304	0.225448	23
CACNA2D4	2.791138	0.310126	9	HOXB3	3.364127	0.146266	23
NOTCH1	2.699126	0.299903	9	PRKCZ	3.297049	0.149866	22
MGMT	2.630872	0.292319	9	SKI	4.176808	0.198896	21
APBA2	2.434052	0.27045	9	FRMD4A	5.580653	0.279033	20
ASPSCR1	4.941479	0.617685	8	SDK1	3.758879	0.187944	20
MSRA	3.824307	0.478038	8	MAD1L1	7.932548	0.417503	19
LHX4	3.00188	0.375235	8	CASZ1	4.757279	0.250383	19
LINC00311	2.710199	0.338775	8	SMG1P2	3.795435	0.19976	19
DLEU1	2.410444	0.301305	8	BOLA2	3.795435	0.19976	19
LINC01140	3.236537	0.462362	7	LOC613038	3.795435	0.19976	19
PCCA	3.02946	0.43278	7	KCNQ1	2.95117	0.155325	19
GAK	2.700565	0.385795	7	CFAP46	2.64123	0.139012	19
C19orf25	2.678181	0.382597	7	FOXK1	5.958762	0.331042	18
LTF	2.474482	0.353497	7	TBC1D16	4.918471	0.273248	18
LHPP	2.438772	0.348396	7	RBFOX1	2.685368	0.149187	18
NAV1	2.355967	0.336567	7	OPCML	3.268202	0.192247	17
FBXL18	3.275702	0.54595	6	FOXP1	3.996994	0.249812	16
CCDC177	2.894281	0.48238	6	SORBS2	2.610353	0.163147	16
COLEC11	2.46434	0.410723	6	GLI2	5.057189	0.337146	15
RUNDC3A	3.816148	0.76323	5	EMX2OS	3.637625	0.242508	15
KLHL25	2.869872	0.573974	5	BAIAP2	3.481082	0.232072	15
TK1	2.503038	0.500608	5	NFIX	2.913399	0.194227	15
EXPH5	2.46519	0.493038	5	SLX1B-			
DICER1	3.31541	1.105137	3	SULT1A4	2.7081	0.18054	15
SLC6A9	2.771843	0.923948	3	SLX1A	2.7081	0.18054	15
SLC25A10	2.783936	1.391968	2	LOC606724	2.7081	0.18054	15
CHTF18	2.668617	1.334309	2	IQSEC1	4.665443	0.333246	14
ANKLE2	2.628808	1.314404	2	RPS6KA2	2.90531	0.207522	14
				CUX1	2.806976	0.200498	14
				PRKAG2	2.420803	0.172914	14
				GSE1	3.850896	0.296223	13
				KIF26B	2.904956	0.223458	13
				GNA12	4.711493	0.392624	12
				TNS3	3.09073	0.257561	12

TABLE 50:				Cancer Type			
				EPN_RELX_Like_C			
Gene site	imp_sum	imp_mean	n				
PTPRN2	6.388245	0.077905	82				
PRDM16	10.31376	0.145264	71				

MAML3	3.052777	0.254398	12	EOGT	2.409254	1.204627	2
ZC3H3	2.892362	0.24103	12	ANKLE2	2.372184	1.186092	2
MEIS2	2.876291	0.239691	12	SLC25A10	2.366913	1.183456	2
CMIP	2.785533	0.232128	12				
ADGRD1	2.366348	0.197196	12				
ZC3H12D	3.563105	0.323919	11	TABLE 51:	Cancer Type	EPN_SPINE	
RAD51B	3.110039	0.282731	11	Gene site	imp_sum	imp_mean	n
ANAPC16	2.658012	0.241637	11	PTPRN2	18.00703	0.219598	82
VGLL4	2.586591	0.235145	11	PRDM16	21.20807	0.298705	71
GAS7	3.014548	0.301455	10	HDAC4	13.01415	0.351734	37
NR2F1-AS1	3.000588	0.300059	10	PAX6	7.995691	0.228448	35
IGF1R	2.660186	0.266019	10	RBFOX3	6.970477	0.199156	35
TSPAN4	2.382834	0.238283	10	DIP2C	10.38479	0.324525	32
SND1	4.833414	0.537046	9	SOX2-OT	6.360972	0.219344	29
AXIN2	3.035017	0.337224	9	GALNT9	5.328999	0.19737	27
TRAPPC12	2.80405	0.311561	9	SHANK2	5.135682	0.197526	26
KCNH2	2.51942	0.279936	9	AGAP1	8.123733	0.324949	25
APBA2	2.505382	0.278376	9	CAMTA1	6.624628	0.264985	25
KAZN	2.494474	0.277164	9	SATB2	4.364773	0.181866	24
KCNMA1	2.478381	0.275376	9	NCOR2	8.301598	0.360939	23
ADAMTS2	2.473136	0.274793	9	RPTOR	8.110635	0.352636	23
LHX4	3.455697	0.431962	8	RIMBP2	4.596968	0.199868	23
DNMT3A	3.206566	0.400821	8	PRKCZ	4.078898	0.185404	22
VRK2	2.814389	0.351799	8	SKI	10.08525	0.48025	21
TRAPPC9	2.399386	0.299923	8	ZIC4	3.955615	0.188363	21
C19orf25	3.027249	0.432464	7	SDK1	5.291577	0.264579	20
NAV1	2.631295	0.375899	7	ABR	4.94313	0.247157	20
WWOX	2.430468	0.34721	7	FRMD4A	4.534796	0.22674	20
AGO2	2.369084	0.338441	7	MAD1L1	10.78786	0.567782	19
FBXL18	3.322959	0.553826	6	CASZ1	7.839378	0.412599	19
SLC22A18AS	3.084762	0.514127	6	ZNF423	7.19556	0.378714	19
STRA6	2.641257	0.440209	6	SMG1P2	5.068935	0.266786	19
C10orf90	2.622107	0.437018	6	BOLA2	5.068935	0.266786	19
COQ8A	2.579869	0.429978	6	LOC613038	5.068935	0.266786	19
CCDC177	2.55317	0.425528	6	SEPTIN9	6.749913	0.374995	18
COLEC11	2.525162	0.42086	6	TBC1D16	6.521948	0.36233	18
STK10	2.519602	0.419934	6	RBFOX1	5.168689	0.287149	18
NUMA1	2.423579	0.40393	6	FO XK1	3.802433	0.211246	18
ARHGEF7	3.999335	0.799867	5	ANKRD11	3.67135	0.203964	18
CACNA1I	3.715944	0.743189	5	OPCML	8.390771	0.493575	17
TK1	2.677213	0.535443	5	NAV2	5.952011	0.372001	16
SDK2	2.515765	0.503153	5	FOXP1	5.76391	0.360244	16
DTNA	2.688749	0.672187	4	EBF3	4.427132	0.276696	16
DICER1	2.758525	0.919508	3	SORBS2	4.389494	0.274343	16
SLC6A9	2.689165	0.896388	3	BAIAP2	5.503545	0.366903	15
DAGLB	2.676754	0.892251	3	GLI2	5.395369	0.359691	15
SLC25A22	2.467789	0.822596	3	LRMDA	4.368683	0.291246	15
SOX10	2.415804	1.207902	2	NFIX	4.022804	0.268187	15

SLX1B-SULT1A4	3.543156	0.23621	15	LRRFIP1	3.599162	0.59986	6
SLX1A	3.543156	0.23621	15	FAM181A	3.597879	0.599647	6
LOC606724	3.543156	0.23621	15	DENND3	3.442411	0.573735	6
RPS6KA2	7.164354	0.51174	14	TSNAX-DISC1	4.470584	0.894117	5
CUX1	6.139501	0.438536	14	BCAR1	4.298052	0.85961	5
C7orf50	3.830526	0.273609	14	RUNDC3A	3.826841	0.765368	5
MIR548F5	3.805653	0.271832	14	PRR5L	3.551702	0.71034	5
IQSEC1	3.699906	0.264279	14	VOPP1	3.871078	0.967769	4
MSI2	6.515431	0.501187	13	DTNA	3.738399	0.9346	4
GSE1	6.362104	0.489393	13	CCDC167	3.465475	1.155158	3
RFX4	5.069011	0.389924	13	SLC25A10	4.701776	2.350888	2
KIF26B	4.02975	0.309981	13	ANKLE2	3.649509	1.824755	2
CLYBL	3.93966	0.303051	13	TABLE 52:	Cancer Type		
ZC3H3	5.204388	0.433699	12		EPN_SPINE_MYCN		
MEIS2	4.613977	0.384498	12	Gene site	imp_sum	imp_mean	n
FBRSL1	4.582972	0.381914	12	PTPRN2	6.492942	0.079182	82
MEGF6	4.143271	0.345273	12	PRDM16	7.7856	0.109656	71
TNS3	3.906942	0.325579	12	PCDHGA1	3.162956	0.053609	59
MAML3	3.574924	0.29791	12	PCDHGA2	3.162956	0.05549	57
TBX4	3.547774	0.295648	12	PCDHGA3	3.162956	0.058573	54
ZC3H12D	6.090734	0.553703	11	PCDHGB1	3.162956	0.059678	53
VGLL4	4.273837	0.388531	11	PCDHGA4	3.162956	0.062019	51
SPON2	3.617264	0.328842	11	PCDHGB2	2.84657	0.058093	49
AKAP13	5.145785	0.514579	10	PCDHGA5	2.530184	0.053834	47
TSPAN4	3.955269	0.395527	10	PCDHGB3	2.530184	0.058841	43
NR2F1-AS1	3.943816	0.394382	10	PCDHGA6	2.530184	0.063255	40
ADGRA1	3.563767	0.356377	10	HDAC4	5.62407	0.152002	37
GAS7	3.524642	0.352464	10	PCDHGA7	2.530184	0.068383	37
SH3RF3	3.482212	0.348221	10	PAX6	3.986653	0.113904	35
SND1	5.671606	0.630178	9	PCDHGB4	2.530184	0.072291	35
TSPAN9	5.566682	0.61852	9	PCDHGA8	2.530184	0.072291	35
ATP11A	4.94636	0.549596	9	DIP2C	4.775328	0.149229	32
CACNA2D4	4.67568	0.51952	9	PCDHGB5	2.213798	0.069181	32
ADAMTS2	4.189157	0.465462	9	PCDHGA9	2.213798	0.071413	31
KCNH2	3.889556	0.432173	9	GALNT9	3.892155	0.144154	27
AXIN2	3.837607	0.426401	9	AGAP1	3.423555	0.136942	25
NOTCH1	3.620084	0.402232	9	CAMTA1	3.338662	0.133546	25
MGMT	3.598229	0.399803	9	SATB2	4.430963	0.184623	24
ASAP1	3.584188	0.398243	9	RPTOR	3.916326	0.170275	23
MSRA	5.061993	0.632749	8	SKI	5.889311	0.280443	21
LHX4	4.717822	0.589728	8	HOXA-AS3	3.973196	0.1892	21
MCC	4.073128	0.509141	8	ZIC4	3.270454	0.155736	21
DLEU1	3.720543	0.465068	8	SIM2	2.463619	0.117315	21
NAV1	4.946607	0.706658	7	ABR	2.43546	0.121773	20
CXXC5	3.859552	0.551365	7	FRMD4A	2.285651	0.114283	20
VPS13D	3.741837	0.534548	7	MAD1L1	4.81219	0.253273	19
SLC22A18AS	4.24026	0.70671	6	SMG1P2	4.027895	0.211994	19

BOLA2	4.027895	0.211994	19	RXRA	2.105226	0.300747	7
LOC613038	4.027895	0.211994	19	ARHGAP45	3.123683	0.520614	6
ZNF423	3.885737	0.204512	19	FBXL18	2.962263	0.49371	6
FOXK1	2.547433	0.141524	18	SATB2-AS1	2.871803	0.478634	6
SIM1	5.801214	0.341248	17	LRRFIP1	2.353039	0.392173	6
OPCML	3.150464	0.185321	17	PRR5L	3.2963	0.65926	5
TBX15	2.737097	0.161006	17	BCAR1	2.164598	0.43292	5
FOXP1	2.73496	0.170935	16	RUNDC3A	2.065769	0.413154	5
NAV2	2.531088	0.158193	16	VOPPI	2.76606	0.691515	4
GLI2	4.935341	0.329023	15	OLFM1	2.67317	0.668293	4
EMX2OS	2.453844	0.16359	15	CRB2	2.620027	0.655007	4
SLX1B-				GABRB3	2.614687	0.653672	4
SULT1A4	2.134165	0.142278	15	LAIR1	2.532069	0.633017	4
SLX1A	2.134165	0.142278	15	DTNA	2.209257	0.552314	4
LOC606724	2.134165	0.142278	15	RBMS3	2.174902	0.543726	4
BAIAP2	2.043891	0.136259	15	NDST1	2.090472	0.522618	4
GNG7	2.455568	0.175398	14	BCAT1	2.182819	0.727606	3
RPS6KA2	2.230171	0.159298	14	SLC25A10	3.725949	1.862975	2
MSI2	2.807782	0.215983	13	HNF1B	2.452458	1.226229	2
CLYBL	2.577345	0.198257	13	ACMSD	2.983202	2.983202	1
MYT1L	2.571778	0.197829	13	ACAD10	2.098791	2.098791	1
FBRSL1	3.083854	0.256988	12				
ZC3H3	2.408241	0.200687	12				
MAML3	2.168862	0.180739	12	TABLE 53:	Cancer Type		
ADGRD1	2.073695	0.172808	12	Gene site	EPN_SPINE_SE_A		
ZC3H12D	4.179757	0.379978	11	imp_sum	imp_mean	n	
RAD51B	2.468987	0.224453	11	PTPRN2	4.467313	0.054479	82
PITX2	3.85557	0.385557	10	PRDM16	5.538834	0.078012	71
ADGRA1	3.749056	0.374906	10	HDAC4	7.257234	0.196141	37
TFAP2B	3.226117	0.322612	10	RBFOX3	2.086675	0.059619	35
ACOT7	3.181729	0.318173	10	DIP2C	2.523885	0.078871	32
NR2F1-AS1	2.785737	0.278574	10	GALNT9	1.812383	0.067125	27
FMN1	2.142563	0.214256	10	ADARB2	2.334298	0.089781	26
ATP11A	3.665884	0.40732	9	AGAP1	3.980887	0.159235	25
SND1	3.162725	0.351414	9	CAMTA1	3.968255	0.15873	25
SLC22A18	2.776862	0.30854	9	SATB2	4.287825	0.178659	24
IGF2BP1	2.408029	0.267559	9	RPTOR	3.996189	0.173747	23
RUNX1	2.348507	0.260945	9	HOXB3	2.9538	0.128426	23
AXIN2	2.162687	0.240299	9	RIMBP2	2.65345	0.115367	23
TSPAN9	2.115413	0.235046	9	NXN	2.034489	0.088456	23
AFF3	2.968832	0.371104	8	SKI	4.451828	0.211992	21
KIF26A	2.695016	0.336877	8	HOXA-AS3	3.749579	0.178551	21
MSRA	2.471942	0.308993	8	ZIC4	3.199024	0.152334	21
DLEU1	2.059775	0.257472	8	SIM2	2.58685	0.123183	21
C1orf94	2.594722	0.370675	7	ZNF423	4.318873	0.227309	19
DUSP6	2.369086	0.338441	7	MAD1L1	4.199438	0.221023	19
CLDN10	2.333333	0.333333	7	SMG1P2	2.016115	0.106111	19
TRIM2	2.136209	0.305173	7	BOLA2	2.016115	0.106111	19
				LOC613038	2.016115	0.106111	19

CASZ1	1.898316	0.099911	19	LINC00311	1.875494	0.234437	8
SEPTIN9	1.764349	0.098019	18	ESRRG	1.771343	0.221418	8
TBX15	2.619569	0.154092	17	DUSP6	2.976121	0.42516	7
OPCML	2.460219	0.144719	17	LHX2	2.213486	0.316212	7
FOXP1	3.242841	0.202678	16	NAV1	1.787504	0.255358	7
EBF3	1.824205	0.114013	16	FAM181A	2.321552	0.386925	6
GLI2	5.087536	0.339169	15	SLC22A18AS	1.888411	0.314735	6
DLX6-AS1	2.789193	0.185946	15	PRR5L	2.943148	0.58863	5
EMX2OS	2.767121	0.184475	15	RUNDC3A	2.868566	0.573713	5
BAIAP2	2.224255	0.148284	15	PDE4B	2.389689	0.477938	5
NFATC1	1.776564	0.118438	15	HOXB6	2.066272	0.413254	5
CUX1	2.87708	0.205506	14	GRIP1	1.946106	0.389221	5
RPS6KA2	2.122895	0.151635	14	KLHL25	1.92724	0.385448	5
IQSEC1	1.951216	0.139373	14	ARHGEF7	1.839995	0.367999	5
MSI2	2.877331	0.221333	13	MCPH1	1.778196	0.355639	5
MYT1L	2.671325	0.205487	13	CRB2	1.947448	0.486862	4
CLYBL	2.480584	0.190814	13	DTNA	1.876086	0.469022	4
RFX4	2.104561	0.161889	13	GATA6	1.875189	0.468797	4
ZC3H3	2.345505	0.195459	12	PPM1H	1.766097	0.441524	4
MIRLET7BHG	2.116093	0.176341	12	GRIN2B	1.967055	0.655685	3
CMIP	2.115268	0.176272	12	DICER1	1.860287	0.620096	3
FBRSL1	2.040479	0.17004	12	SLC25A10	3.588723	1.794361	2
MEGF6	1.757851	0.146488	12	ANKLE2	2.019678	1.009839	2
RAD51B	1.854509	0.168592	11	SOX10	2.000114	1.000057	2
NR2F1-AS1	2.721518	0.272152	10	ACMSD	3.011469	3.011469	1
ACOT7	2.542456	0.254246	10	GRTP1	2.569028	2.569028	1
EBF1	2.314205	0.23142	10	ACAD10	2.131225	2.131225	1
PITX2	2.081013	0.208101	10	C10orf105	1.947394	1.947394	1
NR5A2	2.038764	0.203876	10	AK1	1.790931	1.790931	1
BCL11B	2.027634	0.202763	10				
TFAP2B	1.983684	0.198368	10	TABLE 54:	Cancer Type	EPN_SPINE_SE_B	
SPPL2B	1.761071	0.176107	10	Gene site	imp_sum	imp_mean	n
ATP11A	3.269095	0.363233	9	PTPRN2	20.69829	0.252418	82
RUNX1	2.889558	0.321062	9	PRDM16	22.9618	0.323406	71
SLC22A18	2.832039	0.314671	9	PCDHGA1	4.918729	0.083368	59
SND1	2.665522	0.296169	9	PCDHGA2	4.918729	0.086293	57
KAZN	2.529525	0.281058	9	PCDHGA3	4.198881	0.077757	54
AXIN2	2.34763	0.260848	9	PCDHGB1	4.198881	0.079224	53
TRAPPC12	2.32492	0.258324	9	PCDHGA4	4.198881	0.082331	51
ADAMTS2	2.039645	0.226627	9	PCDHGB2	4.198881	0.085691	49
NOTCH1	1.991879	0.22132	9	PCDHGA5	4.198881	0.089338	47
TSPAN9	1.824324	0.202703	9	HDAC4	14.31085	0.38678	37
GATA4	2.510676	0.313834	8	PAX6	13.13532	0.375295	35
AFF3	2.510149	0.313769	8	RBFOX3	9.970229	0.284864	35
MSRA	2.302983	0.287873	8	DIP2C	11.0602	0.345631	32
DLEU1	2.271895	0.283987	8	SOX2-OT	11.19802	0.386139	29
RORA	2.087459	0.260932	8	GALNT9	7.862966	0.291221	27
PPP2R2B	1.904162	0.23802	8	ADARB2	6.067064	0.233349	26

SHANK2	5.873276	0.225895	26	GSE1	4.684687	0.360361	13
AGAP1	10.57591	0.423036	25	ZC3H3	6.255098	0.521258	12
CAMTA1	6.217241	0.24869	25	MIRLET7BHG	5.826241	0.48552	12
SATB2	7.490794	0.312116	24	TNS3	5.309675	0.442473	12
MEIS1	4.165291	0.173554	24	CMIP	4.284207	0.357017	12
RPTOR	9.826889	0.427256	23	RASA3	4.172052	0.347671	12
NCOR2	9.548187	0.415139	23	ZC3H12D	6.618574	0.601689	11
INPP5A	5.536311	0.240709	23	SPON2	5.097684	0.463426	11
NXN	5.318387	0.231234	23	RAD51B	4.824109	0.438555	11
PRKCZ	6.740115	0.306369	22	GLUD1P2	4.273133	0.388467	11
SKI	13.02695	0.620331	21	VGLL4	4.240334	0.385485	11
ZIC4	4.943805	0.235419	21	ACOT7	4.858882	0.485888	10
ABR	7.6722	0.38361	20	NR2F1-AS1	4.800457	0.480046	10
FRMD4A	5.546184	0.277309	20	SH3RF3	4.580332	0.458033	10
SDK1	5.284686	0.264234	20	ADGRA1	4.305105	0.43051	10
MAD1L1	13.03724	0.686171	19	ATP11A	5.885514	0.653946	9
ZNF423	10.79861	0.568348	19	SND1	5.659362	0.628818	9
CASZ1	7.383993	0.388631	19	ADAMTS2	5.246017	0.582891	9
SMG1P2	5.64007	0.296846	19	CACNA2D4	4.926576	0.547397	9
BOLA2	5.64007	0.296846	19	RUNX1	4.681661	0.520185	9
LOC613038	5.64007	0.296846	19	TSPAN9	4.67902	0.519891	9
FOKK1	9.325676	0.518093	18	GPC6	4.339458	0.482162	9
SEPTIN9	8.261632	0.45898	18	LHX4	6.731641	0.841455	8
ANKRD11	5.545247	0.308069	18	MSRA	5.131543	0.641443	8
OPCML	7.962893	0.468405	17	ESRRG	4.630434	0.578804	8
TBX15	6.519563	0.383504	17	LINC00311	4.613139	0.576642	8
PAX6-AS1	5.623303	0.330783	17	DLEU1	4.323018	0.540377	8
RCN1	5.623303	0.330783	17	SHROOM3	4.278519	0.534815	8
SIM1	5.056549	0.297444	17	AFF3	4.217597	0.5272	8
FOXP1	4.704797	0.29405	16	DUSP6	6.489698	0.9271	7
NAV2	4.700894	0.293806	16	FBXL18	4.174415	0.695736	6
EBF3	4.510004	0.281875	16	RUNDC3A	4.871555	0.974311	5
GLI2	10.22611	0.68174	15	PRR5L	4.840978	0.968196	5
BAIAP2	6.583023	0.438868	15	ARHGEF7	4.4663	0.89326	5
KIRREL3	5.563956	0.37093	15	TSNAX-DISC1	4.405841	0.881168	5
ZBTB20	5.414394	0.36096	15	GRIN2B	4.152206	1.384069	3
NFIX	4.357147	0.290476	15	SLC25A10	4.592854	2.296427	2
SLX1B-SULT1A4	4.258454	0.283897	15	TABLE 55: Cancer Type EPN_ST_ND_A			
SLX1A	4.258454	0.283897	15	Gene site	imp_sum	imp_mean	n
LOC606724	4.258454	0.283897	15	PTPRN2	12.57252	0.153323	82
RPS6KA2	7.391291	0.527949	14	PRDM16	14.33	0.201831	71
PRKAG2	5.627199	0.401943	14	HDAC4	6.155105	0.166354	37
IQSEC1	4.523432	0.323102	14	PAX6	7.762951	0.221799	35
CUX1	4.38091	0.312922	14	RBFOX3	7.065691	0.201877	35
MSI2	7.917794	0.609061	13	DIP2C	6.741237	0.210664	32
RFX4	4.921662	0.378589	13	SOX2-OT	5.040501	0.17381	29
CLYBL	4.856825	0.373602	13	GALNT9	4.874103	0.180522	27

SHANK2	7.288743	0.280336	26	KIF26B	4.176009	0.321231	13
ADARB2	3.906834	0.150263	26	MYT1L	3.563742	0.274134	13
AGAP1	8.912881	0.356515	25	RFX4	3.506892	0.269761	13
CAMTA1	6.869073	0.274763	25	CLYBL	3.150749	0.242365	13
SATB2	7.694246	0.320594	24	GSE1	2.986001	0.229692	13
RPTOR	6.571293	0.285708	23	ZC3H3	5.844641	0.487053	12
INPP5A	4.421946	0.192259	23	TBX4	4.403033	0.366919	12
HOXB3	4.358938	0.189519	23	CMIP	4.392077	0.366006	12
RIMBP2	4.322707	0.187944	23	MEIS2	4.044825	0.337069	12
NCOR2	3.852216	0.167488	23	ADGRD1	4.029529	0.335794	12
PRKCZ	3.722508	0.169205	22	MIRLET7BHG	3.374908	0.281242	12
SKI	10.07708	0.479861	21	CTNNA2	3.246693	0.270558	12
ZIC4	5.448838	0.259468	21	FBRSL1	3.180878	0.265073	12
SDK1	5.266742	0.263337	20	VGLL4	3.209122	0.291738	11
FRMD4A	4.473937	0.223697	20	CACNA1C	3.104733	0.282248	11
ZNF423	8.417935	0.443049	19	RAD51B	2.936205	0.266928	11
MAD1L1	7.875587	0.414505	19	ACOT7	4.858651	0.485865	10
CASZ1	5.26721	0.277222	19	TP73	4.164661	0.416466	10
SMG1P2	3.458359	0.182019	19	NR2F1-AS1	3.072003	0.3072	10
BOLA2	3.458359	0.182019	19	AKAP13	2.999263	0.299926	10
LOC613038	3.458359	0.182019	19	ATP11A	5.059425	0.562158	9
FOKK1	5.183399	0.287967	18	SLC22A18	3.856998	0.428555	9
SEPTIN9	3.899176	0.216621	18	SND1	3.819203	0.424356	9
TBC1D16	3.342098	0.185672	18	ASAP1	3.802296	0.422477	9
MCF2L	3.157815	0.175434	18	RUNX1	3.343484	0.371498	9
OPCML	6.224343	0.366138	17	KCNMA1	3.216977	0.357442	9
TBX15	4.049813	0.238224	17	GPC6	2.958499	0.328722	9
PAX6-AS1	3.515691	0.206805	17	NOTCH1	2.939813	0.326646	9
RCN1	3.515691	0.206805	17	LHX4	4.780661	0.597583	8
FOXP1	5.086289	0.317893	16	DLEU1	3.942974	0.492872	8
NAV2	3.823901	0.238994	16	AFF3	3.384681	0.423085	8
SORBS2	3.076293	0.192268	16	RGS20	3.296919	0.412115	8
GLI2	9.932155	0.662144	15	NAV1	5.090853	0.727265	7
EMX2OS	5.669129	0.377942	15	RXRA	4.045082	0.577869	7
NFIX	4.441511	0.296101	15	TBR1	2.920705	0.417244	7
KNDC1	4.432388	0.295493	15	FAM181A	3.697698	0.616283	6
COL23A1	3.876927	0.258462	15	SATB2-AS1	3.660097	0.610016	6
ZBTB20	3.583497	0.2389	15	FBXL18	3.282771	0.547129	6
NFATC1	3.473814	0.231588	15	PRR5L	3.713016	0.742603	5
BAIAP2	3.181375	0.212092	15	KLHL25	3.472346	0.694469	5
RPS6KA2	5.42418	0.387441	14	TSNAX-DISC1	3.321393	0.664279	5
CUX1	4.397781	0.314127	14	RAPGEF4	3.220098	0.64402	5
PRKAG2	4.248722	0.30348	14	PPM1H	3.137802	0.784451	4
IQSEC1	3.297421	0.23553	14	SLC25A10	3.874652	1.937326	2
ARHGEF10	3.263557	0.233111	14				
C7orf50	3.069573	0.219255	14	TABLE 56:	Cancer Type	EPN_ST_SE	
MIR9-3HG	8.809367	0.677644	13	Gene site	imp_sum	imp_mean	n
MSI2	5.605766	0.431213	13	PTPRN2	14.78757	0.180336	82

PRDM16	21.56532	0.303737	71	MSI2	6.101907	0.469377	13
HDAC4	14.04352	0.379555	37	GSE1	4.626839	0.355911	13
PAX6	11.96461	0.341846	35	CLYBL	4.397876	0.338298	13
RBFOX3	8.961976	0.256056	35	MYT1L	3.996951	0.307458	13
DIP2C	9.608908	0.300278	32	ZC3H3	5.670165	0.472514	12
SOX2-OT	8.497969	0.293033	29	MIRLET7BHG	5.655803	0.471317	12
GALNT9	5.740494	0.212611	27	ADGRD1	5.166093	0.430508	12
SHANK2	7.465656	0.287141	26	TNS3	4.686673	0.390556	12
ADARB2	6.559737	0.252298	26	CMIP	4.095593	0.341299	12
AGAP1	10.25957	0.410383	25	MEGF6	3.732575	0.311048	12
CAMTA1	6.874727	0.274989	25	MEIS2	3.623368	0.301947	12
SATB2	5.351616	0.222984	24	ZC3H12D	6.265589	0.569599	11
RPTOR	9.819349	0.426928	23	RAD51B	4.404139	0.400376	11
NCOR2	7.440985	0.323521	23	ACOT7	5.071909	0.507191	10
RIMBP2	5.916542	0.257241	23	NR2F1-AS1	4.302561	0.430256	10
INPP5A	4.349603	0.189113	23	AKAP13	4.039456	0.403946	10
NXN	3.831029	0.166566	23	KLHL29	3.846141	0.384614	10
PRKCZ	7.157802	0.325355	22	ATP11A	6.082089	0.675788	9
SKI	11.11734	0.529397	21	SND1	5.90144	0.655716	9
ZIC4	7.164295	0.341157	21	ADAMTS2	4.881248	0.542361	9
FRMD4A	6.790834	0.339542	20	TRAPPC12	4.750428	0.527825	9
ABR	6.306589	0.315329	20	KAZN	4.663185	0.518132	9
SDK1	4.903644	0.245182	20	TSPAN9	4.24802	0.472002	9
MAD1L1	10.49204	0.552212	19	RUNX1	4.047814	0.449757	9
ZNF423	9.522139	0.501165	19	KCNH2	3.967067	0.440785	9
CASZ1	7.009732	0.368933	19	CACNA2D4	3.965026	0.440558	9
SMG1P2	5.475582	0.288189	19	AXIN2	3.583753	0.398195	9
BOLA2	5.475582	0.288189	19	LHX4	5.144101	0.643013	8
LOC613038	5.475582	0.288189	19	DLEU1	4.440199	0.555025	8
CFAP46	3.567633	0.18777	19	PPP2R2B	4.044065	0.505508	8
TBC1D16	6.460163	0.358898	18	AFF3	3.839932	0.479992	8
SEPTIN9	5.192761	0.288487	18	MACROD1	3.809808	0.476226	8
FO XK1	4.631213	0.25729	18	DNMT3A	3.694474	0.461809	8
ANKRD11	4.424428	0.245802	18	NAV1	4.94547	0.706496	7
MCF2L	4.332015	0.240667	18	LHX2	4.648095	0.664014	7
OPCML	6.841107	0.402418	17	RXRA	4.29991	0.614273	7
FOXP1	5.663108	0.353944	16	VPS13D	3.874879	0.553554	7
GLI2	9.954524	0.663635	15	PRKCA	3.697941	0.528277	7
BAIAP2	5.130543	0.342036	15	FBXL18	3.844834	0.640806	6
KIRREL3	4.407345	0.293823	15	FAM181A	3.81628	0.636047	6
ZBTB20	4.208394	0.28056	15	TSNAX-DISC1	4.644692	0.928938	5
NFIX	4.099719	0.273315	15	BCAR1	4.280171	0.856034	5
KNDC1	3.923233	0.261549	15	PRR5L	4.19888	0.839776	5
RPS6KA2	7.055123	0.503937	14	ARHGEF7	4.134932	0.826986	5
CUX1	6.973338	0.498096	14	RUNDC3A	4.087877	0.817575	5
PRKAG2	4.477268	0.319805	14	RBMS3	3.986484	0.996621	4
ARHGEF10	3.99234	0.285167	14	DTNA	3.828958	0.957239	4
MIR548F5	3.628218	0.259158	14	PER2	3.731991	0.932998	4

GRIN2B	3.692311	1.23077	3	BAIAP2	5.11409	0.340939	15
SLC25A10	4.834545	2.417272	2	ZBTB20	4.871469	0.324765	15
ANKLE2	4.05317	2.026585	2	SLX1B-SULT1A4	4.493723	0.299582	15
TABLE 57: Cancer Type EPN_YAP				SLX1A	4.493723	0.299582	15
Gene site	imp_sum	imp_mean	n	LOC606724	4.493723	0.299582	15
PTPRN2	17.23822	0.210222	82	NFATC1	4.395464	0.293031	15
PRDM16	23.42478	0.329926	71	RPS6KA2	7.801359	0.55724	14
HDAC4	13.23857	0.357799	37	CUX1	6.376211	0.455444	14
PAX6	21.39254	0.611215	35	PRKAG2	4.412961	0.315211	14
RBFOX3	8.512954	0.243227	35	C7orf50	3.980788	0.284342	14
DIP2C	10.6073	0.331478	32	MSI2	6.990942	0.537765	13
SOX2-OT	8.977742	0.309577	29	GSE1	5.00517	0.385013	13
GALNT9	4.167793	0.154363	27	KIF26B	4.903826	0.377217	13
ADARB2	7.132454	0.274325	26	MIR9-3HG	4.894567	0.376505	13
SHANK2	5.964185	0.229392	26	CLYBL	4.868188	0.374476	13
AGAP1	9.353925	0.374157	25	RFX4	4.587237	0.352864	13
CAMTA1	3.886305	0.155452	25	HOXC4	4.101998	0.315538	13
SATB2	4.927197	0.2053	24	MYT1L	3.95988	0.304606	13
RPTOR	12.46487	0.541951	23	ZC3H3	6.30355	0.525296	12
NCOR2	6.643614	0.288853	23	TNS3	6.209721	0.517477	12
NXN	6.426718	0.279423	23	MIRLET7BHG	5.903381	0.491948	12
HOXB3	5.600506	0.2435	23	CMIP	5.294991	0.441249	12
INPP5A	4.027074	0.17509	23	MEGF6	4.612604	0.384384	12
PRKCZ	6.461544	0.293707	22	FBRSL1	4.480354	0.373363	12
SKI	11.13937	0.530446	21	VGLL4	5.340595	0.485509	11
ZIC4	4.102191	0.195342	21	ZC3H12D	5.005365	0.455033	11
ABR	5.611227	0.280561	20	RAD51B	4.29177	0.390161	11
FRMD4A	5.558851	0.277943	20	OTX1	6.165507	0.616551	10
SDK1	5.420154	0.271008	20	AKAP13	4.68413	0.468413	10
MAD1L1	12.4804	0.656863	19	TFAP2B	4.020065	0.402007	10
ZNF423	9.830616	0.517401	19	SND1	7.518726	0.835414	9
CASZ1	6.916102	0.364005	19	ATP11A	6.410488	0.712276	9
SMG1P2	6.485867	0.341361	19	ADAMTS2	5.174234	0.574915	9
BOLA2	6.485867	0.341361	19	TSPAN9	4.678385	0.519821	9
LOC613038	6.485867	0.341361	19	AXIN2	4.671273	0.51903	9
FOXK1	6.577737	0.36543	18	TRAPPC12	4.393501	0.488167	9
TBC1D16	6.131496	0.340639	18	KAZN	4.306895	0.478544	9
SEPTIN9	5.646419	0.31369	18	KCNMA1	4.166196	0.462911	9
MCF2L	5.28324	0.293513	18	CACNA2D4	3.982821	0.442536	9
ANKRD11	4.767949	0.264886	18	LHX4	6.347496	0.793437	8
OPCML	7.682188	0.451893	17	DLEU1	5.400273	0.675034	8
SIM1	4.439576	0.261152	17	MSRA	4.880909	0.610114	8
SORBS2	5.097365	0.318585	16	SHROOM3	4.771151	0.596394	8
NAV2	4.854781	0.303424	16	LINC00311	4.53473	0.566841	8
FOXP1	4.852911	0.303307	16	DNMT3A	4.117827	0.514728	8
GLI2	9.641517	0.642768	15	RORA	3.996121	0.499515	8
NFIX	7.684088	0.512273	15	AFF3	3.891856	0.486482	8

RBM20	5.579537	0.797077	7	HOXA-AS3	9.306106	0.443148	21
RXRA	4.454168	0.63631	7	ZIC4	5.248086	0.249909	21
IQCE	4.215459	0.602208	7	SIM2	3.686565	0.175551	21
VPS13D	4.017275	0.573896	7	SDK1	8.255789	0.412789	20
TSNAX-DISC1	5.221409	1.044282	5	FRMD4A	6.886077	0.344304	20
RUNDC3A	4.872651	0.97453	5	MAD1L1	11.9611	0.629532	19
ARHGEF7	4.514927	0.902985	5	ZNF423	6.307225	0.331959	19
PRR5L	4.43245	0.88649	5	SMG1P2	5.356851	0.28194	19
RBMS3	4.741908	1.185477	4	BOLA2	5.356851	0.28194	19
SLC25A10	4.793721	2.39686	2	LOC613038	5.356851	0.28194	19
ANKLE2	4.123466	2.061733	2	CASZ1	4.610425	0.242654	19
TABLE 58: Cancer Type ERMS				KCNQ1	4.21475	0.221829	19
				FO XK1	8.336183	0.463121	18
Gene site	imp_sum	imp_mean	n	ANKRD11	6.822507	0.379028	18
PTPRN2	8.157355	0.09948	82	TBC1D16	5.973922	0.331885	18
PRDM16	11.39271	0.160461	71	HOXA3	5.746921	0.319273	18
PCDHGA1	8.984443	0.152279	59	NAV2	5.302418	0.331401	16
PCDHGA2	8.351671	0.146521	57	FOXP1	5.185945	0.324122	16
PCDHGA3	7.402513	0.137084	54	GLI2	8.091988	0.539466	15
PCDHGB1	7.402513	0.13967	53	BAIAP2	5.722795	0.38152	15
PCDHGA4	7.253907	0.142233	51	KIRREL3	5.255829	0.350389	15
PCDHGB2	6.868	0.140163	49	SLX1B-			
PCDHGA5	6.868	0.146128	47	SULT1A4	3.715797	0.24772	15
PCDHGB3	6.28895	0.146255	43	SLX1A	3.715797	0.24772	15
PCDHGA6	5.517177	0.137929	40	LOC606724	3.715797	0.24772	15
HDAC4	16.77947	0.453499	37	IQSEC1	5.40076	0.385769	14
PCDHGA7	5.200791	0.140562	37	PRKAG2	5.122928	0.365923	14
RBFOX3	9.22086	0.263453	35	CUX1	4.153132	0.296652	14
PCDHGB4	4.884405	0.139554	35	C7orf50	3.849158	0.27494	14
PCDHGA8	4.884405	0.139554	35	ARHGEF10	3.740174	0.267155	14
PAX6	4.584193	0.130977	35	GSE1	6.060605	0.4662	13
DIP2C	9.570651	0.299083	32	MSI2	5.450645	0.41928	13
PCDHGB5	4.884405	0.152638	32	SPTBN4	4.880376	0.375414	13
PCDHGA9	4.884405	0.157561	31	MYT1L	4.579967	0.352305	13
PCDHGB6	4.390992	0.151414	29	CMIP	6.003932	0.500328	12
SOX2-OT	3.88906	0.134106	29	ZC3H3	5.82491	0.485409	12
PCDHGA10	4.074606	0.145522	28	GNA12	4.70056	0.391713	12
SHANK2	5.327244	0.204894	26	MEGF6	4.407827	0.367319	12
ADARB2	3.73715	0.143737	26	ISLR2	4.095581	0.341298	12
AGAP1	11.34168	0.453667	25	FBRSL1	3.994867	0.332906	12
CAMTA1	7.539154	0.301566	25	ADGRD1	3.92948	0.327457	12
PDGFRA	4.315036	0.172601	25	TBX4	3.823881	0.318657	12
MEIS1	4.155988	0.173166	24	CCDC140	4.510849	0.410077	11
RPTOR	8.680668	0.37742	23	CTBP2	4.27095	0.388268	11
NCOR2	8.138623	0.353853	23	RAD51B	3.718315	0.338029	11
NXN	5.422937	0.23578	23	AKAP13	3.979031	0.397903	10
HOXB3	3.751074	0.16309	23	CHST11	3.892027	0.389203	10
SKI	9.53873	0.454225	21	SND1	7.687314	0.854146	9

ATP11A	6.268404	0.696489	9	ZNF423	5.361067	0.282161	19
ADAMTS2	4.508347	0.500927	9	CASZ1	3.016508	0.158764	19
ASAP1	4.452648	0.494739	9	FOXK1	5.642007	0.313445	18
CACNA2D4	4.447124	0.494125	9	TBC1D16	4.117118	0.228729	18
MGMT	4.085135	0.453904	9	ANKRD11	3.034833	0.168602	18
PACS2	3.727252	0.414139	9	HOXA3	2.922267	0.162348	18
MSRA	5.063556	0.632945	8	SEPTIN9	2.731261	0.151737	18
LINC00311	4.6416	0.5802	8	FOXP1	5.779804	0.361238	16
VRK2	4.482111	0.560264	8	SORBS2	2.893713	0.180857	16
SYNJ2	4.400104	0.550013	8	EBF3	2.811049	0.175691	16
GAK	5.050612	0.721516	7	GLI2	6.58701	0.439134	15
NAV1	4.685313	0.66933	7	ZBTB20	3.025428	0.201695	15
C19orf25	4.636755	0.662394	7	GNG7	4.644684	0.331763	14
VPS13D	4.124844	0.589263	7	RPS6KA2	4.257981	0.304142	14
LHPP	3.768018	0.538288	7	CUX1	4.252716	0.303765	14
FBXL18	3.763178	0.627196	6	C7orf50	3.545082	0.25322	14
RUNDC3A	5.129459	1.025892	5	MIR548F5	3.302271	0.235876	14
ARHGEF7	3.999063	0.799813	5	IQSEC1	3.015585	0.215399	14
BACH2	3.821299	0.76426	5	PRKAG2	2.958187	0.211299	14
TABLE 59:	Cancer Type ETMR_Atyp			ARHGEF10	2.909369	0.207812	14
				MSI2	4.641112	0.357009	13
Gene site	imp_sum	imp_mean	n	GSE1	3.652304	0.280946	13
PTPRN2	12.61628	0.153857	82	CLYBL	3.521073	0.270852	13
PRDM16	8.961167	0.126214	71	MYT1L	3.206279	0.246637	13
HDAC4	11.88801	0.321298	37	RFX4	2.853878	0.219529	13
PAX6	6.177259	0.176493	35	ZC3H3	5.288032	0.440669	12
DIP2C	6.424846	0.200776	32	ADGRD1	4.848656	0.404055	12
SOX2-OT	7.087108	0.244383	29	CMIP	4.797575	0.399798	12
GALNT9	5.293596	0.196059	27	MAML3	3.145508	0.262126	12
SHANK2	6.11146	0.235056	26	FBRSL1	2.955564	0.246297	12
AGAP1	13.69025	0.54761	25	MIRLET7BHG	2.830016	0.235835	12
CAMTA1	5.010274	0.200411	25	RASA3	2.783277	0.23194	12
PDGFRA	2.953273	0.118131	25	VGLL4	3.948416	0.358947	11
SATB2	2.649146	0.110381	24	ZC3H12D	3.60369	0.327608	11
RPTOR	7.439347	0.32345	23	RAD51B	3.444522	0.313138	11
NCOR2	5.023833	0.218428	23	ACOT7	4.094276	0.409428	10
NXN	3.647387	0.158582	23	MAML2	3.252715	0.325271	10
HOXB3	3.556701	0.154639	23	TFAP2B	2.892127	0.289213	10
INPP5A	3.314745	0.144119	23	SH3RF3	2.647604	0.26476	10
PRKCZ	5.04235	0.229198	22	NR5A2	2.620498	0.26205	10
SKI	7.416808	0.353181	21	ATP11A	4.89493	0.543881	9
HOXA-AS3	3.437471	0.163689	21	SND1	4.120306	0.457812	9
ABR	2.671086	0.133554	20	KCNH2	3.600796	0.400088	9
MAD1L1	9.29656	0.489293	19	PACS2	3.458328	0.384259	9
KCNQ1	6.105397	0.321337	19	EGFR	3.39395	0.377106	9
SMG1P2	5.60813	0.295165	19	ADAMTS2	3.248628	0.360959	9
BOLA2	5.60813	0.295165	19	TSPAN9	3.036751	0.337417	9
LOC613038	5.60813	0.295165	19	PAX3	2.942869	0.326985	9

TRAPPC12	2.920628	0.324514	9	PCDHGB5	4.579852	0.14312	32		
ASAP1	2.714372	0.301597	9	PCDHGA9	4.579852	0.147737	31		
MGMT	2.68465	0.298294	9	SOX2-OT	6.083001	0.209759	29		
APBA2	2.681638	0.29796	9	PCDHGB6	4.263466	0.147016	29		
MACROD1	4.228081	0.52851	8	PCDHGA10	4.263466	0.152267	28		
MSRA	3.444056	0.430507	8	SHANK2	4.651371	0.178899	26		
LINC00311	2.834108	0.354264	8	AGAP1	11.70109	0.468043	25		
RXRA	3.906314	0.558045	7	CAMTA1	4.196368	0.167855	25		
NAV1	3.340597	0.477228	7	PCDHGB7	3.94708	0.164462	24		
VPS13D	3.241423	0.46306	7	MEIS1	3.693835	0.15391	24		
LHPP	2.635364	0.376481	7	RPTOR	10.80714	0.469876	23		
FBXL18	4.520193	0.753365	6	INPP5A	6.427313	0.279448	23		
COQ8A	4.07088	0.67848	6	NCOR2	5.658868	0.246038	23		
SRGAP3	2.948205	0.491368	6	NXN	4.955936	0.215475	23		
TSNAX-DISC1	4.041131	0.808226	5	PCDHGA11	3.94708	0.171612	23		
RUNDC3A	3.966069	0.793214	5	PRKCZ	3.545285	0.161149	22		
PRR5L	2.998843	0.599769	5	SKI	9.076939	0.432235	21		
TK1	2.828315	0.565663	5	ABR	4.939217	0.246961	20		
ARHGEF7	2.778802	0.55576	5	FRMD4A	4.369024	0.218451	20		
RBMS3	4.005949	1.001487	4	SDK1	4.277882	0.213894	20		
NDST1	2.748946	0.687236	4	MAD1L1	11.05499	0.581842	19		
DTNA	2.646445	0.661611	4	SMG1P2	6.12457	0.322346	19		
FBXL17	2.852793	0.950931	3	BOLA2	6.12457	0.322346	19		
SLC12A9	2.814091	0.93803	3	LOC613038	6.12457	0.322346	19		
SOX10	2.739494	1.369747	2	CASZ1	4.750979	0.250052	19		
ANKLE2	2.707781	1.35389	2	ZNF423	4.569673	0.240509	19		
TABLE 60:	Cancer Type ETMR_C19MC			KCNQ1	3.698012	0.194632	19		
				FOXK1	6.360468	0.353359	18		
		Gene site	imp_sum	imp_mean	n	TBC1D16	4.769727	0.264985	18
						ANKRD11	4.507033	0.250391	18
						HOXA3	3.678129	0.204341	18
						TBX15	4.506908	0.265112	17
						PAX6-AS1	4.470024	0.262943	17
						RCN1	4.470024	0.262943	17
						OPCML	3.520633	0.207096	17
						FOXP1	6.167845	0.38549	16
				NAV2	3.968529	0.248033	16		
				GLI2	4.877839	0.325189	15		
				SLX1B-					
				SULT1A4	3.954447	0.26363	15		
				SLX1A	3.954447	0.26363	15		
				LOC606724	3.954447	0.26363	15		
				BAIAP2	3.6137	0.240913	15		
				RPS6KA2	5.856751	0.418339	14		
				CUX1	5.813019	0.415216	14		
				PRKAG2	4.374581	0.31247	14		
				IQSEC1	4.288222	0.306302	14		
				GNG7	4.028826	0.287773	14		

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ARHGEF10	3.516089	0.251149	14
MSI2	7.052339	0.542488	13
GSE1	3.640543	0.280042	13
CMIP	5.66703	0.472252	12
TNS3	4.297541	0.358128	12
ZC3H3	4.223031	0.351919	12
FBRSL1	3.979732	0.331644	12
TBCD	3.690381	0.335489	11
RAD51B	3.664451	0.333132	11
ACOT7	3.998721	0.399872	10
AKAP13	3.628019	0.362802	10
CHST11	3.625287	0.362529	10
SND1	5.409773	0.601086	9
ADAMTS2	5.34484	0.593871	9
ATP11A	5.303516	0.58928	9
TSPAN9	4.594095	0.510455	9
KCNH2	4.047686	0.449743	9
CACNA2D4	4	0.444444	9
AXIN2	3.787404	0.420823	9
TXNRD1	3.62526	0.402807	9
VRK2	7.00172	0.875215	8
MSRA	4.521701	0.565213	8
DNMT3A	4.405394	0.550674	8
PPP2R2B	3.55962	0.444953	8
VPS13D	4.918324	0.702618	7
C19orf25	4.004237	0.572034	7
FBXL18	5.120557	0.853426	6
COQ8A	3.912035	0.652006	6
TSNAX-DISC1	4.890718	0.978144	5
BCAR1	3.714802	0.74296	5
TUBA1C	4.909867	1.227467	4
RBMS3	4.340008	1.085002	4
DAGLB	3.488732	1.162911	3
CHTF18	3.643517	1.821758	2
ANKLE2	3.592778	1.796389	2

TABLE 61: Cancer Type EVNCYT						
Gene site	imp_sum	imp_mean	n			
PTPRN2	14.8685	0.181323	82	MSI2	4.658842	0.358372 13
PRDM16	14.39248	0.202711	71	RFX4	4.112173	0.316321 13
PCDHGA1	4.472651	0.075808	59	MYT1L	3.744602	0.288046 13
PCDHGA2	4.472651	0.078468	57	GSE1	3.63194	0.27938 13
PCDHGA3	3.839879	0.071109	54	MIRLET7BHG	5.061852	0.421821 12
PCDHGB1	3.839879	0.072451	53	ZC3H3	4.551285	0.379274 12
PCDHGA4	3.523493	0.069088	51	CMIP	4.522782	0.376899 12
PCDHGB2	3.523493	0.071908	49	FBRSL1	3.102052	0.258504 12
HDAC4	11.31675	0.305858	37	FGFR2	4.091655	0.371969 11
PAX6	7.318088	0.209088	35	VGLL4	3.826003	0.347818 11
RBFOX3	6.25787	0.178796	35	RAD51B	3.599109	0.327192 11
DIP2C	7.6996	0.240613	32	CCDC140	3.500543	0.318231 11
SOX2-OT	5.155114	0.177763	29	LBX1-AS1	3.794145	0.379414 10
SHANK2	3.287713	0.12645	26	ACOT7	3.731201	0.37312 10
AGAP1	8.012474	0.320499	25	AKAP13	3.709336	0.370934 10
CAMTA1	6.573397	0.262936	25	GAS7	3.353155	0.335316 10
PDGFRA	4.343741	0.17375	25	GRID1	3.317649	0.331765 10
MEIS1	4.274311	0.178096	24	SH3RF3	3.218749	0.321875 10
RPTOR	9.309927	0.404779	23	ADGRB1	5.758616	0.639846 9
INPP5A	4.019441	0.174758	23	SND1	5.419146	0.602127 9
PRKCZ	5.654279	0.257013	22	ATP11A	4.765904	0.529545 9
SKI	9.625199	0.458343	21	ADAMTS2	3.946421	0.438491 9
ZIC4	3.365632	0.160268	21	KCNMA1	3.728571	0.414286 9
MAD1L1	8.895139	0.468165	19	TRAPPC12	3.586849	0.398539 9
ZNF423	8.863756	0.466513	19	AXIN2	3.538599	0.393178 9
SMG1P2	4.795953	0.252419	19	CACNA2D4	3.203809	0.355979 9
BOLA2	4.795953	0.252419	19	NOTCH1	3.186872	0.354097 9
LOC613038	4.795953	0.252419	19	LINC00311	5.007689	0.625961 8
CASZ1	3.443674	0.181246	19	MSRA	4.707704	0.588463 8
ANKRD11	4.230042	0.235002	18	ESRRG	3.942771	0.492846 8
TBC1D16	4.141089	0.230061	18	RORA	3.815378	0.476922 8
FO XK1	3.781959	0.210109	18	DPP6	3.11482	0.389352 8
MCF2L	3.555992	0.197555	18	DUSP6	5.324422	0.760632 7
RBFOX1	3.30935	0.183853	18	LINC00461	4.77633	0.682333 7
OPCML	6.346396	0.373317	17	NAV1	4.164379	0.594911 7
FOXP1	4.952197	0.309512	16	FHIT	4.122583	0.58894 7
SORBS2	3.853856	0.240866	16	ITPKB	3.575263	0.510752 7
NAV2	3.128093	0.195506	16	FBXL18	4.33218	0.72203 6
GLI2	10.08569	0.672379	15	FAM181A	3.378516	0.563086 6
ZBTB20	3.560998	0.2374	15	SLC22A18AS	3.30902	0.551503 6
NFIX	3.498528	0.233235	15	RUNDC3A	5.339258	1.067852 5
RPS6KA2	4.441852	0.317275	14	ARHGEF7	3.476753	0.695351 5
PRKAG2	4.119838	0.294274	14	THRB	3.433111	0.686622 5
IQSEC1	3.75183	0.267988	14	CACNA1I	3.363004	0.672601 5
ARHGEF10	3.411972	0.243712	14	TK1	3.296835	0.659367 5
				TSNAX-DISC1	3.226471	0.645294 5
				STAP2	3.52695	0.881738 4
				CORO2B	3.398559	0.84964 4

RBMS3	3.3878	0.84695	4	FOXP1	3.051477	0.190717	16
DTNA	3.265761	0.81644	4	GLI2	6.11288	0.407525	15
GRIN2B	4.117413	1.372471	3	ZBTB20	4.576408	0.305094	15
DAGLB	3.313942	1.104647	3	BAIAP2	3.671115	0.244741	15
DLL1	3.178605	1.059535	3	RPS6KA2	7.520536	0.537181	14
SOX10	4.950309	2.475154	2	IQSEC1	5.627224	0.401945	14
SLC25A10	3.296161	1.64808	2	PRKAG2	4.309802	0.307843	14
TABLE 62: Cancer Type EWS				C7orf50	4.272252	0.305161	14
				PPP2R2A	3.526415	0.251887	14
Gene site	imp_sum	imp_mean	n	MIR548F5	3.246979	0.231927	14
PTPRN2	6.594466	0.08042	82	CUX1	3.035699	0.216836	14
PRDM16	8.444389	0.118935	71	MSI2	5.781775	0.444752	13
PCDHGA1	3.163841	0.053624	59	GSE1	3.471098	0.267008	13
PCDHGA2	3.163841	0.055506	57	MYT1L	3.140211	0.241555	13
PCDHGA3	3.163841	0.05859	54	HOXC4	3.032424	0.233263	13
PCDHGB1	3.163841	0.059695	53	FBRSL1	5.401794	0.450149	12
PCDHGA4	3.163841	0.062036	51	CMIP	4.698304	0.391525	12
PCDHGB2	3.163841	0.064568	49	ADGRD1	4.340891	0.361741	12
PCDHGA5	3.163841	0.067316	47	GNA12	3.997858	0.333155	12
PCDHGB3	3.480227	0.080936	43	MEGF6	3.603341	0.300278	12
HDAC4	8.759235	0.236736	37	RAD51B	3.352156	0.304741	11
RBFOX3	4.953792	0.141537	35	CTBP2	3.021814	0.27471	11
PAX6	4.909085	0.14026	35	BCL11B	5.072798	0.50728	10
DIP2C	7.742061	0.241939	32	AKAP13	4.448844	0.444884	10
GALNT9	3.783787	0.14014	27	CHST11	3.972987	0.397299	10
SHANK2	4.063047	0.156271	26	FMN1	3.795513	0.379551	10
AGAP1	10.22599	0.40904	25	ACOT7	3.710255	0.371026	10
CAMTA1	5.832812	0.233312	25	KLHL29	3.646232	0.364623	10
SATB2	3.268379	0.136182	24	GAS7	2.932857	0.293286	10
MEIS1	3.164186	0.131841	24	RGS12	2.919996	0.292	10
RPTOR	10.08952	0.438675	23	IGF1R	2.912019	0.291202	10
INPP5A	6.721586	0.292243	23	ATP11A	6.351578	0.705731	9
NCOR2	5.642924	0.245345	23	SND1	4.100007	0.455556	9
PRKCZ	3.891859	0.176903	22	MGMT	3.877867	0.430874	9
SKI	8.625603	0.410743	21	TSPAN9	3.575338	0.39726	9
FRMD4A	3.761279	0.188064	20	TRAPPC12	3.24621	0.36069	9
ABR	3.155898	0.157795	20	ADAMTS2	2.987984	0.331998	9
SMG1P2	5.64643	0.297181	19	PACS2	2.966455	0.329606	9
BOLA2	5.64643	0.297181	19	DNMT3A	4.267716	0.533464	8
LOC613038	5.64643	0.297181	19	VRK2	3.403344	0.425418	8
ZNF423	5.470921	0.287943	19	DLEU1	3.081545	0.385193	8
CASZ1	4.319583	0.227346	19	SHROOM3	3.073762	0.38422	8
MAD1L1	3.31708	0.174583	19	GRIK2	3.050294	0.381287	8
ANKRD11	4.595043	0.25528	18	MSRA	3.047019	0.380877	8
SEPTIN9	4.030671	0.223926	18	C19orf25	5.392038	0.770291	7
TBC1D16	3.436328	0.190907	18	NAV1	4.318606	0.616944	7
OPCML	3.748227	0.220484	17	PTPN20	2.995701	0.427957	7
EBF3	3.578374	0.223648	16	KCNAB2	2.943331	0.420476	7

FBXL18	3.959427	0.659904	6	IQSEC1	2.230874	0.159348	14
CRADD	3.504241	0.58404	6	TBX5	1.898316	0.135594	14
CCDC177	3.049015	0.508169	6	PRKAG2	1.407036	0.100503	14
PAX1	3.010346	0.501724	6	MYT1L	1.690763	0.130059	13
RUNDC3A	4.677137	0.935427	5	MIR9-3HG	1.58193	0.121687	13
ARHGEF7	4.245753	0.849151	5	SPTBN4	1.521369	0.117028	13
TSNAX-DISC1	4.070083	0.814017	5	MIRLET7BHG	3.578224	0.298185	12
IDI2	3.253075	0.650615	5	TBX4	2.297014	0.191418	12
KLHL25	3.148576	0.629715	5	CMIP	1.565499	0.130458	12
DONSON	3.503814	1.167938	3	MAML3	1.411568	0.117631	12
DAGLB	3.381121	1.12704	3	ADGRD1	1.391228	0.115936	12
DICER1	3.264558	1.088186	3	CCDC140	2.278284	0.207117	11
CHTF18	3.388371	1.694186	2	VGLL4	1.650163	0.150015	11
SLC25A10	3.07935	1.539675	2	GLUD1P2	1.584414	0.144038	11
TABLE 63:	Cancer Type GBM_CBM			LBX1-AS1	3.359792	0.335979	10
				TSPAN4	2.514486	0.251449	10
Gene site	imp_sum	imp_mean	n	OTX1	2.43546	0.243546	10
PTPRN2	4.219585	0.051458	82	ACOT7	2.384765	0.238476	10
PRDM16	5.223884	0.073576	71	NR2F1-AS1	1.584295	0.15843	10
HDAC4	4.968689	0.134289	37	TFAP2A	1.529399	0.15294	10
PAX6	3.924259	0.112122	35	ATP11A	2.97819	0.33091	9
RBFOX3	2.757375	0.078782	35	RUNX1	1.959724	0.217747	9
DIP2C	2.740991	0.085656	32	TSPAN9	1.787018	0.198558	9
SOX2-OT	3.59743	0.124049	29	ZNF833P	1.704292	0.189366	9
PDGFRA	2.993496	0.11974	25	ADGRB1	1.656848	0.184094	9
AGAP1	2.315682	0.092627	25	NOTCH1	1.622247	0.18025	9
CAMTA1	1.729468	0.069179	25	GPC6	1.497155	0.166351	9
SATB2	4.371957	0.182165	24	APBA2	1.495026	0.166114	9
RPTOR	4.110492	0.178717	23	SND1	1.401819	0.155758	9
NCOR2	1.999787	0.086947	23	GRIK2	2.572652	0.321582	8
INPP5A	1.963659	0.085376	23	MSRA	2.151155	0.268894	8
PRKCZ	2.262767	0.102853	22	MACROD1	1.432446	0.179056	8
SIM2	2.459611	0.117124	21	RORA	1.422077	0.17776	8
FRMD4A	1.52728	0.076364	20	NR2E1	1.392098	0.174012	8
MAD1L1	3.476252	0.182961	19	DLEU1	1.384263	0.173033	8
ZNF423	1.960736	0.103197	19	TACC2	2.292627	0.327518	7
CASZ1	1.76757	0.09303	19	NAV1	2.179499	0.311357	7
FO XK1	4.095143	0.227508	18	LINC00461	2.036008	0.290858	7
SEPTIN9	2.346494	0.130361	18	RBM20	1.829679	0.261383	7
ANKRD11	2.23996	0.124442	18	DUSP6	1.605871	0.22941	7
TBX15	2.832461	0.166615	17	FBXL18	2.118706	0.353118	6
OPCML	2.132107	0.125418	17	FAM181A	2.084256	0.347376	6
FOXP1	2.240363	0.140023	16	VAX2	1.780092	0.296682	6
NAV2	1.612654	0.100791	16	SATB2-AS1	1.739164	0.289861	6
BAIAP2	2.22624	0.148416	15	TRAK1	1.680758	0.280126	6
GLI2	1.827958	0.121864	15	FMNL2	1.58193	0.263655	6
PPP2R2A	2.990556	0.213611	14	SLC22A18AS	1.512488	0.252081	6
CUX1	2.290274	0.163591	14	MYO16	1.493941	0.24899	6

LRRFIP1	1.420423	0.236737	6	ADARB2	5.055486	0.194442	26
RUNDC3A	2.517392	0.503478	5	AGAP1	8.358635	0.334345	25
LOC100132215	2.087629	0.417526	5	CAMTA1	8.271489	0.33086	25
CACNA1I	1.661515	0.332303	5	PDGFRA	6.358749	0.25435	25
KLHL25	1.518958	0.303792	5	SATB2	9.115991	0.379833	24
ARHGEF7	1.457993	0.291599	5	MEIS1	6.622748	0.275948	24
RAPGEF4	1.396595	0.279319	5	PCDHGB7	4.126915	0.171955	24
STAP2	2.002651	0.500663	4	RPTOR	9.815838	0.426776	23
RBMS3	1.956574	0.489144	4	INPP5A	6.802927	0.295779	23
DTNA	1.634875	0.408719	4	NCOR2	5.704298	0.248013	23
TUBA1C	1.486045	0.371511	4	PRKCZ	6.501686	0.295531	22
FRMPD2	1.396595	0.349149	4	SKI	7.97741	0.379877	21
TTC12	1.91512	0.638373	3	FRMD4A	4.932228	0.246611	20
LOXL3	1.633668	0.544556	3	MAD1L1	11.39993	0.599996	19
METAP1D	1.453821	0.484607	3	SMG1P2	8.181284	0.430594	19
SLC25A22	1.429634	0.476545	3	BOLA2	8.181284	0.430594	19
SLC4A8	1.389227	0.463076	3	LOC613038	8.181284	0.430594	19
SOX10	2.79619	1.398095	2	ZNF423	7.825319	0.411859	19
SLC25A10	1.591924	0.795962	2	CASZ1	4.801215	0.252696	19
ANKLE2	1.498168	0.749084	2	CFAP46	4.05837	0.213598	19
PHF19	1.38402	0.69201	2	KCNQ1	3.952958	0.20805	19
TABLE 64:	Cancer Type GBM_G34			FOXK1	6.041595	0.335644	18
				SEPTIN9	5.392621	0.29959	18
Gene site	imp_sum	imp_mean	n	MCF2L	3.795464	0.210859	18
PTPRN2	19.89897	0.24267	82	OPCML	6.854193	0.403188	17
PRDM16	14.43818	0.203355	71	TBX15	4.596928	0.270408	17
PCDHGA1	7.473345	0.126667	59	FOXP1	5.462874	0.34143	16
PCDHGA2	7.473345	0.131111	57	EBF3	4.291585	0.268224	16
PCDHGA3	7.473345	0.138395	54	GLI2	8.64613	0.576409	15
PCDHGB1	7.473345	0.141007	53	EMX2OS	4.110559	0.274037	15
PCDHGA4	7.473345	0.146536	51	ZBTB20	3.936085	0.262406	15
PCDHGB2	7.460566	0.152256	49	RPS6KA2	5.824749	0.416053	14
PCDHGA5	7.096471	0.150989	47	CUX1	5.076042	0.362574	14
PCDHGB3	6.379765	0.148367	43	IQSEC1	4.752308	0.339451	14
PCDHGA6	5.796002	0.1449	40	MYT1L	5.537306	0.425947	13
HDAC4	11.11229	0.300332	37	MSI2	4.925849	0.378911	13
PCDHGA7	5.322527	0.143852	37	KIF26B	3.854842	0.296526	13
RBFOX3	11.3611	0.324603	35	MIRLET7BHG	5.363207	0.446934	12
PAX6	7.229973	0.206571	35	TNS3	4.797854	0.399821	12
PCDHGB4	5.322527	0.152072	35	CMIP	4.72135	0.393446	12
PCDHGA8	5.322527	0.152072	35	TBX4	4.663755	0.388646	12
DIP2C	6.139385	0.191856	32	ZC3H12D	5.092555	0.46296	11
PCDHGB5	5.006141	0.156442	32	ANAPC16	4.847683	0.440698	11
PCDHGA9	5.006141	0.161488	31	SORCS2	3.899277	0.35448	11
SOX2-OT	10.3488	0.356855	29	SH3RF3	4.611812	0.461181	10
PCDHGB6	4.443301	0.153217	29	ACOT7	4.229379	0.422938	10
PCDHGA10	4.443301	0.158689	28	GRID1	4.011402	0.40114	10
SHANK2	5.9963	0.230627	26	ATP11A	7.379091	0.819899	9

SND1	5.619648	0.624405	9	RIMBP2	2.708516	0.117762	23
AXIN2	4.860437	0.540049	9	INPP5A	2.477152	0.107702	23
TSPAN9	4.587217	0.509691	9	PRKCZ	2.809272	0.127694	22
ADAMTS2	3.97508	0.441676	9	SKI	4.27164	0.203411	21
TRAPPC12	3.971414	0.441268	9	FRMD4A	3.782863	0.189143	20
LINC00311	4.648027	0.581003	8	SDK1	3.117634	0.155882	20
DNMT3A	4.303718	0.537965	8	ABR	2.594189	0.129709	20
MSRA	4.272627	0.534078	8	MAD1L1	7.157094	0.376689	19
LHX2	4.517777	0.645397	7	ZNF423	3.094365	0.162861	19
GDNF	4.454709	0.636387	7	SMG1P2	2.938503	0.154658	19
LINC00461	4.403363	0.629052	7	BOLA2	2.938503	0.154658	19
CDYL	4.356803	0.6224	7	LOC613038	2.938503	0.154658	19
DUSP6	4.317444	0.616778	7	KCNQ1	2.773978	0.145999	19
GLI3	3.890153	0.555736	7	CASZ1	2.31299	0.121736	19
LYPD1	5.224149	0.870691	6	ANKRD11	5.108699	0.283817	18
FBXL18	4.850918	0.808486	6	FOXK1	4.541819	0.252323	18
SATB2-AS1	4.373285	0.728881	6	TBC1D16	3.514847	0.195269	18
FAM181A	4.254141	0.709023	6	SEPTIN9	3.070805	0.1706	18
ARHGEF7	4.251735	0.850347	5	PAX6-AS1	3.440958	0.202409	17
CASC15	4.150169	0.830034	5	RCN1	3.440958	0.202409	17
ATP2B4	3.866019	0.773204	5	TBX15	2.685264	0.157957	17
IGSF21	4.438775	1.109694	4	FOXP1	3.750495	0.234406	16
STAP2	4.287031	1.071758	4	EBF3	3.173477	0.198342	16
DTNA	3.80024	0.95006	4	NAV2	3.098199	0.193637	16
ARHGAP23	4.72853	1.576177	3	SORBS2	2.531166	0.158198	16
SRRM3	3.870911	1.290304	3	GLI2	4.379243	0.29195	15
OLIG2	4.617618	2.308809	2	BAIAP2	2.897856	0.19319	15
SOX10	3.854589	1.927294	2	NFIX	2.366496	0.157766	15
TABLE 65:	Cancer Type GBM_MES_Atyp			KNDC1	2.361173	0.157412	15
				PRKAG2	4.298671	0.307048	14
				RPS6KA2	4.264028	0.304573	14
				CUX1	3.672298	0.262307	14
Gene site	imp_sum	imp_mean	n				
PTPRN2	8.433087	0.102843	82	ARHGEF10	2.952753	0.210911	14
PRDM16	6.780965	0.095507	71	IQSEC1	2.923624	0.20883	14
HDAC4	7.186587	0.194232	37	MIR548F5	2.413638	0.172403	14
PAX6	4.903338	0.140095	35	TBX5	2.300758	0.16434	14
RBFOX3	3.107038	0.088773	35	MSI2	3.096241	0.238172	13
DIP2C	6.504262	0.203258	32	CMIP	4.54422	0.378685	12
SOX2-OT	2.911348	0.100391	29	MAML3	3.456282	0.288023	12
SHANK2	3.576954	0.137575	26	ADGRD1	3.143607	0.261967	12
ADARB2	2.697827	0.103763	26	FBRSL1	2.786601	0.232217	12
CAMTA1	5.335488	0.21342	25	CTNNA2	2.585921	0.215493	12
PDGFRA	4.368188	0.174728	25	SORCS2	2.993974	0.272179	11
AGAP1	3.977791	0.159112	25	ANAPC16	2.493181	0.226653	11
SATB2	4.514819	0.188117	24	SLC38A10	2.475242	0.225022	11
MEIS1	3.689164	0.153715	24	VGLL4	2.324173	0.211288	11
RPTOR	7.619219	0.33127	23	SH3RF3	3.976811	0.397681	10
NCOR2	4.33597	0.18852	23	TSPAN4	3.618876	0.361888	10

AKAP13	3.113099	0.31131	10	PCDHGA5	8.422682	0.179206	47	
BCL11B	3.084883	0.308488	10	PCDHGB3	7.473524	0.173803	43	
GAS7	2.404786	0.240479	10	PCDHGA6	6.709864	0.167747	40	
FMN1	2.334601	0.23346	10	HDAC4	15.91135	0.430036	37	
SND1	3.742607	0.415845	9	PCDHGA7	6.393478	0.172797	37	
AXIN2	3.283112	0.36479	9	PAX6	11.66539	0.333297	35	
RUNX1	3.232644	0.359183	9	RBFOX3	7.368602	0.210531	35	
ADAMTS2	3.075889	0.341765	9	PCDHGB4	6.288867	0.179682	35	
TRAPPC12	2.869826	0.31887	9	PCDHGA8	6.288867	0.179682	35	
NOTCH1	2.600302	0.288922	9	DIP2C	10.53407	0.32919	32	
ASAP1	2.478045	0.275338	9	PCDHGB5	6.288867	0.196527	32	
ADGRB1	2.463991	0.273777	9	PCDHGA9	6.288867	0.202867	31	
MCC	3.597978	0.449747	8	SOX2-OT	7.7339	0.266686	29	
LINC00311	2.817797	0.352225	8	PCDHGB6	5.473696	0.188748	29	
LHX4	2.589797	0.323725	8	PCDHGA10	5.473696	0.195489	28	
DNMT3A	2.573273	0.321659	8	SHANK2	6.019655	0.231525	26	
MSRA	2.46484	0.308105	8	ADARB2	5.68846	0.218787	26	
DLEU1	2.384677	0.298085	8	AGAP1	10.45411	0.418164	25	
AFF3	2.306736	0.288342	8	CAMTA1	7.166051	0.286642	25	
MACROD1	2.300575	0.287572	8	PDGFRA	6.769784	0.270791	25	
C19orf25	3.355938	0.47942	7	MEIS1	6.634768	0.276449	24	
ITPK1	3.117822	0.445403	7	SATB2	6.269327	0.261222	24	
CDYL	2.714648	0.387807	7	PCDHGB7	5.802861	0.241786	24	
NAV1	2.690872	0.38441	7	RPTOR	12.93967	0.562595	23	
SLC22A18AS	3.300956	0.550159	6	RIMBP2	6.255045	0.271958	23	
MIR100HG	2.84836	0.474727	6	NCOR2	6.172236	0.268358	23	
LRRFIP1	2.530759	0.421793	6	NXN	6.129696	0.266509	23	
FMNL2	2.440385	0.406731	6	PCDHGA11	5.561293	0.241795	23	
MIR548G	2.379921	0.396653	6	INPP5A	4.458401	0.193844	23	
KLHL25	3.043751	0.60875	5	PRKCZ	6.232476	0.283294	22	
ARHGEF7	2.408625	0.481725	5	SKI	10.62373	0.505892	21	
TUBA1C	2.46219	0.615547	4	HOXA-AS3	4.545824	0.216468	21	
DAGLB	2.838583	0.946194	3	ZIC4	4.536976	0.216046	21	
ACSL1	2.293654	0.764551	3	SIM2	4.451726	0.211987	21	
SOX10	2.94264	1.47132	2	FRMD4A	7.193395	0.35967	20	
SLC25A10	2.649164	1.324582	2	ABR	5.89055	0.294528	20	
TABLE 66:	Cancer_Type GBM_MES_Typ	imp_sum	imp_mean	n	SDK1	5.592627	0.279631	20
					MAD1L1	12.94929	0.681541	19
					ZNF423	7.647999	0.402526	19
					CASZ1	7.56223	0.398012	19
					SMG1P2	6.857681	0.360931	19
					BOLA2	6.857681	0.360931	19
					LOC613038	6.857681	0.360931	19
					KCNQ1	5.770086	0.303689	19
					ANKRD11	7.654705	0.425261	18
					FOXK1	7.432383	0.41291	18
PTPRN2	23.49127	0.286479	82	MCF2L	6.444539	0.35803	18	
PRDM16	22.97156	0.323543	71	TBC1D16	5.943273	0.330182	18	
PCDHGA1	10.84728	0.183852	59					
PCDHGA2	10.21451	0.179202	57					
PCDHGA3	9.06282	0.16783	54					
PCDHGB1	9.06282	0.170997	53					
PCDHGA4	9.06282	0.177702	51					
PCDHGB2	8.931951	0.182285	49					

RBFOX1	4.392738	0.244041	18	PTPRN2	4.660027	0.05683	82
PAX6-AS1	6.660589	0.391799	17	PRDM16	1.212407	0.017076	71
RCN1	6.660589	0.391799	17	PCDHGA1	1.98213	0.033595	59
OPCML	6.571515	0.38656	17	PCDHGA2	1.98213	0.034774	57
FOXP1	7.921231	0.495077	16	PCDHGA3	1.98213	0.036706	54
NAV2	6.202516	0.387657	16	PCDHGB1	1.98213	0.037399	53
EBF3	4.524319	0.28277	16	PCDHGA4	1.665744	0.032662	51
GLI2	9.308291	0.620553	15	PCDHGB2	1.665744	0.033995	49
KIRREL3	6.247889	0.416526	15	PCDHGA5	1.265544	0.026926	47
KNDC1	5.324119	0.354941	15	PCDHGB3	1.265544	0.029431	43
NFIX	5.277974	0.351865	15	PCDHGA6	1.265544	0.031639	40
BAIAP2	4.98361	0.332241	15	HDAC4	2.229184	0.060248	37
ZBTB20	4.772255	0.31815	15	DIP2C	2.621531	0.081923	32
RPS6KA2	6.525278	0.466091	14	SOX2-OT	2.793191	0.096317	29
PRKAG2	6.037694	0.431264	14	SHANK2	1.387906	0.053381	26
C7orf50	5.965491	0.426107	14	ADARB2	1.080209	0.041547	26
MIR548F5	4.766224	0.340445	14	CAMTA1	2.15173	0.086069	25
GNG7	4.731929	0.337995	14	AGAP1	1.310034	0.052401	25
MSI2	8.116375	0.624337	13	SATB2	3.618022	0.150751	24
SPTBN4	5.54136	0.426258	13	RPTOR	1.304413	0.056714	23
MYT1L	5.028356	0.386797	13	RIMBP2	1.265544	0.055024	23
ZC3H3	5.032763	0.419397	12	PRKCZ	1.835344	0.083425	22
CMIP	4.971106	0.414259	12	SKI	2.527028	0.120335	21
FBRSL1	4.79912	0.399927	12	ZIC4	1.396595	0.066505	21
TNS3	4.75218	0.396015	12	ZNF423	2.805755	0.147671	19
SORCS2	4.921415	0.447401	11	MAD1L1	2.765159	0.145535	19
VGLL4	4.606674	0.418789	11	SMG1P2	2.46524	0.129749	19
COL4A1	4.48589	0.407808	11	BOLA2	2.46524	0.129749	19
ACOT7	5.030053	0.503005	10	LOC613038	2.46524	0.129749	19
AKAP13	4.56057	0.456057	10	CASZ1	2.132961	0.112261	19
SND1	7.281794	0.809088	9	FOXK1	2.36923	0.131624	18
ADAMTS2	5.153743	0.572638	9	SEPTIN9	1.792162	0.099565	18
TSPAN9	4.538052	0.504228	9	MCF2L	1.431384	0.079521	18
TRAPPC12	4.457085	0.495232	9	RBFOX1	1.38183	0.076768	18
SSBP3	4.353363	0.483707	9	TBX15	1.93143	0.113614	17
LINC00311	4.787609	0.598451	8	OPCML	1.606827	0.094519	17
DLEU1	4.646289	0.580786	8	PAX6-AS1	1.265544	0.074444	17
RGS20	4.459601	0.55745	8	RCN1	1.265544	0.074444	17
DUSP6	5.217385	0.745341	7	GLI2	2.853675	0.190245	15
LINC00461	4.68498	0.669283	7	LRMDA	1.58193	0.105462	15
NAV1	4.450325	0.635761	7	CUX1	2.424641	0.173189	14
FBXL18	4.963335	0.827222	6	RPS6KA2	2.029367	0.144955	14
TSNAX-DISC1	4.412335	0.882467	5	PRKAG2	1.396595	0.099757	14
SOX10	4.332658	2.166329	2	CLYBL	1.712981	0.131768	13
				ADGRD1	1.743981	0.145332	12
				FBRSL1	1.298956	0.108246	12
				TBX4	1.265544	0.105462	12
				CMIP	1.180952	0.098413	12

TABLE 67:

Cancer Type
GBM_ped_ND_A

Gene site

imp_sum

imp_mean

n

ZC3H12D	2.137458	0.194314	11	DAGLB	1.703494	0.567831	3
RAD51B	1.387906	0.126173	11	SLC6A9	1.086286	0.362095	3
TBCD	1.080209	0.098201	11	TLX1NB	1.080209	0.36007	3
NTM	1.918556	0.191856	10	SLC25A10	2.125032	1.062516	2
TFAP2B	1.34721	0.134721	10	TABLE 68:	Cancer Type		
ACOT7	1.227596	0.12276	10		GBM_ped_ND_B		
BCL11B	1.206764	0.120676	10	Gene site	imp_sum	imp_mean	n
AUTS2	1.080209	0.108021	10	PTPRN2	12.14662	0.14813	82
ATP11A	1.929964	0.21444	9	PRDM16	6.993189	0.098496	71
AXIN2	1.916799	0.212978	9	PCDHGA1	5.102496	0.086483	59
SND1	1.197867	0.133096	9	PCDHGA2	5.102496	0.089517	57
TSPAN9	1.174158	0.130462	9	PCDHGA3	4.681997	0.086704	54
SYNJ2	1.650285	0.206286	8	PCDHGB1	4.681997	0.08834	53
RGS20	1.387906	0.173488	8	PCDHGA4	4.365611	0.0856	51
LHX4	1.265544	0.158193	8	PCDHGB2	4.365611	0.089094	49
NR2E1	1.080209	0.135026	8	PCDHGA5	3.843487	0.081776	47
LINC00311	1.080209	0.135026	8	PCDHGB3	3.527101	0.082026	43
CDYL	1.884525	0.269218	7	PCDHGA6	3.527101	0.088178	40
TRIM2	1.396595	0.199514	7	HDAC4	6.965959	0.188269	37
ITPKB	1.205787	0.172255	7	PCDHGA7	3.210715	0.086776	37
LHX2	1.193883	0.170555	7	PAX6	8.183288	0.233808	35
OTX2-AS1	1.080209	0.154316	7	RBFOX3	4.508841	0.128824	35
FBXL18	1.784169	0.297362	6	PCDHGB4	3.210715	0.091735	35
ACTR3C	1.704515	0.284086	6	PCDHGA8	3.210715	0.091735	35
SATB2-AS1	1.681932	0.280322	6	DIP2C	5.416515	0.169266	32
FAM181A	1.440657	0.24011	6	PCDHGB5	3.210715	0.100335	32
LRRFIP1	1.330824	0.221804	6	PCDHGA9	3.210715	0.103571	31
SLC22A18AS	1.202572	0.200429	6	PCDHGB6	2.584559	0.089123	29
LIMCH1	1.20248	0.200413	6	SHANK2	3.321582	0.127753	26
FMNL2	1.097757	0.18296	6	ADARB2	3.108278	0.119549	26
CDK6	1.080209	0.180035	6	AGAP1	5.4006	0.216024	25
JAKMIP1	1.080209	0.180035	6	PDGFRA	2.602431	0.104097	25
CELSR1	1.075712	0.179285	6	CAMTA1	2.419096	0.096764	25
TRABD2B	1.071723	0.178621	6	SATB2	7.161246	0.298385	24
CACNA2D3	1.07152	0.178587	6	MEIS1	3.279392	0.136641	24
MNX1	2.115646	0.423129	5	NCOR2	4.341474	0.18876	23
HLX	1.527647	0.305529	5	RPTOR	3.937426	0.171192	23
ARHGEF7	1.354671	0.270934	5	INPP5A	3.519542	0.153024	23
TMEM132C	1.160199	0.23204	5	SKI	5.30783	0.252754	21
SHOX2	1.119658	0.223932	5	SIM2	3.927126	0.187006	21
CPZ	1.07152	0.214304	5	ABR	2.58979	0.12949	20
NPHP4	1.06875	0.21375	5	FRMD4A	2.396029	0.119801	20
RBMS3	1.492019	0.373005	4	MAD1L1	6.393482	0.336499	19
IGF2BP3	1.432903	0.358226	4	ZNF423	6.385805	0.336095	19
VOPPI	1.354583	0.338646	4	SMG1P2	4.47727	0.235646	19
PPM1H	1.24313	0.310783	4	BOLA2	4.47727	0.235646	19
UNQ6494	1.241017	0.310254	4	LOC613038	4.47727	0.235646	19
LIPE-AS1	1.076052	0.269013	4				

CASZ1	4.285857	0.225571	19	ACTR3C	2.897499	0.482916	6
MCF2L	4.109657	0.228314	18	FAM181A	2.66049	0.443415	6
ANKRD11	2.709106	0.150506	18	FBXL18	2.482766	0.413794	6
SEPTIN9	2.548878	0.141604	18	ARHGEF7	3.550002	0.71	5
SIM1	5.797883	0.341052	17	RUNDC3A	2.678331	0.535666	5
TBX15	4.177295	0.245723	17	TSNAX-DISC1	2.443815	0.488763	5
OPCML	4.163199	0.244894	17	RBMS3	2.902629	0.725657	4
FOXP1	2.710848	0.169428	16	UNQ6494	2.490583	0.622646	4
EBF3	2.326947	0.145434	16	CRB2	2.432396	0.608099	4
GLI2	7.550957	0.503397	15	SLC25A10	3.623653	1.811826	2
LRMDA	2.788694	0.185913	15	ANKLE2	2.456756	1.228378	2
CUX1	4.424777	0.316056	14	ACAD10	2.40091	2.40091	1
C7orf50	2.990176	0.213584	14				
RPS6KA2	2.923735	0.208838	14	TABLE 69: Cancer Type GBM_pedMYCN			
IQSEC1	2.848773	0.203484	14	Gene site	imp_sum	imp_mean	n
ARHGEF10	2.658323	0.18988	14	PTPRN2	13.7309	0.16745	82
PRKAG2	2.548134	0.18201	14	PRDM16	14.16247	0.199471	71
SPTBN4	3.758864	0.289143	13	PCDHGA1	8.092392	0.137159	59
MSI2	3.316939	0.255149	13	PCDHGA2	7.776006	0.136421	57
CLYBL	2.507192	0.192861	13	PCDHGA3	7.143234	0.132282	54
TBX4	3.229651	0.269138	12	PCDHGB1	7.45962	0.140748	53
ZC3H3	3.02575	0.252146	12	PCDHGA4	7.45962	0.146267	51
TNS3	2.80412	0.233677	12	PCDHGB2	7.143234	0.14578	49
CMIP	2.559671	0.213306	12	PCDHGA5	6.332692	0.134738	47
FBRSL1	2.511935	0.209328	12	PCDHGB3	5.629493	0.130918	43
ADGRD1	2.397913	0.199826	12	PCDHGA6	5.313107	0.132828	40
TBCD	3.339869	0.303624	11	HDAC4	6.570127	0.177571	37
RAD51B	3.175857	0.288714	11	PCDHGA7	4.996721	0.135047	37
ZC3H12D	2.811273	0.25557	11	PAX6	11.10894	0.317398	35
TFAP2B	3.53736	0.353736	10	RBFOX3	5.104816	0.145852	35
AKAP13	2.601768	0.260177	10	PCDHGB4	4.984633	0.142418	35
LBX1-AS1	2.447679	0.244768	10	PCDHGA8	4.984633	0.142418	35
ATP11A	4.313543	0.479283	9	DIP2C	8.089298	0.252791	32
SND1	3.356261	0.372918	9	PCDHGB5	4.809739	0.150304	32
ADAMTS2	2.928678	0.325409	9	PCDHGA9	4.493353	0.144947	31
RUNX1	2.889622	0.321069	9	SOX2-OT	3.57114	0.123143	29
TRAPPC12	2.864223	0.318247	9	PCDHGB6	3.322727	0.114577	29
NOTCH1	2.764459	0.307162	9	ADARB2	4.248209	0.163393	26
ASAP1	2.588346	0.287594	9	SHANK2	4.211053	0.161964	26
LHX9	2.382751	0.26475	9	CAMTA1	8.757924	0.350317	25
DMRTA2	2.361578	0.262398	9	PDGFRA	5.018825	0.200753	25
LINC00311	3.544951	0.443119	8	AGAP1	4.881521	0.195261	25
NR2E1	2.462557	0.30782	8	SATB2	10.03345	0.41806	24
GRIK2	2.427412	0.303426	8	MEIS1	4.687863	0.195328	24
CDYL	3.880029	0.55429	7	NCOR2	5.290152	0.230007	23
LHX2	2.714765	0.387824	7	RPTOR	4.949618	0.215201	23
SATB2-AS1	3.780636	0.630106	6	RIMBP2	4.056962	0.17639	23
PAX1	3.657875	0.609646	6				

INPP5A	3.448069	0.149916	23	KCNH2	3.411673	0.379075	9
SKI	6.838609	0.325648	21	SND1	3.364139	0.373793	9
HOXA-AS3	3.484558	0.165931	21	LINC00311	3.722809	0.465351	8
ABR	5.172557	0.258628	20	VEPH1	3.630206	0.453776	8
SDK1	4.600207	0.23001	20	DLEU1	3.626791	0.453349	8
MAD1L1	7.765849	0.408729	19	LRRC61	3.498689	0.437336	8
ZNF423	5.615465	0.295551	19	RGS20	3.332919	0.416615	8
CASZ1	4.149527	0.218396	19	AFF3	3.311203	0.4139	8
SMG1P2	3.848223	0.202538	19	DNMT3A	3.195727	0.399466	8
BOLA2	3.848223	0.202538	19	ASPSCR1	3.123	0.390375	8
LOC613038	3.848223	0.202538	19	CDYL	4.192885	0.598984	7
KCNQ1	3.783269	0.199119	19	LHX2	3.769659	0.538523	7
FO XK1	6.938724	0.385485	18	DUSP6	3.465504	0.495072	7
SEPTIN9	5.291204	0.293956	18	SATB2-AS1	4.890843	0.81514	6
RBFOX1	4.540653	0.252258	18	ACTR3C	3.265273	0.544212	6
TBC1D16	3.39222	0.188457	18	ATP2B4	4.18037	0.836074	5
OPCML	5.532892	0.325464	17	ARHGEF7	3.279377	0.655875	5
TBX15	5.350234	0.31472	17	SHOX2	3.12614	0.625228	5
PAX6-AS1	3.345572	0.196798	17	GRIN2B	3.309093	1.103031	3
RCN1	3.345572	0.196798	17	SOX10	3.801967	1.900984	2
FOXP1	3.748139	0.234259	16	SLC25A10	3.604396	1.802198	2
GLI2	4.770497	0.318033	15				
SLX1B-SULT1A4	4.051811	0.270121	15	TABLE 70: Cancer Type GBM_pedRTK1a			
SLX1A	4.051811	0.270121	15	Gene site	imp_sum	imp_mean	n
LOC606724	4.051811	0.270121	15	PTPRN2	24.80392	0.302487	82
RPS6KA2	4.640371	0.331455	14	PRDM16	16.05384	0.22611	71
CUX1	4.195972	0.299712	14	PCDHGA1	9.715844	0.164675	59
PRKAG2	3.509503	0.250679	14	PCDHGA2	9.715844	0.170453	57
MSI2	3.661582	0.28166	13	PCDHGA3	10.03223	0.185782	54
CLYBL	3.430496	0.263884	13	PCDHGB1	10.34862	0.195257	53
RFX4	3.323302	0.255639	13	PCDHGA4	10.34862	0.202914	51
ZC3H3	5.034914	0.419576	12	PCDHGB2	10.03223	0.204739	49
MIRLET7BHG	4.906574	0.408881	12	PCDHGA5	9.858888	0.209764	47
TBX4	4.513305	0.376109	12	PCDHGB3	9.516396	0.221312	43
TNS3	4.300972	0.358414	12	PCDHGA6	8.883624	0.222091	40
CMIP	3.897793	0.324816	12	HDAC4	11.62845	0.314282	37
SPON2	3.155581	0.286871	11	PCDHGA7	9.516396	0.2572	37
ZC3H12D	3.130966	0.284633	11	RBFOX3	10.31311	0.29466	35
TFAP2B	4.794462	0.479446	10	PCDHGB4	8.883624	0.253818	35
LBX1-AS1	4.313126	0.431313	10	PCDHGA8	8.883624	0.253818	35
OTX1	3.891279	0.389128	10	PAX6	8.730832	0.249452	35
NTM	3.878567	0.387857	10	DIP2C	12.67672	0.396148	32
ACOT7	3.560066	0.356007	10	PCDHGB5	8.567238	0.267726	32
NR5A2	3.307077	0.330708	10	PCDHGA9	8.136833	0.262478	31
ADGRA1	3.244699	0.32447	10	SOX2-OT	10.55781	0.364062	29
GAS7	3.133788	0.313379	10	PCDHGB6	7.482216	0.258007	29
ATP11A	5.134152	0.570461	9	PCDHGA10	7.482216	0.267222	28

SHANK2	4.574269	0.175933	26	VGLL4	5.44074	0.494613	11
AGAP1	9.283145	0.371326	25	RAD51B	4.763093	0.433008	11
PDGFRA	7.722014	0.308881	25	PCDHGC3	4.647271	0.422479	11
CAMTA1	6.438737	0.257549	25	FGFR2	4.172656	0.379332	11
SATB2	9.78528	0.40772	24	GLUD1P2	4.096334	0.372394	11
MEIS1	7.400244	0.308343	24	LBX1-AS1	6.643877	0.664388	10
PCDHGB7	7.16583	0.298576	24	ACOT7	4.245559	0.424556	10
RPTOR	8.582795	0.373165	23	GRID1	4.217946	0.421795	10
PCDHGA11	6.458615	0.280809	23	NR2F1-AS1	4.198591	0.419859	10
INPP5A	6.355389	0.276321	23	SH3RF3	4.070687	0.407069	10
PRKCZ	5.929783	0.269536	22	SND1	6.143544	0.682616	9
SKI	11.02648	0.52507	21	ATP11A	5.905842	0.656205	9
SIM2	6.157468	0.293213	21	ASAP1	5.312638	0.590293	9
ABR	6.332246	0.316612	20	ADGRB1	5.153716	0.572635	9
FRMD4A	5.456517	0.272826	20	TRAPPC12	4.912758	0.545862	9
SDK1	4.58138	0.229069	20	NOTCH1	4.490583	0.498954	9
MAD1L1	12.11511	0.637637	19	ADAMTS2	4.435597	0.492844	9
ZNF423	10.45062	0.550033	19	LINC00311	4.672861	0.584108	8
SMG1P2	6.194484	0.326025	19	NXPH1	4.415364	0.55192	8
BOLA2	6.194484	0.326025	19	DUSP6	6.259741	0.894249	7
LOC613038	6.194484	0.326025	19	VPS13D	4.510809	0.644401	7
CASZ1	5.647379	0.29723	19	LHX2	4.153165	0.593309	7
FOXK1	7.159214	0.397734	18	FBXL18	4.458406	0.743068	6
MCF2L	4.622141	0.256786	18	RUNDC3A	5.156	1.0312	5
TBX15	5.525197	0.325012	17	ATP2B4	5.053604	1.010721	5
PAX6-AS1	4.792128	0.28189	17	STAP2	5.171362	1.292841	4
RCN1	4.792128	0.28189	17	RBMS3	4.424791	1.106198	4
OPCML	4.748257	0.279309	17	GRIN2B	4.55116	1.517053	3
NAV2	4.932821	0.308301	16	SOX10	4.786496	2.393248	2
GLI2	9.602972	0.640198	15				
ZBTB20	6.998146	0.466543	15				
LRMDA	4.327524	0.288502	15				
COL23A1	4.216483	0.281099	15				
PCDHGA12	5.596429	0.399745	14				
RPS6KA2	5.49329	0.392378	14				
PRKAG2	4.76182	0.34013	14				
CUX1	4.426468	0.316176	14				
TBX5	4.404041	0.314574	14				
C7orf50	4.382117	0.313008	14				
MSI2	6.547676	0.503667	13				
MYT1L	5.523665	0.424897	13				
RFX4	5.099645	0.39228	13				
GSE1	4.415732	0.339672	13				
CMIP	6.031148	0.502596	12				
MEIS2	5.728016	0.477335	12				
ZC3H3	5.622596	0.46855	12				
TNS3	4.046921	0.337243	12				
FBRSL1	4.044398	0.337033	12				

				TABLE 71: Cancer Type GBM_pedRTK1b			
				Gene site	imp_sum	imp_mean	n
				PTPRN2	16.8441	0.205416	82
				PRDM16	8.257376	0.116301	71
				PCDHGA1	4.124719	0.06991	59
				PCDHGA2	4.124719	0.072363	57
				PCDHGA3	4.441105	0.082243	54
				PCDHGB1	4.441105	0.083794	53
				PCDHGA4	4.124719	0.080877	51
				PCDHGB2	4.2585	0.086908	49
				PCDHGA5	3.96155	0.084288	47
				PCDHGB3	3.923728	0.091249	43
				PCDHGA6	3.607342	0.090184	40
				HDAC4	11.9522	0.323032	37
				PCDHGA7	3.607342	0.097496	37
				RBFOX3	11.41951	0.326272	35
				PAX6	7.858159	0.224519	35

PCDHGB4	3.607342	0.103067	35	KIF26B	3.910967	0.300844	13
PCDHGA8	3.607342	0.103067	35	MIRLET7BHG	5.539514	0.461626	12
DIP2C	8.969986	0.280312	32	CMIP	4.937353	0.411446	12
SOX2-OT	8.36321	0.288387	29	ZC3H3	4.925995	0.4105	12
ADARB2	4.170747	0.160413	26	FBRSL1	3.8216	0.318467	12
SHANK2	4.005233	0.154047	26	RAD51B	4.467921	0.406175	11
PDGFRA	7.265464	0.290619	25	GLUD1P2	4.168221	0.378929	11
AGAP1	7.15294	0.286118	25	VGLL4	4.132147	0.37565	11
CAMTA1	5.170631	0.206825	25	CCDC140	3.554233	0.323112	11
SATB2	5.301858	0.220911	24	LBX1-AS1	7.500434	0.750043	10
MEIS1	4.769272	0.19872	24	TSPAN4	4.208367	0.420837	10
RPTOR	10.70811	0.46557	23	NR2F1-AS1	4.171545	0.417154	10
INPP5A	5.238358	0.227755	23	SND1	5.542731	0.615859	9
NCOR2	3.92109	0.170482	23	ATP11A	5.413101	0.601456	9
PRKCZ	3.654551	0.166116	22	ZNF833P	4.763877	0.52932	9
SKI	6.381008	0.303858	21	ASAP1	4.354548	0.483839	9
FRMD4A	5.678504	0.283925	20	TRAPPC12	4.284941	0.476105	9
ABR	3.950629	0.197531	20	NOTCH1	3.817776	0.424197	9
SDK1	3.726003	0.1863	20	GRIK2	4.906423	0.613303	8
MAD1L1	6.973862	0.367045	19	LINC00311	4.410606	0.551326	8
ZNF423	6.674353	0.351282	19	DLEU1	3.741214	0.467652	8
SMG1P2	4.768102	0.250953	19	MSRA	3.471661	0.433958	8
BOLA2	4.768102	0.250953	19	NR2E1	3.463409	0.432926	8
LOC613038	4.768102	0.250953	19	SOX6	5.964048	0.852007	7
CASZ1	4.337346	0.228281	19	DUSP6	5.893848	0.841978	7
KCNQ1	3.811966	0.20063	19	NAV1	3.867131	0.552447	7
FO XK1	6.494021	0.360779	18	GALNT2	3.781673	0.540239	7
SEPTIN9	5.08708	0.282616	18	FBXL18	5.063272	0.843879	6
RBFOX1	5.08074	0.282263	18	CRACR2A	3.885679	0.647613	6
TBC1D16	4.43256	0.246253	18	DNAJB6	3.881887	0.646981	6
MCF2L	3.741877	0.207882	18	HOXD4	3.774326	0.629054	6
OPCML	5.119027	0.301119	17	VAX2	3.636933	0.606156	6
TBX15	4.511745	0.265397	17	RUNDC3A	5.488615	1.097723	5
PAX6-AS1	4.025643	0.236803	17	TSNAX-DISC1	4.149847	0.829969	5
RCN1	4.025643	0.236803	17	STAP2	3.883946	0.970986	4
FOXP1	4.976041	0.311003	16	GRIN2B	4.116633	1.372211	3
GLI2	10.24092	0.682728	15	SOX10	5.368365	2.684182	2
ZBTB20	6.312985	0.420866	15				
NFIX	3.690353	0.246024	15	TABLE 72: Cancer Type			
BAIAP2	3.667221	0.244481	15	GBM_pedRTK1c			
KIRREL3	3.462071	0.230805	15	Gene site	imp_sum	imp_mean	n
NFATC1	3.451441	0.230096	15	PTPRN2	21.58137	0.263187	82
CUX1	5.320574	0.380041	14	PRDM16	15.24929	0.214779	71
C7orf50	4.81344	0.343817	14	PCDHGA1	13.78797	0.233694	59
RPS6KA2	4.752512	0.339465	14	PCDHGA2	13.78797	0.241894	57
IQSEC1	4.536437	0.324031	14	PCDHGA3	13.11033	0.242784	54
MSI2	5.416546	0.416657	13	PCDHGB1	13.11033	0.247365	53
MYT1L	4.465743	0.343519	13	PCDHGA4	13.11033	0.257065	51

PCDHGB2	12.31356	0.251297	49	TBX15	6.876137	0.404479	17
PCDHGA5	11.60184	0.246848	47	OPCML	4.769349	0.28055	17
PCDHGB3	10.59932	0.246496	43	FOXP1	6.147698	0.384231	16
PCDHGA6	9.643087	0.241077	40	SORBS2	4.38522	0.274076	16
PCDHGA7	9.195832	0.248536	37	GLI2	11.62047	0.774698	15
HDAC4	8.502729	0.229803	37	ZBTB20	4.843045	0.32287	15
RBFOX3	9.03437	0.258125	35	NFIX	3.97448	0.264965	15
PCDHGB4	8.879446	0.253698	35	CUX1	5.937357	0.424097	14
PCDHGA8	8.879446	0.253698	35	RPS6KA2	4.826212	0.344729	14
PAX6	5.81069	0.16602	35	C7orf50	4.504922	0.32178	14
DIP2C	10.58032	0.330635	32	MYT1L	6.483682	0.498745	13
PCDHGB5	8.795632	0.274863	32	MSI2	5.743576	0.441814	13
PCDHGA9	8.479246	0.273524	31	RFX4	4.041167	0.310859	13
SOX2-OT	7.604816	0.262235	29	ADGRD1	5.342894	0.445241	12
PCDHGB6	7.51977	0.259302	29	MIRLET7BHG	4.044424	0.337035	12
PCDHGA10	7.51977	0.268563	28	CMIP	4.025176	0.335431	12
SHANK2	4.015922	0.154459	26	ZC3H3	3.947124	0.328927	12
CAMTA1	8.165847	0.326634	25	VGLL4	5.135635	0.466876	11
PDGFRA	7.934166	0.317367	25	RAD51B	4.162093	0.378372	11
AGAP1	6.960914	0.278437	25	LBX1-AS1	7.429146	0.742915	10
SATB2	9.605772	0.40024	24	GRID1	5.065253	0.506525	10
PCDHGB7	6.570612	0.273776	24	NR2F1-AS1	4.644931	0.464493	10
RPTOR	7.988668	0.347333	23	SH3RF3	4.491597	0.44916	10
INPP5A	6.102587	0.26533	23	AKAP13	3.898361	0.389836	10
PCDHGA11	6.042179	0.262703	23	ZNF833P	6.168989	0.685443	9
HOXB3	4.130717	0.179596	23	ATP11A	5.682604	0.6314	9
RIMBP2	4.09859	0.1782	23	ASAP1	5.017223	0.557469	9
NCOR2	4.009765	0.174338	23	SND1	4.822785	0.535865	9
PRKCZ	6.119476	0.278158	22	ADAMTS2	4.475024	0.497225	9
SKI	6.474332	0.308302	21	GPC6	4.225264	0.469474	9
SIM2	5.283129	0.251578	21	NEAT1	4.193073	0.465897	9
ZIC4	4.033671	0.19208	21	LINC00311	4.876328	0.609541	8
FRMD4A	6.903309	0.345165	20	GRIK2	4.622532	0.577816	8
ABR	5.841206	0.29206	20	NR2E1	4.620947	0.577618	8
SDK1	4.903843	0.245192	20	RORA	4.290015	0.536252	8
MAD1L1	9.776501	0.514553	19	PPP2R2B	4.121802	0.515225	8
ZNF423	6.705634	0.352928	19	DUSP6	5.596834	0.799548	7
SMG1P2	5.695178	0.299746	19	NAV1	5.228216	0.746888	7
BOLA2	5.695178	0.299746	19	ITPKB	4.251161	0.607309	7
LOC613038	5.695178	0.299746	19	LHX2	4.084893	0.583556	7
CASZ1	5.679773	0.298935	19	RUNDC3A	4.809346	0.961869	5
KCNQ1	5.066135	0.266639	19	ARHGEF7	3.962916	0.792583	5
FO XK1	6.058288	0.336572	18	STAP2	4.016796	1.004199	4
TBC1D16	5.42445	0.301358	18	GRIN2B	4.484791	1.49493	3
MCF2L	5.130007	0.285	18	SOX10	5.491093	2.745546	2
ANKRD11	4.908939	0.272719	18				
RBFOX1	3.99222	0.22179	18				
SEPTIN9	3.846863	0.213715	18				

TABLE 73:

Cancer Type
GBM_pedRTK2a

Gene site	imp_sum	imp_mean	n	LOC613038	6.95649	0.366131	19
PTPRN2	28.1641	0.343465	82	CFAP46	4.887135	0.257218	19
PRDM16	21.49848	0.302796	71	FOXK1	7.572598	0.4207	18
PCDHGA1	10.54351	0.178704	59	TBC1D16	5.958143	0.331008	18
PCDHGA2	9.783748	0.171645	57	ANKRD11	4.911447	0.272858	18
PCDHGA3	9.467362	0.175322	54	MCF2L	4.815097	0.267505	18
PCDHGB1	9.467362	0.178629	53	OPCML	6.655209	0.391483	17
PCDHGA4	9.783748	0.191838	51	PAX6-AS1	5.534909	0.325583	17
PCDHGB2	9.807264	0.200148	49	RCN1	5.534909	0.325583	17
PCDHGA5	9.379782	0.19957	47	TBX15	5.496154	0.323303	17
PCDHGB3	8.128167	0.189027	43	HBG2	4.603913	0.270818	17
PCDHGA6	8.128167	0.203204	40	NAV2	5.046775	0.315423	16
HDAC4	12.80694	0.346133	37	FOXP1	4.916724	0.307295	16
PCDHGA7	8.030161	0.217031	37	GLI2	9.048138	0.603209	15
PAX6	13.01784	0.371938	35	ZBTB20	5.031503	0.335434	15
RBFOX3	9.143529	0.261244	35	BAIAP2	4.611745	0.30745	15
PCDHGB4	8.278399	0.236526	35	RPS6KA2	7.976409	0.569744	14
PCDHGA8	8.278399	0.236526	35	CUX1	6.534683	0.466763	14
DIP2C	10.34585	0.323308	32	PRKAG2	5.038111	0.359865	14
PCDHGB5	7.731808	0.241619	32	MSI2	7.113944	0.547226	13
PCDHGA9	7.731808	0.249413	31	MYT1L	6.357355	0.489027	13
SOX2-OT	12.30557	0.42433	29	CLYBL	4.987379	0.383645	13
PCDHGB6	7.002877	0.241479	29	RFX4	4.929773	0.379213	13
PCDHGA10	7.002877	0.250103	28	SPTBN4	4.556067	0.350467	13
GALNT9	6.062111	0.224523	27	MIRLET7BHG	6.349523	0.529127	12
ADARB2	8.59359	0.330523	26	CMIP	5.979667	0.498306	12
SHANK2	6.854793	0.263646	26	TBX4	5.161419	0.430118	12
AGAP1	8.555426	0.342217	25	TNS3	5.124884	0.427074	12
CAMTA1	8.267775	0.330711	25	ZC3H12D	7.204827	0.654984	11
PDGFRA	7.508267	0.300331	25	RAD51B	5.065146	0.460468	11
SATB2	11.18465	0.466027	24	AKAP13	4.664413	0.466441	10
MEIS1	6.644202	0.276842	24	NR5A2	4.618816	0.461882	10
PCDHGB7	6.555907	0.273163	24	ATP11A	7.175656	0.797295	9
RPTOR	11.37789	0.494691	23	SND1	6.615857	0.735095	9
NCOR2	7.036286	0.305925	23	ADAMTS2	6.153891	0.683766	9
PCDHGA11	6.047336	0.262928	23	TSPAN9	5.140176	0.571131	9
RIMBP2	4.742972	0.206216	23	KCNH2	5.02434	0.55826	9
PRKCZ	5.937995	0.269909	22	TRAPPC12	4.909557	0.545506	9
SKI	12.07293	0.574901	21	ADGRB1	4.550072	0.505564	9
HOXA-AS3	4.937572	0.235122	21	LINC00311	5.588942	0.698618	8
FRMD4A	6.668317	0.333416	20	DUSP6	6.487949	0.92685	7
SDK1	6.323901	0.316195	20	LINC01551	5.202681	0.74324	7
ABR	5.327392	0.26637	20	CDYL	4.932539	0.704648	7
MAD1L1	11.44563	0.602402	19	FBXL18	5.24403	0.874005	6
ZNF423	9.669321	0.508912	19	FAM181A	4.729407	0.788235	6
CASZ1	7.624501	0.40129	19	SATB2-AS1	4.656288	0.776048	6
SMG1P2	6.95649	0.366131	19	ATP2B4	5.000298	1.00006	5
BOLA2	6.95649	0.366131	19	RUNDC3A	4.913925	0.982785	5

ARHGEF7	4.639519	0.927904	5	SMG1P2	4.421746	0.232723	19
STAP2	4.549002	1.137251	4	BOLA2	4.421746	0.232723	19
METAP1D	5.050681	1.68356	3	LOC613038	4.421746	0.232723	19
OLIG2	5.738568	2.869284	2	CASZ1	3.503762	0.184409	19
SOX10	4.568744	2.284372	2	FOXK1	3.481892	0.193438	18
TABLE 74:	Cancer Type	GBM_pedRTK2b		SEPTIN9	2.899965	0.161109	18
				MCF2L	2.827648	0.157092	18
Gene site	imp_sum	imp_mean	n	TBX15	4.863068	0.286063	17
PTPRN2	11.04087	0.134645	82	OPCML	4.147014	0.243942	17
PRDM16	8.286591	0.116713	71	NAV2	3.194876	0.19968	16
PCDHGA1	5.501873	0.093252	59	GLI2	6.363292	0.424219	15
PCDHGA2	5.501873	0.096524	57	LRMDA	2.353996	0.156933	15
PCDHGA3	5.818259	0.107746	54	RPS6KA2	3.202018	0.228716	14
PCDHGB1	5.818259	0.109778	53	PRKAG2	2.939428	0.209959	14
PCDHGA4	5.818259	0.114084	51	PCDHGA12	2.755248	0.196803	14
PCDHGB2	5.818259	0.11874	49	CUX1	2.690397	0.192171	14
PCDHGA5	5.376909	0.114402	47	MOB2	2.625962	0.187569	14
PCDHGB3	4.744137	0.110329	43	MIR548F5	2.444184	0.174585	14
PCDHGA6	5.060523	0.126513	40	MSI2	3.469356	0.266874	13
HDAC4	8.161755	0.220588	37	CLYBL	3.086376	0.237414	13
PCDHGA7	5.376909	0.145322	37	RFX4	2.839211	0.218401	13
PAX6	6.948512	0.198529	35	ADGRD1	3.516245	0.29302	12
PCDHGB4	5.376909	0.153626	35	MEGF6	2.874126	0.239511	12
PCDHGA8	5.376909	0.153626	35	TNS3	2.58521	0.215434	12
RBFOX3	4.667296	0.133351	35	MIRLET7BHG	2.470717	0.205893	12
PCDHGB5	5.060523	0.158141	32	ZC3H3	2.325213	0.193768	12
DIP2C	3.099325	0.096854	32	ANAPC16	3.200292	0.290936	11
PCDHGA9	4.744137	0.153037	31	VGLL4	2.922761	0.265706	11
SOX2-OT	5.636251	0.194353	29	RAD51B	2.753059	0.250278	11
PCDHGB6	3.986475	0.137465	29	ZC3H12D	2.366425	0.21513	11
PCDHGA10	3.986475	0.142374	28	AKAP13	3.046862	0.304686	10
GALNT9	2.756451	0.102091	27	NR2F1-AS1	2.926888	0.292689	10
SHANK2	3.6576	0.140677	26	ACOT7	2.851214	0.285121	10
AGAP1	4.791877	0.191675	25	TFAP2B	2.488557	0.248856	10
CAMTA1	4.553356	0.182134	25	BCL11B	2.409928	0.240993	10
SATB2	7.4428	0.310117	24	AUTS2	2.313751	0.231375	10
PCDHGB7	4.020792	0.167533	24	ATP11A	3.937952	0.43755	9
INPP5A	4.580119	0.199136	23	KCNH2	3.612538	0.401393	9
RPTOR	4.330385	0.188278	23	TSPAN9	3.420374	0.380042	9
PCDHGA11	4.020792	0.174817	23	SND1	2.556235	0.284026	9
NCOR2	3.21157	0.139633	23	TRAPPC12	2.513835	0.279315	9
RIMBP2	2.324574	0.101068	23	JPH3	2.327109	0.258568	9
PRKCZ	4.457482	0.202613	22	ESRRG	3.313599	0.4142	8
SKI	6.52049	0.3105	21	MCC	2.724467	0.340558	8
ABR	3.258228	0.162911	20	ANK1	2.680844	0.335106	8
MAD1L1	5.960424	0.313707	19	MBP	2.522589	0.315324	8
ZNF423	5.395207	0.283958	19	CDYL	3.198895	0.456985	7
				DUSP6	2.847414	0.406773	7

RBM20	2.626792	0.375256	7	ZIC4	3.52581	0.167896	21
SATB2-AS1	4.193875	0.698979	6	FRMD4A	2.726461	0.136323	20
FAM181A	3.402264	0.567044	6	ABR	2.57363	0.128681	20
FBXL18	3.214322	0.53572	6	ZNF423	5.300859	0.278993	19
COL26A1	2.824265	0.470711	6	SMG1P2	3.971251	0.209013	19
ATP2B4	3.761507	0.752301	5	BOLA2	3.971251	0.209013	19
RUNDC3A	2.668414	0.533683	5	LOC613038	3.971251	0.209013	19
ARHGEF7	2.51674	0.503348	5	MAD1L1	3.297692	0.173563	19
RBMS3	3.232868	0.808217	4	CASZ1	2.676858	0.140887	19
STAP2	2.547391	0.636848	4	FOXK1	5.10052	0.283362	18
SASH1	2.332012	0.583003	4	SEPTIN9	2.752116	0.152895	18
SOX10	2.350214	1.175107	2	OPCML	4.969368	0.292316	17
SLC25A10	2.344204	1.172102	2	TBX15	4.693877	0.27611	17
				SIM1	3.561681	0.209511	17
TABLE 75:	Cancer Type GBM_PNC			PAX6-AS1	3.028129	0.178125	17
Gene site	imp_sum	imp_mean	n	RCN1	3.028129	0.178125	17
PTPRN2	6.423062	0.07833	82	NAV2	4.319793	0.269987	16
PRDM16	2.898317	0.040821	71	FOXP1	4.003332	0.250208	16
PCDHGA1	6.790692	0.115096	59	GLI2	5.244434	0.349629	15
PCDHGA2	7.107078	0.124686	57	EMX2OS	3.026256	0.20175	15
PCDHGA3	6.027488	0.11162	54	SLX1B-			
PCDHGB1	6.027488	0.113726	53	SULT1A4	2.81556	0.187704	15
PCDHGA4	6.027488	0.118186	51	SLX1A	2.81556	0.187704	15
PCDHGB2	5.394716	0.110096	49	LOC606724	2.81556	0.187704	15
PCDHGA5	5.07833	0.10805	47	ZBTB20	2.709311	0.180621	15
PCDHGB3	5.394716	0.125459	43	KNDC1	2.633055	0.175537	15
PCDHGA6	5.711102	0.142778	40	RPS6KA2	3.433396	0.245243	14
HDAC4	6.431201	0.173816	37	IQSEC1	2.953314	0.210951	14
PCDHGA7	5.272353	0.142496	37	CUX1	2.779521	0.198537	14
PAX6	6.287148	0.179633	35	PRKAG2	2.722693	0.194478	14
PCDHGB4	5.272353	0.150639	35	PCDHGA12	2.612582	0.186613	14
PCDHGA8	5.272353	0.150639	35	SPTBN4	5.213154	0.401012	13
RBFOX3	3.210057	0.091716	35	MSI2	4.418725	0.339902	13
PCDHGB5	4.955967	0.154874	32	MYT1L	2.901417	0.223186	13
DIP2C	3.948744	0.123398	32	MIRLET7BHG	3.722823	0.310235	12
PCDHGA9	4.955967	0.15987	31	TNS3	3.361623	0.280135	12
PCDHGB6	4.114368	0.141875	29	FBRSL1	3.348249	0.279021	12
PCDHGA10	4.114368	0.146942	28	ZC3H3	3.273033	0.272753	12
AGAP1	6.176979	0.247079	25	TBX4	2.979561	0.248297	12
CAMTA1	4.11764	0.164706	25	ZC3H12D	3.001307	0.272846	11
PDGFRA	3.491247	0.13965	25	SKOR1	3.370501	0.33705	10
SATB2	3.653961	0.152248	24	LBX1-AS1	2.881476	0.288148	10
PCDHGB7	3.352383	0.139683	24	OBI1-AS1	2.81532	0.281532	10
RPTOR	6.97111	0.303092	23	KLHL29	2.755884	0.275588	10
NCOR2	3.367096	0.146395	23	ACOT7	2.743144	0.274314	10
PCDHGA11	2.905452	0.126324	23	ATP11A	5.442526	0.604725	9
PRKCZ	4.050971	0.184135	22	ASAP1	3.670701	0.407856	9
SKI	5.862098	0.279148	21	SND1	3.64327	0.404808	9

TSPAN9	3.445264	0.382807	9	ADARB2	7.490435	0.288094	26
CACNA2D4	3.278697	0.3643	9	SHANK2	5.723285	0.220126	26
ADAMTS2	3.192983	0.354776	9	AGAP1	9.620862	0.384834	25
KCNH2	3.135611	0.348401	9	CAMTA1	7.42271	0.296908	25
AXIN2	2.668943	0.296549	9	PDGFRA	6.579112	0.263164	25
LINC00311	3.914549	0.489319	8	MEIS1	9.833254	0.409719	24
DNMT3A	3.17287	0.396609	8	PCDHGB7	6.762717	0.28178	24
PRDM6	2.737071	0.342134	8	RPTOR	10.48325	0.455793	23
RORA	2.6248	0.3281	8	INPP5A	7.884809	0.342818	23
MCC	2.578296	0.322287	8	RIMBP2	6.547014	0.284653	23
TRAPPC9	2.557848	0.319731	8	PCDHGA11	6.150797	0.267426	23
NAV1	3.346483	0.478069	7	NCOR2	5.982639	0.260115	23
CDYL	2.959039	0.42272	7	PRKCZ	8.395716	0.381623	22
MIR548H4	2.759179	0.394168	7	SKI	10.55635	0.502683	21
FBXL18	4.388585	0.731431	6	SIM2	6.320251	0.300964	21
STK10	2.64978	0.44163	6	HOXA-AS3	5.76096	0.274331	21
RUNDC3A	4.488731	0.897746	5	FRMD4A	7.221386	0.361069	20
DAGLB	2.714242	0.904747	3	ABR	5.131695	0.256585	20
DICER1	2.613815	0.871272	3	SDK1	5.003845	0.250192	20
SOX10	2.866816	1.433408	2	MAD1L1	12.34894	0.649944	19
SLC25A10	2.644748	1.322374	2	ZNF423	9.475006	0.498685	19
TABLE 76: Cancer Type GBM_RTK1				CASZ1	6.441073	0.339004	19
				SMG1P2	6.064086	0.319162	19
Gene site	imp_sum	imp_mean	n	BOLA2	6.064086	0.319162	19
PTPRN2	28.44191	0.346853	82	LOC613038	6.064086	0.319162	19
PRDM16	20.84059	0.293529	71	FOXK1	8.450817	0.46949	18
PCDHGA1	12.39232	0.210039	59	SEPTIN9	5.128235	0.284902	18
PCDHGA2	12.07594	0.211859	57	PAX6-AS1	6.095445	0.358556	17
PCDHGA3	11.12678	0.206051	54	RCN1	6.095445	0.358556	17
PCDHGB1	11.12678	0.209939	53	TBX15	5.67349	0.333735	17
PCDHGA4	11.12678	0.218172	51	OPCML	5.359936	0.31529	17
PCDHGB2	10.49401	0.214163	49	FOXP1	5.657345	0.353584	16
PCDHGA5	9.753145	0.207514	47	NAV2	5.487794	0.342987	16
PCDHGB3	9.449537	0.219757	43	SORBS2	4.740616	0.296288	16
PCDHGA6	9.133151	0.228329	40	GLI2	10.48235	0.698823	15
HDAC4	12.30965	0.332693	37	BAIAP2	6.399272	0.426618	15
PCDHGA7	9.14593	0.247187	37	ZBTB20	6.189875	0.412658	15
RBFOX3	12.19811	0.348517	35	SLX1B-			
PAX6	11.04636	0.31561	35	SULT1A4	4.983773	0.332252	15
PCDHGB4	9.14593	0.261312	35	SLX1A	4.983773	0.332252	15
PCDHGA8	9.14593	0.261312	35	LOC606724	4.983773	0.332252	15
DIP2C	9.579993	0.299375	32	RPS6KA2	7.065162	0.504654	14
PCDHGB5	8.597751	0.26868	32	CUX1	6.693427	0.478102	14
PCDHGA9	8.281365	0.267141	31	PRKAG2	5.619134	0.401367	14
SOX2-OT	11.87077	0.409337	29	C7orf50	5.0646	0.361757	14
PCDHGB6	7.520914	0.259342	29	IQSEC1	4.856892	0.346921	14
PCDHGA10	7.520914	0.268604	28	MYT1L	6.962197	0.535554	13
GALNT9	4.804374	0.17794	27	SPTBN4	5.549333	0.426872	13

MSI2	5.429656	0.417666	13	PCDHGB4	8.268738	0.23625	35
GSE1	5.293354	0.407181	13	PCDHGA8	8.268738	0.23625	35
HOXA10-				PCDHGB5	8.268738	0.258398	32
HOXA9	4.962239	0.381711	13	DIP2C	7.532289	0.235384	32
CMIP	5.283035	0.440253	12	PCDHGA9	8.268738	0.266733	31
ZC3H3	4.974593	0.414549	12	SOX2-OT	8.995953	0.310205	29
MAML3	4.830029	0.402502	12	PCDHGB6	7.071556	0.243847	29
VGLL4	5.27689	0.479717	11	PCDHGA10	7.071556	0.252556	28
RAD51B	5.159886	0.469081	11	SHANK2	6.280585	0.241561	26
ZC3H12D	4.848675	0.440789	11	ADARB2	4.727206	0.181816	26
LBX1-AS1	6.275327	0.627533	10	AGAP1	9.622224	0.384889	25
ACOT7	5.334854	0.533485	10	CAMTA1	7.433597	0.297344	25
SH3RF3	5.188231	0.518823	10	PDGFRA	5.709785	0.228391	25
AKAP13	4.795264	0.479526	10	SATB2	10.64248	0.443437	24
SND1	6.244847	0.693872	9	MEIS1	7.688916	0.320371	24
ATP11A	5.774312	0.64159	9	PCDHGB7	6.307733	0.262822	24
TSPAN9	5.127746	0.56975	9	RPTOR	12.03723	0.523358	23
ASAP1	5.047038	0.560782	9	NCOR2	8.962317	0.389666	23
AXIN2	4.911017	0.545669	9	NXN	6.297388	0.273799	23
ADAMTS2	4.847841	0.538649	9	HOXB3	5.798086	0.252091	23
ADGRB1	4.763301	0.529256	9	PCDHGA11	5.732892	0.249256	23
LINC00311	5.827952	0.728494	8	INPP5A	5.068774	0.220381	23
DUSP6	6.547525	0.935361	7	PRKCZ	6.517701	0.296259	22
LINC00461	5.023787	0.717684	7	SKI	10.8709	0.517662	21
NAV1	4.941564	0.705938	7	HOXA-AS3	5.410938	0.257664	21
FBXL18	5.08984	0.848307	6	ZIC4	4.773249	0.227298	21
RUNDC3A	5.299092	1.059818	5	ABR	8.490465	0.424523	20
STAP2	5.035557	1.258889	4	FRMD4A	5.641957	0.282098	20
GRIN2B	4.823391	1.607797	3	SDK1	4.713856	0.235693	20
SOX10	5.5945	2.79725	2	MAD1L1	11.38517	0.599219	19
TABLE 77: Cancer Type GBM_RTK2				ZNF423	8.122477	0.427499	19
				SMG1P2	6.862892	0.361205	19
Gene site	imp_sum	imp_mean	n	BOLA2	6.862892	0.361205	19
PTPRN2	19.6513	0.23965	82	LOC613038	6.862892	0.361205	19
PRDM16	18.95536	0.266977	71	CASZ1	5.755603	0.302926	19
PCDHGA1	13.06176	0.221386	59	ANKRD11	7.390952	0.410608	18
PCDHGA2	12.74538	0.223603	57	FO XK1	7.256107	0.403117	18
PCDHGA3	11.57895	0.214425	54	SEPTIN9	5.800177	0.322232	18
PCDHGB1	11.57895	0.218471	53	MCF2L	5.699282	0.316627	18
PCDHGA4	10.94618	0.214631	51	OPCML	6.8263	0.401547	17
PCDHGB2	10.94618	0.223391	49	TBX15	6.010796	0.353576	17
PCDHGA5	10.46056	0.222565	47	PAX6-AS1	4.937854	0.290462	17
PCDHGB3	9.740708	0.226528	43	RCN1	4.937854	0.290462	17
PCDHGA6	9.107936	0.227698	40	FOXP1	6.393653	0.399603	16
HDAC4	14.32705	0.387217	37	NAV2	5.910149	0.369384	16
PCDHGA7	8.79155	0.237609	37	GLI2	10.11008	0.674006	15
RBFOX3	11.54054	0.32973	35	LRMDA	5.176466	0.345098	15
PAX6	11.22163	0.320618	35	BAIAP2	5.016139	0.334409	15

SLX1B-SULT1A4	4.974586	0.331639	15	PCDHGA4	2.974028	0.058314	51
SLX1A	4.974586	0.331639	15	PCDHGB2	2.974028	0.060694	49
LOC606724	4.974586	0.331639	15	PCDHGA5	2.974028	0.063277	47
RPS6KA2	7.413005	0.5295	14	PCDHGB3	2.974028	0.069163	43
IQSEC1	5.770443	0.412175	14	PCDHGA6	2.341256	0.058531	40
CUX1	5.510593	0.393614	14	HDAC4	10.80254	0.291961	37
MSI2	8.266631	0.635895	13	PCDHGA7	2.341256	0.063277	37
MYT1L	5.590905	0.43007	13	PAX6	4.725962	0.135027	35
SPTBN4	5.57676	0.428982	13	RBFOX3	3.270117	0.093432	35
GSE1	5.208374	0.400644	13	PCDHGB4	2.341256	0.066893	35
ZC3H3	6.33547	0.527956	12	PCDHGA8	2.341256	0.066893	35
MIRLET7BHG	6.225246	0.518771	12	DIP2C	4.662698	0.145709	32
TNS3	5.933709	0.494476	12	SOX2-OT	2.662139	0.091798	29
CMIP	5.395776	0.449648	12	AGAP1	6.21563	0.248625	25
ADGRD1	4.719988	0.393332	12	CAMTA1	2.834911	0.113396	25
VGLL4	4.902711	0.445701	11	SATB2	2.57308	0.107212	24
SH3RF3	5.296941	0.529694	10	RPTOR	6.923574	0.301025	23
LBX1-AS1	5.044842	0.504484	10	INPP5A	3.284902	0.142822	23
NR2F1-AS1	4.856945	0.485695	10	NCOR2	2.447521	0.106414	23
ATP11A	6.945317	0.771702	9	SKI	6.513082	0.310147	21
SND1	6.758195	0.750911	9	ZIC4	3.927683	0.187033	21
AXIN2	5.341699	0.593522	9	SDK1	2.463619	0.123181	20
ADAMTS2	5.162272	0.573586	9	MAD1L1	4.754699	0.250247	19
TRAPPC12	5.068641	0.563182	9	SMG1P2	2.985947	0.157155	19
ASAP1	4.919802	0.546645	9	BOLA2	2.985947	0.157155	19
TSPAN9	4.90379	0.544866	9	LOC613038	2.985947	0.157155	19
DMRTA2	4.730823	0.525647	9	ZNF423	2.952116	0.155375	19
LINC00311	5.353218	0.669152	8	CASZ1	2.272645	0.119613	19
DLEU1	5.160303	0.645038	8	TBC1D16	4.224717	0.234707	18
PPP2R2B	4.979109	0.622389	8	FOXK1	3.763196	0.209066	18
MBP	4.625602	0.5782	8	SEPTIN9	3.473925	0.192996	18
DUSP6	6.155281	0.879326	7	ANKRD11	3.207682	0.178205	18
NAV1	5.179188	0.739884	7	OPCML	3.696412	0.217436	17
CDYL	5.115782	0.730826	7	NAV2	3.016295	0.188518	16
TSNAX-DISC1	4.793222	0.958644	5	FOXP1	2.315913	0.144745	16
ARHGEF7	4.65138	0.930276	5	NFIX	3.557653	0.237177	15
SOX10	5.000024	2.500012	2	SLX1B-SULT1A4	3.248136	0.216542	15
				SLX1A	3.248136	0.216542	15
				LOC606724	3.248136	0.216542	15
				ZBTB20	2.616493	0.174433	15
				GLI2	2.424166	0.161611	15
				NFATC1	2.332888	0.155526	15
				RPS6KA2	5.447932	0.389138	14
				MIR548F5	3.459727	0.247123	14
				IQSEC1	3.360687	0.240049	14
				GNG7	2.978525	0.212752	14
				C7orf50	2.941557	0.210111	14

TABLE 78: Cancer Type GCT_GERM_A			
Gene site	imp_sum	imp_mean	n
PTPRN2	9.101473	0.110994	82
PRDM16	8.043839	0.113294	71
PCDHGA1	2.974028	0.050407	59
PCDHGA2	2.974028	0.052176	57
PCDHGA3	2.974028	0.055075	54
PCDHGB1	2.974028	0.056114	53

CUX1	2.854477	0.203891	14
PRKAG2	2.623327	0.187381	14
ARHGEF10	2.531088	0.180792	14
MSI2	3.74575	0.288135	13
MYT1L	3.317276	0.255175	13
GSE1	2.318814	0.17837	13
CMIP	3.895785	0.324649	12
ADGRD1	2.926081	0.24384	12
ZC3H3	2.88618	0.240515	12
GNA12	2.495305	0.207942	12
ISLR2	2.4525	0.204375	12
TBX4	2.325781	0.193815	12
ZC3H12D	2.609661	0.237242	11
WNT5A	2.549258	0.231751	11
ACOT7	3.651995	0.365199	10
NR2F1-AS1	2.902074	0.290207	10
BCL11B	2.337443	0.233744	10
TSPAN4	2.231434	0.223143	10
SND1	4.244156	0.471573	9
TRAPPC12	3.440843	0.382316	9
ATP11A	3.195474	0.355053	9
SSBP3	3.053275	0.339253	9
CACNA2D4	2.342664	0.260296	9
KCNH2	2.310504	0.256723	9
MSRA	3.189972	0.398746	8
SYNJ2	2.727817	0.340977	8
DLEU1	2.683196	0.3354	8
CDH4	2.395494	0.299437	8
DNMT3A	2.392436	0.299055	8
TENM2	2.339529	0.292441	8
SHROOM3	2.255323	0.281915	8
C19orf25	4.052101	0.578872	7
GAK	2.852329	0.407476	7
MIR548H4	2.571419	0.367346	7
VPS13D	2.460848	0.35155	7
STK10	3.198507	0.533084	6
RADIL	3.066899	0.51115	6
FBXL18	2.858599	0.476433	6
CCDC177	2.672475	0.445412	6
RUNDC3A	3.376471	0.675294	5
CCR6	3.187996	0.637599	5
TSNAX-DISC1	3.062186	0.612437	5
ARHGEF7	2.892383	0.578477	5
AP2A2	2.57388	0.514776	5
ARHGAP26	2.557087	0.511417	5
DTNA	2.421815	0.605454	4
TBC1D7	3.196945	1.065648	3

TABLE 79:

Cancer Type
GCT_GERM_B

Gene site	imp_sum	imp_mean	n
PTPRN2	19.31761	0.235581	82
PRDM16	18.84404	0.265409	71
PCDHGA1	11.03441	0.187024	59
PCDHGA2	10.71803	0.188036	57
PCDHGA3	9.768867	0.180905	54
PCDHGB1	9.452481	0.178349	53
PCDHGA4	9.452481	0.185343	51
PCDHGB2	9.136095	0.186451	49
PCDHGA5	8.819709	0.187653	47
PCDHGB3	8.396513	0.195268	43
PCDHGA6	8.080127	0.202003	40
HDAC4	13.99709	0.3783	37
PCDHGA7	7.447355	0.20128	37
RBFOX3	9.974812	0.284995	35
PAX6	7.738563	0.221102	35
PCDHGB4	7.130969	0.203742	35
PCDHGA8	7.130969	0.203742	35
DIP2C	10.74588	0.335809	32
PCDHGB5	6.217327	0.194291	32
PCDHGA9	6.217327	0.200559	31
SOX2-OT	7.245309	0.249838	29
PCDHGB6	5.584555	0.192571	29
PCDHGA10	5.584555	0.199448	28
GALNT9	5.550231	0.205564	27
ADARB2	7.655789	0.294453	26
SHANK2	6.731637	0.258909	26
AGAP1	9.790224	0.391609	25
CAMTA1	7.134214	0.285369	25
PDGFRA	6.733768	0.269351	25
SATB2	6.469941	0.269581	24
PCDHGB7	5.165607	0.215234	24
RPTOR	11.22884	0.488211	23
NCOR2	7.659987	0.333043	23
NXN	6.652723	0.289249	23
INPP5A	6.507467	0.282933	23
HOXB3	4.777145	0.207702	23
PCDHGA11	4.723644	0.205376	23
PRKCZ	8.538897	0.388132	22
SKI	7.434102	0.354005	21
ZIC4	4.447648	0.211793	21
HOXA-AS3	4.239343	0.201873	21
ABR	5.742782	0.287139	20
FRMD4A	5.473026	0.273651	20
SDK1	4.769503	0.238475	20
MADIL1	10.94435	0.576018	19

ZNF423	6.837359	0.359861	19	DLEU1	3.93938	0.492422	8
CASZ1	5.715937	0.300839	19	PPP2R2B	3.861173	0.482647	8
SMG1P2	4.984773	0.262356	19	NAV1	4.691965	0.670281	7
BOLA2	4.984773	0.262356	19	DUSP6	4.203916	0.600559	7
LOC613038	4.984773	0.262356	19	GAK	3.708546	0.529792	7
SEPTIN9	7.182444	0.399025	18	FBXL18	3.708094	0.618016	6
TBC1D16	6.250265	0.347237	18	TSNAX-DISC1	4.859345	0.971869	5
ANKRD11	6.040036	0.335558	18	RUNDC3A	3.725693	0.745139	5
HOXA3	4.762563	0.264587	18	TABLE 80: Cancer Type GCT_TERA			
FOXK1	4.554552	0.253031	18	Gene site	imp_sum	imp_mean	n
MCF2L	3.738665	0.207704	18	PTPRN2	17.87431	0.217979	82
OPCML	7.256601	0.426859	17	PRDM16	15.90775	0.224053	71
PAX6-AS1	3.966804	0.233341	17	PCDHGA1	4.154031	0.070407	59
RCN1	3.966804	0.233341	17	PCDHGA2	4.470417	0.078428	57
FOXP1	5.738304	0.358644	16	PCDHGA3	4.018183	0.074411	54
GLI2	8.145145	0.54301	15	PCDHGA4	4.018183	0.078788	51
KNDC1	4.826227	0.321748	15	PCDHGB1	4.018183	0.075815	53
SLX1B-				PCDHGA4	4.018183	0.078788	51
SULT1A4	3.946591	0.263106	15	PCDHGB2	4.018183	0.082004	49
SLX1A	3.946591	0.263106	15	PCDHGA5	4.295947	0.091403	47
LOC606724	3.946591	0.263106	15	HDAC4	17.99685	0.486401	37
RPS6KA2	7.147811	0.510558	14	RBFOX3	9.614951	0.274713	35
CUX1	6.450239	0.460731	14	PAX6	9.381022	0.268029	35
PRKAG2	5.410973	0.386498	14	DIP2C	9.374361	0.292949	32
CACNA1H	4.776324	0.341166	14	SOX2-OT	4.59365	0.158402	29
MOB2	4.437151	0.316939	14	GALNT9	4.846109	0.179486	27
IQSEC1	4.235867	0.302562	14	SHANK2	5.967514	0.22952	26
MYT1L	5.984541	0.460349	13	AGAP1	10.10199	0.40408	25
MSI2	5.847016	0.44977	13	CAMTA1	9.78895	0.391558	25
RFX4	4.210517	0.323886	13	PDGFRA	6.632905	0.265316	25
KIF26B	3.750733	0.288518	13	MEIS1	6.378497	0.265771	24
FBRSL1	4.946713	0.412226	12	SATB2	5.7202	0.238342	24
ADGRD1	4.94334	0.411945	12	RPTOR	13.34639	0.580278	23
MAML3	3.926583	0.327215	12	NCOR2	9.562957	0.415781	23
RASA3	3.885229	0.323769	12	NXN	5.929367	0.257799	23
CMIP	3.883371	0.323614	12	PRKCZ	6.904633	0.313847	22
ZC3H3	3.800354	0.316696	12	SKI	8.750163	0.416674	21
ZC3H12D	4.564659	0.414969	11	FRMD4A	7.225964	0.361298	20
TBCD	3.721824	0.338348	11	SDK1	6.522443	0.326122	20
TRAPPC12	5.592923	0.621436	9	MAD1L1	11.14816	0.586745	19
SND1	5.51222	0.612469	9	CASZ1	7.408534	0.389923	19
ATP11A	4.466621	0.496291	9	ZNF423	6.4314	0.338495	19
RUNX1	4.068281	0.452031	9	SMG1P2	6.203487	0.326499	19
AXIN2	3.879315	0.431035	9	BOLA2	6.203487	0.326499	19
TSPAN9	3.811645	0.423516	9	LOC613038	6.203487	0.326499	19
CACNA2D4	3.738174	0.415353	9	TBC1D16	7.737052	0.429836	18
VRK2	4.449892	0.556237	8	ANKRD11	6.607758	0.367098	18
AFF3	4.052908	0.506614	8	FOXK1	6.211291	0.345072	18

MCF2L	5.36849	0.298249	18	MGMT	4.018641	0.446516	9
RBFOX1	3.760071	0.208893	18	ASAP1	3.692621	0.410291	9
PAX6-AS1	5.905532	0.347384	17	DLEU1	5.903349	0.737919	8
RCN1	5.905532	0.347384	17	MSRA	4.837281	0.60466	8
OPCML	3.974252	0.23378	17	LHX4	4.117693	0.514712	8
FOXP1	5.642803	0.352675	16	DNMT3A	3.852664	0.481583	8
SORBS2	5.266291	0.329143	16	RORA	3.836926	0.479616	8
NAV2	4.03055	0.251909	16	VRK2	3.678644	0.45983	8
BAIAP2	5.289703	0.352647	15	NAV1	4.495543	0.64222	7
GLI2	4.695861	0.313057	15	GAK	4.323294	0.617613	7
KIRREL3	4.319986	0.287999	15	FBXL18	5.140929	0.856822	6
NFIX	4.191253	0.279417	15	RUNDC3A	5.185511	1.037102	5
ZBTB20	4.018173	0.267878	15	ARHGEF7	4.182116	0.836423	5
COL23A1	3.724193	0.24828	15	BCAR1	3.830265	0.766053	5
RPS6KA2	6.902618	0.493044	14	TSNAX-DISC1	3.757437	0.751487	5
ARHGEF10	5.265573	0.376112	14				
PRKAG2	4.694434	0.335317	14				
C7orf50	4.404999	0.314643	14				
MOB2	4.213358	0.300954	14	TABLE 81:	Cancer Type GCT_YOLKSAC		
TBX5	4.202229	0.300159	14	Gene site	imp_sum	imp_mean	n
MSI2	5.703035	0.438695	13	PTPRN2	4.99835	0.060955	82
MIR9-3HG	4.989205	0.383785	13	PRDM16	5.801836	0.081716	71
SPTBN4	4.626165	0.355859	13	PCDHGA3	2.502743	0.046347	54
RFX4	4.49132	0.345486	13	PCDHGB1	2.502743	0.047222	53
MYT1L	4.371628	0.336279	13	PCDHGA4	2.502743	0.049073	51
GSE1	3.778988	0.290691	13	HDAC4	11.14682	0.301266	37
ZC3H3	5.296445	0.44137	12	RBFOX3	4.511934	0.128912	35
LRBA	5.208066	0.434005	12	PAX6	3.453012	0.098657	35
ADGRD1	4.681358	0.390113	12	DIP2C	6.987383	0.218356	32
CMIP	4.38781	0.365651	12	SHANK2	3.496089	0.134465	26
TNS3	4.246333	0.353861	12	AGAP1	7.738	0.30952	25
FBRSL1	4.013577	0.334465	12	CAMTA1	4.366767	0.174671	25
MIRLET7BHG	3.678431	0.306536	12	PDGFRA	2.790693	0.111628	25
ANAPC16	4.975722	0.452338	11	RPTOR	8.298155	0.360789	23
CTBP2	4.523532	0.41123	11	NCOR2	6.257643	0.272071	23
ZC3H12D	4.448097	0.404372	11	NXN	5.325576	0.231547	23
TBCD	4.235393	0.385036	11	PRKCZ	3.769165	0.171326	22
RAD51B	4.092926	0.372084	11	SKI	6.772891	0.322519	21
CCDC140	3.835235	0.348658	11	ABR	2.749045	0.137452	20
PCDHGC3	3.759371	0.341761	11	SDK1	2.517911	0.125896	20
TP73	5.395891	0.539589	10	MAD1L1	8.328458	0.43834	19
KLHL29	4.211312	0.421131	10	CASZ1	3.960116	0.208427	19
RGS12	4.028726	0.402873	10	KCNQ1	3.539228	0.186275	19
SH3RF3	3.735144	0.373514	10	SMG1P2	2.739954	0.144208	19
SND1	5.405361	0.600596	9	BOLA2	2.739954	0.144208	19
ATP11A	5.190054	0.576673	9	LOC613038	2.739954	0.144208	19
ADAMTS2	4.816169	0.53513	9	FOXK1	6.469351	0.359408	18
CACNA2D4	4.7708	0.530089	9	TBC1D16	4.904479	0.272471	18

SEPTIN9	2.749956	0.152775	18	SYNJ2	2.540975	0.317622	8
PAX6-AS1	2.751846	0.161873	17	RXRA	3.981993	0.568856	7
RCN1	2.751846	0.161873	17	CXXC5	3.667471	0.523924	7
FOXP1	4.98589	0.311618	16	MIR548H4	2.932401	0.418914	7
EBF3	3.495841	0.21849	16	OTX2-AS1	2.720198	0.3886	7
GLI2	3.827065	0.255138	15	CRADD	4.975217	0.829203	6
SLX1B-				FBXL18	4.219659	0.703277	6
SULT1A4	3.01742	0.201161	15	TRAK1	3.020541	0.503424	6
SLX1A	3.01742	0.201161	15	MYO16	2.676559	0.446093	6
LOC606724	3.01742	0.201161	15	FMNL2	2.639078	0.439846	6
PRKAG2	4.033346	0.288096	14	RUNDC3A	3.406303	0.681261	5
CUX1	3.696431	0.264031	14	ARHGEF7	3.345842	0.669168	5
C7orf50	3.680209	0.262872	14	BCAR1	2.989539	0.597908	5
IQSEC1	3.21317	0.229512	14	FAM53B	2.816195	0.563239	5
ARHGEF10	2.563992	0.183142	14	AP2A2	2.728119	0.545624	5
RPS6KA2	2.556839	0.182631	14	ZMIZ1	2.638003	0.659501	4
MSI2	5.590865	0.430067	13	DUSP5	2.553512	0.638378	4
GSE1	5.181869	0.398605	13	LPP	2.466561	0.61664	4
CMIP	5.62367	0.468639	12	DTNA	2.44406	0.611015	4
ZC3H3	3.288293	0.274024	12	SLC6A9	2.449393	0.816464	3
GNA12	3.222275	0.268523	12	RALGAPA2	3.817503	1.908751	2
RASA3	2.940557	0.245046	12	RAB11FIP3	2.739979	1.36999	2
MEIS2	2.75406	0.229505	12	ERI3	2.704809	1.352405	2
TBX4	2.530601	0.210883	12	TRIM65	2.64978	1.32489	2
ADGRD1	2.482515	0.206876	12	KCNV2	2.795229	2.795229	1
GLUD1P2	4.223631	0.383966	11				
RAD51B	3.500001	0.318182	11				
CTBP2	3.119431	0.283585	11	TABLE 82:	Cancer Type		
VGLL4	2.636152	0.23965	11	Gene site	imp_sum	imp_mean	n
ZC3H12D	2.51935	0.229032	11	PTPRN2	25.34553	0.309092	82
FGFR2	2.458012	0.223456	11	PRDM16	29.31827	0.412933	71
TSPAN4	3.917092	0.391709	10	PCDHGA1	9.194939	0.155846	59
ACOT7	3.318852	0.331885	10	PCDHGA2	8.878553	0.155764	57
AKAP13	3.17245	0.317245	10	PCDHGA3	9.194939	0.170277	54
CHST11	2.657571	0.265757	10	PCDHGB1	9.194939	0.173489	53
SH3RF3	2.64241	0.264241	10	PCDHGA4	9.194939	0.180293	51
KLHL29	2.557927	0.255793	10	PCDHGB2	9.511325	0.194109	49
SND1	5.450853	0.60565	9	PCDHGA5	8.625482	0.183521	47
ATP11A	5.3636	0.595956	9	PCDHGB3	7.99271	0.185877	43
MGMT	3.116205	0.346245	9	PCDHGA6	7.676324	0.191908	40
AXIN2	2.804539	0.311615	9	HDAC4	17.47931	0.472414	37
TSPAN9	2.737463	0.304163	9	PCDHGA7	7.043552	0.190366	37
MACROD1	3.046225	0.380778	8	PAX6	15.42818	0.440805	35
TRIM71	2.748109	0.343514	8	RBFOX3	13.02851	0.372243	35
DNMT3A	2.729414	0.341177	8	PCDHGB4	6.813347	0.194667	35
LINC00311	2.713531	0.339191	8	PCDHGA8	6.813347	0.194667	35
DLEU1	2.630831	0.328854	8	DIP2C	13.69455	0.427955	32
TRAPPC9	2.590092	0.323761	8	PCDHGB5	6.813347	0.212917	32

PCDHGA9	6.813347	0.219785	31	PRKAG2	5.297489	0.378392	14
SOX2-OT	12.0816	0.416607	29	MSI2	8.236219	0.633555	13
PCDHGB6	5.734782	0.197751	29	GSE1	6.344139	0.488011	13
PCDHGA10	5.734782	0.204814	28	KIF26B	5.955905	0.458147	13
SHANK2	8.764206	0.337085	26	RFX4	5.736025	0.441233	13
ADARB2	7.918374	0.304553	26	MYT1L	5.609456	0.431497	13
AGAP1	10.13629	0.405452	25	SPTBN4	5.601586	0.430891	13
CAMTA1	8.46813	0.338725	25	ZC3H3	6.473633	0.539469	12
PDGFRA	6.710821	0.268433	25	TNS3	6.410599	0.534217	12
SATB2	8.66246	0.360936	24	CMIP	5.938821	0.494902	12
MEIS1	7.857727	0.327405	24	TBX4	5.883156	0.490263	12
RPTOR	13.73371	0.597118	23	MIRLET7BHG	5.653598	0.471133	12
NCOR2	8.935001	0.388478	23	ADGRD1	5.444733	0.453728	12
HOXB3	7.16603	0.311567	23	MEGF6	5.315412	0.442951	12
INPP5A	7.097167	0.308572	23	MAML3	5.176265	0.431355	12
NXN	6.273458	0.272759	23	ZC3H12D	7.116886	0.64699	11
RIMBP2	5.900218	0.256531	23	VGLL4	5.735209	0.521383	11
PRKCZ	7.814398	0.3552	22	RAD51B	5.701272	0.518297	11
SKI	13.60206	0.647717	21	SPON2	5.238344	0.476213	11
SIM2	7.465344	0.355493	21	ACOT7	5.762192	0.576219	10
ZIC4	6.097637	0.290364	21	OTX1	5.712617	0.571262	10
ABR	9.118534	0.455927	20	IGF1R	5.600259	0.560026	10
FRMD4A	8.819341	0.440967	20	SND1	6.771402	0.752378	9
SDK1	5.901252	0.295063	20	ATP11A	6.746126	0.74957	9
MAD1L1	13.06315	0.687534	19	ASAP1	5.982675	0.664742	9
ZNF423	10.99371	0.578616	19	AXIN2	5.952509	0.66139	9
CASZ1	8.968132	0.472007	19	TSPAN9	5.389787	0.598865	9
SMG1P2	6.003089	0.315952	19	LHX4	6.42543	0.803179	8
BOLA2	6.003089	0.315952	19	LINC00311	5.699983	0.712498	8
LOC613038	6.003089	0.315952	19	ASPSCR1	5.1551	0.644388	8
FOKK1	8.454174	0.469676	18	DUSP6	6.819031	0.974147	7
ANKRD11	6.82245	0.379025	18	LINC00461	5.320591	0.760084	7
MCF2L	6.745235	0.374735	18	FBXL18	5.134469	0.855745	6
SEPTIN9	5.530185	0.307233	18				
TBC1D16	5.445359	0.30252	18	TABLE 83:	Cancer Type GNT_ND		
OPCML	8.474402	0.498494	17	Gene site	imp_sum	imp_mean	n
TBX15	7.334093	0.431417	17	PTPRN2	11.49988	0.140242	82
PAX6-AS1	5.324681	0.313217	17	PRDM16	10.36101	0.14593	71
RCN1	5.324681	0.313217	17	PCDHGA1	2.628587	0.044552	59
FOXP1	8.364046	0.522753	16	PCDHGA2	2.628587	0.046116	57
NAV2	5.598424	0.349902	16	PCDHGA3	2.944973	0.054537	54
GLI2	12.02527	0.801685	15	PCDHGB1	2.944973	0.055566	53
ZBTB20	6.936051	0.462403	15	PCDHGA4	2.628587	0.051541	51
NFIX	5.624007	0.374934	15	PCDHGA5	2.628587	0.055927	47
LRMDA	5.508807	0.367254	15	PCDHGB3	3.577745	0.083203	43
RPS6KA2	7.775948	0.555425	14	PCDHGA6	2.807114	0.070178	40
C7orf50	6.54699	0.467642	14	HDAC4	9.886463	0.267202	37
CUX1	6.333639	0.452403	14	RBFOX3	7.509306	0.214552	35

PAX6	5.357323	0.153066	35	ADGRB1	5.36614	0.596238	9
DIP2C	8.208457	0.256514	32	ATP11A	5.061607	0.562401	9
SOX2-OT	8.728742	0.300991	29	SND1	3.843547	0.427061	9
ADARB2	3.267447	0.125671	26	ASAP1	3.648247	0.405361	9
CAMTA1	6.086511	0.24346	25	NOTCH1	3.530086	0.392232	9
PDGFRA	5.626339	0.225054	25	ZNF833P	3.196336	0.355148	9
AGAP1	5.331453	0.213258	25	RUNX1	3.10094	0.344549	9
PCDHGB7	2.759321	0.114972	24	TRAPPC12	3.083809	0.342645	9
RPTOR	6.427431	0.279454	23	KCNMA1	2.976558	0.330729	9
NCOR2	4.320246	0.187837	23	AXIN2	2.910305	0.323367	9
RIMBP2	3.703202	0.161009	23	TSPAN9	2.775641	0.308405	9
NXN	2.693327	0.117101	23	ADAMTS2	2.645081	0.293898	9
PRKCZ	4.280145	0.194552	22	GPC6	2.638177	0.293131	9
SKI	8.403006	0.400143	21	LINC00311	2.95298	0.369122	8
FRMD4A	5.84965	0.292483	20	GRIK2	2.800493	0.350062	8
ZNF423	7.989529	0.420502	19	ESRRG	2.688412	0.336052	8
MAD1L1	6.742287	0.354857	19	MSRA	2.685591	0.335699	8
SMG1P2	5.493399	0.289126	19	DUSP6	4.29677	0.613824	7
BOLA2	5.493399	0.289126	19	LINC00461	3.812362	0.544623	7
LOC613038	5.493399	0.289126	19	NAV1	3.484596	0.497799	7
CASZ1	3.400766	0.178988	19	SOX6	3.175191	0.453599	7
MCF2L	4.583134	0.254619	18	FHIT	2.908577	0.415511	7
FO XK1	3.13369	0.174094	18	LHX2	2.781746	0.397392	7
SEPTIN9	2.728531	0.151585	18	LINC01140	2.688698	0.3841	7
TBX15	4.164269	0.244957	17	CXXC5	2.684351	0.383479	7
OPCML	4.137456	0.24338	17	FBXL18	3.966795	0.661133	6
FOXP1	4.774371	0.298398	16	FAM181A	3.321132	0.553522	6
GLI2	9.168754	0.61125	15	MYO16	3.110838	0.518473	6
KIRREL3	3.814096	0.254273	15	RUNDC3A	4.597805	0.919561	5
LRMDA	3.771615	0.251441	15	PRR5L	3.231042	0.646208	5
ZBTB20	3.032585	0.202172	15	TSNAX-DISC1	3.12277	0.624554	5
CUX1	3.015518	0.215394	14	ARHGEF7	3.056062	0.611212	5
MYT1L	4.276737	0.32898	13	THRB	2.723247	0.544649	5
MSI2	3.848376	0.296029	13	RBMS3	3.544672	0.886168	4
RFX4	2.894789	0.222676	13	STAP2	3.066668	0.766667	4
SPTBN4	2.681901	0.2063	13	LINC00856	2.744387	0.686097	4
CMIP	5.471674	0.455973	12	GRIN2B	3.331979	1.11066	3
ZC3H3	3.35249	0.279374	12	DAGLB	2.993153	0.997718	3
MIRLET7BHG	2.987944	0.248995	12	SOX10	4.597364	2.298682	2
ADGRD1	2.913691	0.242808	12	SLC25A10	2.817577	1.408788	2
TNS3	2.719485	0.226624	12				
TBX4	2.638051	0.219838	12	TABLE 84:	Cancer Type HGAP		
FGFR2	4.110203	0.373655	11	Gene site	imp_sum	imp_mean	n
RAD51B	3.301774	0.300161	11	PTPRN2	24.4535	0.298213	82
VGLL4	3.180565	0.289142	11	PRDM16	19.6305	0.276486	71
LBX1-AS1	5.781882	0.578188	10	PCDHGA1	12.32161	0.208841	59
ACOT7	4.055634	0.405563	10	PCDHGA2	12.00523	0.210618	57
SH3RF3	3.706206	0.370621	10	PCDHGA3	10.70417	0.198225	54

PCDHGB1	10.70417	0.201966	53	TBX15	6.224702	0.366159	17
PCDHGA4	10.56268	0.207111	51	PAX6-AS1	5.918508	0.348148	17
PCDHGB2	9.92991	0.202651	49	RCN1	5.918508	0.348148	17
PCDHGA5	9.267611	0.197183	47	NAV2	5.629729	0.351858	16
PCDHGB3	8.503787	0.197762	43	SORBS2	5.629435	0.35184	16
PCDHGA6	8.318986	0.207975	40	FOXP1	5.595224	0.349701	16
HDAC4	14.08724	0.380736	37	GLI2	10.32721	0.688481	15
PCDHGA7	7.686214	0.207736	37	BAIAP2	6.495956	0.433064	15
PAX6	12.7288	0.36368	35	SLX1B-			
RBFOX3	10.1735	0.290671	35	SULT1A4	5.023958	0.334931	15
PCDHGB4	7.686214	0.219606	35	SLX1A	5.023958	0.334931	15
PCDHGA8	7.686214	0.219606	35	LOC606724	5.023958	0.334931	15
DIP2C	12.73497	0.397968	32	COL23A1	4.715474	0.314365	15
PCDHGB5	7.053442	0.22042	32	LRMDA	4.577949	0.305197	15
PCDHGA9	7.053442	0.22753	31	C7orf50	5.186346	0.370453	14
SOX2-OT	11.2276	0.387159	29	RPS6KA2	5.142733	0.367338	14
PCDHGB6	6.465793	0.222958	29	MSI2	6.845577	0.526583	13
PCDHGA10	6.149407	0.219622	28	MYT1L	5.449512	0.419193	13
SHANK2	5.314729	0.204413	26	SPTBN4	5.417407	0.416724	13
CAMTA1	9.327048	0.373082	25	RFX4	5.175823	0.39814	13
AGAP1	8.252622	0.330105	25	MIR9-3HG	4.57855	0.352196	13
PDGFRA	5.639808	0.225592	25	ZC3H3	7.215793	0.601316	12
SATB2	7.592696	0.316362	24	CMIP	5.485913	0.457159	12
MEIS1	7.443434	0.310143	24	MIRLET7BHG	4.868696	0.405725	12
PCDHGB7	5.833021	0.243043	24	ADGRD1	4.826819	0.402235	12
RPTOR	9.629501	0.418674	23	VGLL4	5.635849	0.51235	11
NCOR2	7.868925	0.342127	23	FGFR2	5.206888	0.473353	11
INPP5A	6.119086	0.266047	23	RAD51B	5.131747	0.466522	11
NXN	5.884705	0.255857	23	LBX1-AS1	6.227283	0.622728	10
RIMBP2	5.5258	0.240252	23	AKAP13	4.714159	0.471416	10
PCDHGA11	5.385766	0.234164	23	CHST11	4.491095	0.449109	10
PRKCZ	6.311547	0.286888	22	OTX1	4.46974	0.446974	10
SKI	10.8685	0.517548	21	ADGRB1	5.954707	0.661634	9
SIM2	7.261332	0.345778	21	ATP11A	5.724009	0.636001	9
HOXA-AS3	4.630083	0.22048	21	TSPAN9	5.3629	0.595878	9
FRMD4A	5.211017	0.260551	20	ASAP1	4.940787	0.548976	9
ABR	4.617089	0.230854	20	NEAT1	4.925836	0.547315	9
MAD1L1	12.86645	0.677181	19	ADAMTS2	4.535995	0.503999	9
ZNF423	9.219133	0.485218	19	KCNH2	4.42098	0.49122	9
SMG1P2	7.153844	0.376518	19	LINC00311	4.67027	0.583784	8
BOLA2	7.153844	0.376518	19	ASPSCR1	4.437863	0.554733	8
LOC613038	7.153844	0.376518	19	DUSP6	6.379713	0.911388	7
KCNQ1	6.379811	0.33578	19	LINC00461	5.629928	0.804275	7
SEPTIN9	5.374577	0.298588	18	NAV1	5.075466	0.725067	7
FOKK1	5.363211	0.297956	18	FAM181A	4.627874	0.771312	6
MCF2L	5.30329	0.294627	18	RUNDC3A	4.993431	0.998686	5
ANKRD11	4.888001	0.271556	18	TSNAX-DISC1	4.881004	0.976201	5
OPCML	7.865005	0.462647	17	STAP2	4.615269	1.153817	4

TABLE 85: Cancer Type HGNET_BCOR_Fus				Gene site	imp_sum	imp_mean	n				
				PTPRN2	8.695059	0.106037	82	PPP2R2A	2.952354	0.210882	14
				PRDM16	9.086343	0.127977	71	RPS6KA2	2.287237	0.163374	14
				HDAC4	6.063527	0.163879	37	MYT1L	2.76295	0.212535	13
				RBFOX3	9.137664	0.261076	35	GSE1	2.657642	0.204434	13
				PAX6	7.319629	0.209132	35	MSI2	2.521813	0.193986	13
				DIP2C	3.760208	0.117507	32	CMIP	3.396818	0.283068	12
				SOX2-OT	4.818061	0.16614	29	MIRLET7BHG	2.83575	0.236313	12
				GALNT9	2.927062	0.10841	27	TNS3	2.352031	0.196003	12
				ADARB2	2.991152	0.115044	26	RAD51B	2.971816	0.270165	11
				SHANK2	2.288362	0.088014	26	SLC9A3	2.200231	0.200021	11
				CAMTA1	5.018457	0.200738	25	ACOT7	3.51291	0.351291	10
				AGAP1	4.193611	0.167744	25	GRID1	2.803667	0.280367	10
				PDGFRA	3.368038	0.134722	25	FMN1	2.770846	0.277085	10
				SATB2	4.754808	0.198117	24	LBX1-AS1	2.677234	0.267723	10
				RPTOR	5.570949	0.242215	23	NR2F1-AS1	2.490698	0.24907	10
				NCOR2	4.164385	0.18106	23	NR5A2	2.331394	0.233139	10
				NXN	3.100555	0.134807	23	ATP11A	4.224137	0.469349	9
				RIMBP2	2.694694	0.117161	23	SND1	3.840995	0.426777	9
				PRKCZ	3.816924	0.173497	22	AXIN2	2.695001	0.299445	9
				SKI	7.813392	0.372066	21	ASAP1	2.500677	0.277853	9
				ZIC4	2.983964	0.142094	21	RUNX1	2.490049	0.276672	9
				SIM2	2.501738	0.11913	21	TSPAN9	2.272582	0.252509	9
				FRMD4A	3.927263	0.196363	20	LHX4	10.54497	1.318122	8
				SDK1	3.048273	0.152414	20	DLEU1	3.431598	0.42895	8
				MAD1L1	7.395283	0.389225	19	ESRRG	2.898586	0.362323	8
				ZNF423	5.272324	0.277491	19	NR2E1	2.736802	0.3421	8
				SMG1P2	2.630407	0.138442	19	LINC00311	2.598862	0.324858	8
				BOLA2	2.630407	0.138442	19	MSRA	2.415583	0.301948	8
				LOC613038	2.630407	0.138442	19	AFF3	2.262456	0.282807	8
				CASZ1	2.241851	0.117992	19	MCC	2.244619	0.280577	8
				FO XK1	5.409171	0.30051	18	LHX2	3.357274	0.479611	7
				ANKRD11	3.080524	0.17114	18	CDYL	3.302677	0.471811	7
				SEPTIN9	2.188115	0.121562	18	DUSP6	3.1137	0.444814	7
				OPCML	4.080539	0.240032	17	EBF2	2.757276	0.393897	7
				FOXP1	2.904035	0.181502	16	TACC2	2.218472	0.316925	7
				SORBS2	2.43297	0.152061	16	WNT6	3.408692	0.568115	6
				EBF3	2.260408	0.141276	16	SATB2-AS1	3.133854	0.522309	6
				GLI2	7.058917	0.470594	15	PAX1	3.129753	0.521625	6
				BAIAP2	3.808955	0.25393	15	FAM181A	2.728883	0.454814	6
				EMX2OS	3.695112	0.246341	15	ROR1	2.626658	0.437776	6
				ZBTB20	2.56894	0.171263	15	CALD1	2.603399	0.4339	6
				COL23A1	2.468116	0.164541	15	FBXL18	2.481157	0.413526	6
				CUX1	3.79665	0.271189	14	VAX2	2.406599	0.4011	6
				PRKAG2	3.465237	0.247517	14	AGAP2	3.285679	0.657136	5
								RUNDC3A	3.030862	0.606172	5
								ARHGEF7	2.881976	0.576395	5
								MNX1	2.619473	0.523895	5
								CCR6	2.475371	0.495074	5

TSNAX-DISC1	2.4505	0.4901	5	RCN1	4.633497	0.272559	17
VAV2	2.274903	0.454981	5	EBF3	6.410784	0.400674	16
DTNA	2.296774	0.574194	4	NAV2	5.476947	0.342309	16
RBMS3	2.192891	0.548223	4	FOXP1	5.298004	0.331125	16
LHX5	2.424746	0.808249	3	GLI2	9.711034	0.647402	15
GRIN2B	2.213335	0.737778	3	ZBTB20	5.106156	0.34041	15
ICAM5	3.406453	1.703226	2	NFIX	4.639626	0.309308	15
SOX10	2.655583	1.327791	2	RPS6KA2	6.94009	0.495721	14
TABLE 86:	Cancer Type	HGNET_BCOR_ITD	n	CUX1	5.863901	0.41885	14
				PRKAG2	5.374298	0.383878	14
Gene site	imp_sum	imp_mean		MOB2	4.099752	0.292839	14
PTPRN2	19.0009	0.231718	82	C7orf50	4.038509	0.288465	14
PRDM16	12.49491	0.175985	71	ARHGEF10	3.669185	0.262085	14
HDAC4	9.725468	0.26285	37	MSI2	5.523823	0.424909	13
RBFOX3	9.104029	0.260115	35	KIF26B	4.504027	0.346464	13
PAX6	5.207629	0.148789	35	MYT1L	3.890961	0.299305	13
DIP2C	11.88098	0.371281	32	GSE1	3.703098	0.284854	13
SOX2-OT	5.587138	0.19266	29	CMIP	5.333268	0.444439	12
GALNT9	5.693217	0.21086	27	MIRLET7BHG	5.215694	0.434641	12
SHANK2	6.847045	0.263348	26	ZC3H3	4.979102	0.414925	12
ADARB2	6.108296	0.234934	26	MEGF6	4.063235	0.338603	12
AGAP1	7.80205	0.312082	25	RASA3	3.849104	0.320759	12
CAMTA1	6.115775	0.244631	25	FBRSL1	3.633048	0.302754	12
PDGFRA	4.349081	0.173963	25	WNT5A	5.464912	0.49681	11
SATB2	8.841752	0.368406	24	VGLL4	4.877535	0.443412	11
RPTOR	12.31693	0.535519	23	GLUD1P2	4.790063	0.43546	11
NCOR2	6.809669	0.296073	23	ZC3H12D	4.175176	0.379561	11
RIMBP2	6.235802	0.271122	23	RAD51B	4.078728	0.370793	11
NXN	6.083741	0.26451	23	CTBP2	3.650224	0.331839	11
PRKCZ	6.466025	0.29391	22	ACOT7	4.879087	0.487909	10
SKI	10.71215	0.510102	21	TSPAN4	4.690828	0.469083	10
SIM2	4.336066	0.206479	21	NR2F1-AS1	4.247365	0.424737	10
FRMD4A	6.19085	0.309543	20	SH3RF3	4.173414	0.417341	10
ABR	4.797977	0.239899	20	ATP11A	7.025335	0.780593	9
SDK1	3.99684	0.199842	20	SND1	6.735886	0.748432	9
MAD1L1	12.21106	0.642687	19	ADAMTS2	6.151802	0.683534	9
ZNF423	7.681063	0.404266	19	AXIN2	5.23349	0.581499	9
CASZ1	6.387941	0.336207	19	TSPAN9	5.193186	0.577021	9
SMG1P2	5.249663	0.276298	19	KAZN	4.72919	0.525466	9
BOLA2	5.249663	0.276298	19	RUNX1	4.116735	0.457415	9
LOC613038	5.249663	0.276298	19	NOTCH1	3.965165	0.440574	9
FOKK1	6.729168	0.373843	18	CACNA2D4	3.931642	0.436849	9
TBC1D16	4.621618	0.256757	18	ASAP1	3.624512	0.402724	9
SEPTIN9	4.199987	0.233333	18	LHX4	10.1066	1.263325	8
MCF2L	4.174511	0.231917	18	RGS20	4.895937	0.611992	8
OPCML	7.484302	0.440253	17	MSRA	4.804917	0.600615	8
PAX6-AS1	4.633497	0.272559	17	LINC00311	4.611899	0.576487	8
				DLEU1	4.342586	0.542823	8

PPP2R2B	3.963711	0.495464	8	MAD1L1	9.370734	0.493197	19
NAV1	4.892823	0.698975	7	ZNF423	6.724885	0.353941	19
DUSP6	4.672967	0.667567	7	KCNQ1	3.554033	0.187054	19
CPQ	3.824497	0.637416	6	CASZ1	3.474681	0.182878	19
CRADD	3.798747	0.633124	6	SMG1P2	3.135122	0.165006	19
MIR100HG	3.683164	0.613861	6	BOLA2	3.135122	0.165006	19
TSNAX-DISC1	5.490268	1.098054	5	LOC613038	3.135122	0.165006	19
ARHGEF7	4.757762	0.951552	5	SEPTIN9	5.11153	0.283974	18
RUNDC3A	3.670234	0.734047	5	FOXK1	3.764631	0.209146	18
RBMS3	3.732722	0.933181	4	RBFOX1	3.750624	0.208368	18
DTNA	3.700063	0.925016	4	TBC1D16	3.252347	0.180686	18
DAGLB	3.795143	1.265048	3	ANKRD11	2.628618	0.146034	18
GRIN2B	3.695401	1.2318	3	FOXP1	4.369803	0.273113	16
SOX10	4.134033	2.067016	2	ZBTB20	4.816536	0.321102	15
SLC25A10	4.098196	2.049098	2	BAIAP2	4.473171	0.298211	15
ANKLE2	3.947945	1.973972	2	GLI2	3.099998	0.206667	15
				CUX1	4.203818	0.300273	14
TABLE 87:	Cancer Type HGNET_BEND2			RPS6KA2	4.011043	0.286503	14
Gene site	imp_sum	imp_mean	n	PRKAG2	3.903697	0.278835	14
PTPRN2	11.65657	0.142153	82	IQSEC1	2.754749	0.196768	14
PRDM16	12.43657	0.175163	71	MSI2	5.503119	0.423317	13
PCDHGA1	4.072552	0.069026	59	RFX4	4.552872	0.350221	13
PCDHGA2	3.756166	0.065898	57	MYT1L	3.535586	0.271968	13
PCDHGA3	3.756166	0.069559	54	CLYBL	2.869046	0.220696	13
PCDHGB1	3.756166	0.070871	53	TNS3	6.128524	0.51071	12
PCDHGA4	3.756166	0.07365	51	CMIP	4.165661	0.347138	12
PCDHGB2	3.43978	0.0702	49	ADGRD1	3.521824	0.293485	12
PCDHGA5	3.43978	0.073187	47	MEGF6	3.426526	0.285544	12
PCDHGB3	3.123394	0.072637	43	GNA12	2.844038	0.237003	12
HDAC4	9.431211	0.254898	37	SPON2	4.630129	0.420921	11
PAX6	8.609217	0.245978	35	ZC3H12D	3.845786	0.349617	11
RBFOX3	5.355051	0.153001	35	TBCD	2.7058	0.245982	11
DIP2C	8.138146	0.254317	32	TSPAN4	3.978882	0.397888	10
SOX2-OT	4.38671	0.151266	29	CHST11	3.670097	0.36701	10
GALNT9	3.528299	0.130678	27	AUTS2	3.093549	0.309355	10
ADARB2	4.905996	0.188692	26	NR2F1-AS1	3.03703	0.303703	10
CAMTA1	5.38565	0.215426	25	ACOT7	3.002526	0.300253	10
AGAP1	5.293279	0.211731	25	LMF1	2.675611	0.267561	10
PDGFRA	5.028399	0.201136	25	ATP11A	5.470725	0.607858	9
SATB2	5.258892	0.219121	24	SND1	5.344849	0.593872	9
NXN	8.321484	0.361804	23	ADAMTS2	3.427103	0.380789	9
RPTOR	5.518358	0.239929	23	KAZN	3.061964	0.340218	9
RIMBP2	3.241004	0.140913	23	CACNA2D4	2.703012	0.300335	9
PRKCZ	6.480769	0.29458	22	AXIN2	2.666413	0.296268	9
SKI	4.733328	0.225397	21	TSPAN9	2.628527	0.292059	9
FRMD4A	5.660585	0.283029	20	DLEU1	4.043543	0.505443	8
ABR	5.165881	0.258294	20	LHX4	4.02215	0.502769	8
SDK1	2.552309	0.127615	20	DNMT3A	3.144953	0.393119	8

PPP2R2B	3.102758	0.387845	8	SKI	4.368183	0.208009	21
MACROD1	3.028968	0.378621	8	ABR	3.446806	0.17234	20
AFF3	2.958851	0.369856	8	SDK1	2.216034	0.110802	20
DLX5	2.698816	0.337352	8	MAD1L1	3.129601	0.164716	19
TRIM2	3.572583	0.510369	7	ZNF423	2.543212	0.133853	19
NAV1	3.009561	0.429937	7	KCNQ1	1.500359	0.078966	19
C19orf25	2.80825	0.401179	7	TBC1D16	2.402423	0.133468	18
LHX2	2.68695	0.38385	7	FOXK1	2.33257	0.129587	18
FAM181A	3.475105	0.579184	6	MCF2L	1.418762	0.07882	18
SATB2-AS1	3.344044	0.557341	6	SEPTIN9	1.396595	0.077589	18
CELSR1	3.153194	0.525532	6	OPCML	2.399511	0.141148	17
FMNL2	3.035279	0.50588	6	EBF3	2.809053	0.175566	16
DNAJC17	2.948643	0.491441	6	FOXP1	1.790086	0.11188	16
LRRFIP1	2.732459	0.45541	6	GLI2	2.267675	0.151178	15
TSNAX-DISC1	3.759786	0.751957	5	NFATC1	1.58193	0.105462	15
ARHGEF7	3.698422	0.739684	5	SLX1B-			
BCAR1	2.750124	0.550025	5	SULT1A4	1.518958	0.101264	15
NPHP4	2.647374	0.529475	5	SLX1A	1.518958	0.101264	15
VOPP1	2.754547	0.688637	4	LOC606724	1.518958	0.101264	15
EXT1	2.639232	0.659808	4	RPS6KA2	2.496148	0.178296	14
GRIN2B	3.046582	1.015527	3	CUX1	1.532479	0.109463	14
DAGLB	2.845096	0.948365	3	GSE1	2.132961	0.164074	13
SOX10	3.388138	1.694069	2	MSI2	2.033189	0.156399	13
				MYT1L	1.337815	0.102909	13
				CMIP	1.709623	0.142469	12
TABLE 88:	Cancer Type HGNET_CXXC5			MIRLET7BHG	1.69019	0.140849	12
Gene site	imp_sum	imp_mean	n	CSMD1	1.492681	0.12439	12
PTPRN2	2.49268	0.030399	82	FBRSL1	1.472528	0.122711	12
PRDM16	8.149901	0.114787	71	VGLL4	1.298956	0.118087	11
PCDHGA1	1.396595	0.023671	59	GRID1	1.743341	0.174334	10
PCDHGA2	1.396595	0.024502	57	GAS7	1.704292	0.170429	10
PCDHGA3	1.396595	0.025863	54	RGS12	1.392098	0.13921	10
PCDHGB1	1.396595	0.026351	53	ATP11A	1.748129	0.194237	9
PCDHGA4	1.396595	0.027384	51	ADAMTS2	1.58545	0.176161	9
PCDHGB2	1.396595	0.028502	49	ASAP1	1.516276	0.168475	9
PCDHGA5	1.396595	0.029715	47	TSPAN9	1.397071	0.15523	9
PCDHGB3	1.396595	0.032479	43	SND1	1.289476	0.143275	9
PCDHGA6	1.396595	0.034915	40	TRAPPC12	1.279397	0.142155	9
HDAC4	6.832493	0.184662	37	AFF3	1.779233	0.222404	8
PCDHGA7	1.396595	0.037746	37	SMAD3	1.598138	0.199767	8
PAX6	2.536371	0.072468	35	LINC00311	1.476182	0.184523	8
DIP2C	2.990636	0.093457	32	DLEU1	1.384494	0.173062	8
SOX2-OT	1.396595	0.048158	29	GAK	1.678084	0.239726	7
ADARB2	1.396595	0.053715	26	C19orf25	1.61115	0.230164	7
CAMTA1	3.160176	0.126407	25	CDYL	1.563736	0.223391	7
AGAP1	2.907156	0.116286	25	TBR1	1.392098	0.198871	7
NXN	2.882371	0.12532	23	KDM4B	2.065877	0.344313	6
INPP5A	2.303654	0.100159	23	PSD3	1.622697	0.270449	6
NCOR2	1.836913	0.079866	23				

MIR100HG	1.529752	0.254959	6	PCDHGB5	2.223121	0.069473	32	
SLC22A18AS	1.517593	0.252932	6	PCDHGA9	2.223121	0.071714	31	
GPR39	1.482671	0.247112	6	SOX2-OT	4.323853	0.149098	29	
LRRFIP1	1.396987	0.232831	6	SHANK2	2.334295	0.089781	26	
CCDC177	1.387906	0.231318	6	AGAP1	4.297918	0.171917	25	
MYO16	1.381014	0.230169	6	PDGFRA	3.281884	0.131275	25	
EPHB1	1.286386	0.214398	6	CAMTA1	3.235869	0.129435	25	
TSNAX-DISC1	1.85738	0.371476	5	MEIS1	6.112786	0.254699	24	
ARHGEF7	1.687341	0.337468	5	SATB2	3.003986	0.125166	24	
CABLES1	1.527647	0.305529	5	RPTOR	4.919096	0.213874	23	
TK1	1.518958	0.303792	5	INPP5A	2.831969	0.123129	23	
THRB	1.497338	0.299468	5	PRKCZ	3.058304	0.139014	22	
RNLS	1.387906	0.277581	5	SKI	5.751564	0.273884	21	
CASP8	1.387906	0.277581	5	FRMD4A	3.997671	0.199884	20	
TEAD1	1.307323	0.261465	5	SDK1	2.415599	0.12078	20	
MAPK8IP3	2.130606	0.532651	4	MAD1L1	5.24362	0.27598	19	
EDNRB	1.881066	0.470266	4	ZNF423	4.461305	0.234806	19	
FOXO1	1.546283	0.386571	4	SMG1P2	3.210425	0.16897	19	
STOX2	1.40626	0.351565	4	BOLA2	3.210425	0.16897	19	
LINC00856	1.396128	0.349032	4	LOC613038	3.210425	0.16897	19	
VOPPI	1.383603	0.345901	4	CASZ1	2.630815	0.138464	19	
NDST1	1.316257	0.329064	4	FOXK1	4.570601	0.253922	18	
MYT1	1.303009	0.325752	4	MCF2L	3.630234	0.20168	18	
EPAS1	1.841716	0.613905	3	SEPTIN9	3.195472	0.177526	18	
DICER1	1.56627	0.52209	3	OPCML	6.284087	0.369652	17	
SLC6A9	1.450121	0.483374	3	TBX15	4.028118	0.236948	17	
DAGLB	1.305795	0.435265	3	NAV2	2.630111	0.164382	16	
SLC25A10	1.882719	0.94136	2	FOXP1	2.224576	0.139036	16	
SOX10	1.72484	0.86242	2	GLI2	5.770352	0.38469	15	
UFSP2	1.653183	0.826591	2	BAIAP2	4.016603	0.267774	15	
DISC1	1.330762	0.665381	2	ZBTB20	2.599909	0.173327	15	
TABLE 89:	Cancer Type HGNET_ND_B			MIR548F5	3.480232	0.248588	14	
				RPS6KA2	2.764372	0.197455	14	
				CUX1	2.612496	0.186607	14	
				PRKAG2	2.487324	0.177666	14	
				MSI2	3.219484	0.247653	13	
				MYT1L	2.901918	0.223224	13	
				SPTBN4	2.502449	0.192496	13	
				CMIP	4.42819	0.369016	12	
				MIRLET7BHG	2.426833	0.202236	12	
				VGLL4	5.39493	0.490448	11	
Gene site	imp_sum	imp_mean	n		GLUD1P2	2.888543	0.262595	11
PTPRN2	11.57447	0.141152	82		CACNA1C	2.659495	0.241772	11
PRDM16	4.038915	0.056886	71		ATP11A	3.97013	0.441126	9
PCDHGA1	3.488665	0.05913	59		ADAMTS2	3.669879	0.407764	9
PCDHGA2	3.488665	0.061205	57		AXIN2	3.418227	0.379803	9
PCDHGA3	3.172279	0.058746	54		RUNX1	3.347958	0.371995	9
PCDHGB1	3.172279	0.059854	53		SND1	3.134135	0.348237	9
PCDHGA4	2.855893	0.055998	51					
PCDHGB2	2.855893	0.058284	49					
PCDHGA5	2.223121	0.0473	47					
HDAC4	6.376827	0.172347	37					
PAX6	5.147216	0.147063	35					
RBFOX3	4.611426	0.131755	35					
DIP2C	6.615504	0.206735	32					

NOTCH1	2.670621	0.296736	9	DIP2C	4.067567	0.127111	32
ASAP1	2.47974	0.275527	9	SOX2-OT	5.505808	0.189855	29
CACNB2	2.449655	0.272184	9	ADARB2	4.089054	0.157271	26
TRAPPC12	2.194112	0.24379	9	SHANK2	3.054717	0.117489	26
GRIK2	6.924673	0.865584	8	AGAP1	6.291578	0.251663	25
LINC00311	2.704552	0.338069	8	CAMTA1	2.683617	0.107345	25
ASPSCR1	2.620689	0.327586	8	PDGFRA	2.01336	0.080534	25
MBP	2.552522	0.319065	8	SATB2	4.086095	0.170254	24
ESRRG	2.400991	0.300124	8	RPTOR	4.202601	0.182722	23
NR2E1	2.262175	0.282772	8	INPP5A	2.531088	0.110047	23
NAV1	3.393725	0.484818	7	NCOR2	2.446499	0.10637	23
DUSP6	2.942372	0.420339	7	PRKCZ	3.53049	0.160477	22
ADAMTS17	2.832985	0.404712	7	SKI	4.931482	0.234832	21
TBR1	2.483161	0.354737	7	FRMD4A	3.027059	0.151353	20
LINC00461	2.476002	0.353715	7	MAD1L1	5.636523	0.296659	19
VPS13D	2.406937	0.343848	7	KCNQ1	2.847474	0.149867	19
SOX6	2.305773	0.329396	7	ZNF423	2.584632	0.136033	19
ITPKB	2.303968	0.329138	7	SEPTIN9	6.304789	0.350266	18
SLC22A18AS	2.76306	0.46051	6	FOXK1	2.265772	0.125876	18
FBXL18	2.717941	0.45299	6	RBFOX1	1.710245	0.095014	18
COQ8A	2.380451	0.396742	6	FOXP1	3.143963	0.196498	16
LIMCH1	2.275298	0.379216	6	SORBS2	2.899457	0.181216	16
FMNL2	2.225253	0.370876	6	EBF3	2.255027	0.140939	16
RUNDC3A	3.568779	0.713756	5	GLI2	3.951824	0.263455	15
GAREM2	2.432091	0.486418	5	ZBTB20	2.759924	0.183995	15
TK1	2.28875	0.45775	5	NFATC1	2.025083	0.135006	15
TSNAX-DISC1	2.244638	0.448928	5	CUX1	2.824382	0.201742	14
ARHGEF7	2.206025	0.441205	5	IQSEC1	2.472231	0.176588	14
NFIB	4.010649	1.002662	4	ARHGEF10	2.345753	0.167554	14
DTNA	3.340887	0.835222	4	RPS6KA2	2.249066	0.160648	14
ONECUT2	3.070253	0.767563	4	PRKAG2	2.103343	0.150239	14
STAP2	2.550313	0.637578	4	C7orf50	1.875874	0.133991	14
RBMS3	2.471495	0.617874	4	MYT1L	2.655877	0.204298	13
SASH1	2.315015	0.578754	4	MIR9-3HG	2.582158	0.198628	13
GRIN2B	3.638806	1.212935	3	KIF26B	1.803358	0.13872	13
DAGLB	2.323308	0.774436	3	MSI2	1.769056	0.136081	13
LOXL3	2.31565	0.771883	3	ZC3H3	3.083274	0.256939	12
TTC12	2.28273	0.76091	3	CMIP	3.058493	0.254874	12
MAP2K3	2.157708	1.078854	2	RASA3	2.896784	0.241399	12
TABLE 90:	Cancer Type			TBX4	2.123167	0.176931	12
	HGNET_ND_C			TNS3	1.935834	0.161319	12
	Gene site			CTNNA2	1.926265	0.160522	12
	imp_sum	imp_mean	n	TBCD	2.487809	0.226164	11
	PTPRN2	9.737831	82	RAD51B	1.82219	0.165654	11
	PRDM16	5.153874	71	AKAP13	2.800951	0.280095	10
	HDAC4	4.968572	37	CHST11	2.72077	0.272077	10
	RBFOX3	5.080853	35	BCL11B	2.6064	0.26064	10
	PAX6	4.020079	35	ACOT7	2.500636	0.250064	10

LBX1-AS1	2.461608	0.246161	10	TABLE 91:	Cancer Type HGNET_ND_D		
KLHL29	2.348852	0.234885	10		Gene site	imp_sum	imp_mean
ETS1	1.756824	0.175682	10	PTPRN2	9.864449	0.120298	82
ATP11A	3.391144	0.376794	9	PRDM16	9.259115	0.13041	71
RUNX1	3.20046	0.355607	9	PCDHGA1	3.439024	0.058289	59
ASAP1	2.892005	0.321334	9	PCDHGA2	3.439024	0.060334	57
NOTCH1	2.535825	0.281758	9	PCDHGA3	3.014547	0.055825	54
APBA2	1.926545	0.214061	9	PCDHGB1	3.014547	0.056878	53
PAX3	1.841296	0.204588	9	PCDHGA4	3.014547	0.059109	51
SND1	1.791119	0.199013	9	PCDHGB2	3.014547	0.061521	49
KCNMA1	1.738471	0.193163	9	PCDHGA5	3.014547	0.064139	47
SSBP3	1.731396	0.192377	9	PCDHGB3	3.014547	0.070106	43
AXIN2	1.717771	0.190863	9	PCDHGA6	3.014547	0.075364	40
MACROD1	3.289917	0.41124	8	HDAC4	6.917241	0.186952	37
MSRA	2.995025	0.374378	8	PCDHGA7	2.698161	0.072923	37
BAHCC1	2.627357	0.32842	8	PAX6	6.524986	0.186428	35
LINC00311	2.386556	0.29832	8	RBFOX3	3.342572	0.095502	35
VRK2	1.942024	0.242753	8	PCDHGB4	2.381775	0.068051	35
AFF3	1.797905	0.224738	8	PCDHGA8	2.381775	0.068051	35
TRAPPC9	1.776346	0.222043	8	DIP2C	7.027478	0.219609	32
SYNJ2	1.77498	0.221872	8	PCDHGB5	2.357303	0.073666	32
DUSP6	3.619583	0.517083	7	SOX2-OT	4.8712	0.167972	29
RBMS1	1.893431	0.27049	7	GALNT9	2.278284	0.084381	27
PRKCA	1.810447	0.258635	7	SHANK2	2.623623	0.100909	26
TRIM2	1.810327	0.258618	7	AGAP1	5.019296	0.200772	25
ZNF664-RFLNA	1.796796	0.256685	7	PDGFRA	4.475775	0.179031	25
CXXC5	1.764596	0.252085	7	CAMTA1	3.807931	0.152317	25
FBXL18	2.644251	0.440709	6	MEIS1	2.889276	0.120387	24
SLC22A18AS	2.461434	0.410239	6	SATB2	2.52298	0.105124	24
TG	2.157854	0.359642	6	RPTOR	5.902472	0.256629	23
SATB2-AS1	2.04251	0.340418	6	NCOR2	2.516777	0.109425	23
HOXD4	1.836799	0.306133	6	PRKCZ	3.91809	0.178095	22
SRGAP3	1.739316	0.289886	6	SKI	5.236337	0.249349	21
ARHGEF7	2.395104	0.479021	5	FRMD4A	4.373247	0.218662	20
BCAR1	1.866178	0.373236	5	MAD1L1	6.162868	0.324361	19
PRR5L	1.74963	0.349926	5	SMG1P2	3.647932	0.191996	19
SASH1	2.149578	0.537394	4	BOLA2	3.647932	0.191996	19
VOPPI	1.976727	0.494182	4	LOC613038	3.647932	0.191996	19
RBMS3	1.940124	0.485031	4	ZNF423	3.494232	0.183907	19
ACOX3	1.719939	0.429985	4	CASZ1	2.658986	0.139947	19
GRIN2B	3.178745	1.059582	3	SEPTIN9	3.617041	0.200947	18
DICER1	2.067448	0.689149	3	MCF2L	3.531901	0.196217	18
SLC6A9	1.970891	0.656964	3	FOXK1	3.184272	0.176904	18
IFFO1	1.811975	0.603992	3	ANKRD11	2.73067	0.151704	18
EPAS1	1.765209	0.588403	3	FOXP1	4.188119	0.261757	16
SOX10	3.343898	1.671949	2	ZBTB20	2.583813	0.172254	15
KIF21B	1.814686	0.907343	2	GLI2	2.570217	0.171348	15

RPS6KA2	4.104399	0.293171	14	THRA	3.34908	1.11636	3
CUX1	3.949712	0.282122	14	GRIN2B	2.508702	0.836234	3
C7orf50	3.928659	0.280619	14	DAGLB	2.390514	0.796838	3
IQSEC1	3.089471	0.220677	14	CNP	2.335046	0.778349	3
TBX5	2.692247	0.192303	14	SOX10	3.171381	1.585691	2
GNG7	2.415288	0.172521	14	DENND11	2.860855	1.430428	2
MSI2	3.746287	0.288176	13	NR1D1	2.395607	1.197804	2
MYT1L	3.666093	0.282007	13				
SPTBN4	2.632143	0.202473	13	TABLE 92:	Cancer Type		
CMIP	3.366597	0.28055	12		HGNET_PATZ		
FBRSL1	2.872354	0.239363	12	Gene site	imp_sum	imp_mean	n
CTBP2	3.574491	0.324954	11	PTPRN2	17.14336	0.209065	82
VGLL4	3.287994	0.298909	11	PRDM16	12.51692	0.176295	71
SPON2	2.968323	0.269848	11	PCDHGA1	3.803542	0.064467	59
GLUD1P2	2.744848	0.249532	11	PCDHGB2	3.487156	0.071166	49
ZC3H12D	2.33304	0.212095	11	PCDHGA5	3.933456	0.083691	47
RAD51B	2.318825	0.210802	11	PCDHGA6	3.648056	0.091201	40
CHST11	3.437065	0.343707	10	HDAC4	13.10879	0.354292	37
ACOT7	3.064985	0.306499	10	RBFOX3	9.455681	0.270162	35
NTM	2.596398	0.25964	10	PAX6	6.343311	0.181237	35
ATP11A	3.703061	0.411451	9	DIP2C	11.99765	0.374927	32
SND1	2.984411	0.331601	9	SOX2-OT	6.001773	0.206958	29
PACS2	2.978543	0.330949	9	GALNT9	5.841	0.216333	27
ADAMTS2	2.841953	0.315773	9	SHANK2	6.679166	0.256891	26
RUNX1	2.765462	0.307274	9	ADARB2	5.552845	0.213571	26
SSBP3	2.762278	0.30692	9	AGAP1	6.78803	0.271521	25
TRAPPC12	2.469924	0.274436	9	CAMTA1	5.56868	0.222747	25
CACNA2D4	2.321527	0.257947	9	SATB2	4.700124	0.195839	24
TSPAN9	2.300269	0.255585	9	RPTOR	10.83693	0.471171	23
NR2E1	2.795337	0.349417	8	NCOR2	7.807486	0.339456	23
DLEU1	2.774543	0.346818	8	RIMBP2	6.394636	0.278028	23
MSRA	2.533345	0.316668	8	HOXB3	4.338576	0.188634	23
ESRRG	2.476585	0.309573	8	NXN	3.893343	0.169276	23
SYNJ2	2.466121	0.308265	8	PRKCZ	5.89598	0.267999	22
LINC00461	3.138709	0.448387	7	SKI	10.8308	0.515752	21
FBXL18	3.766261	0.62771	6	SIM2	4.655035	0.221668	21
PVT1	2.654909	0.442485	6	ZIC4	4.491162	0.213865	21
COQ8A	2.392082	0.39868	6	HOXA-AS3	3.87165	0.184364	21
FMNL2	2.28478	0.380797	6	FRMD4A	6.736049	0.336802	20
RUNDC3A	3.898227	0.779645	5	ABR	6.342327	0.317116	20
ARHGEF7	3.104328	0.620866	5	SDK1	4.559424	0.227971	20
PRR5L	2.514518	0.502904	5	ZNF423	10.68511	0.562374	19
TGFB3	2.282278	0.456456	5	MAD1L1	7.895225	0.415538	19
STOX2	2.85666	0.714165	4	CASZ1	6.119203	0.322063	19
RBMS3	2.687846	0.671961	4	SMG1P2	3.883388	0.204389	19
VOPPI	2.621298	0.655325	4	BOLA2	3.883388	0.204389	19
SASH1	2.344511	0.586128	4	LOC613038	3.883388	0.204389	19
PRDM2	3.809634	1.269878	3	CFAP46	3.554014	0.187053	19

FO XK1	7.423561	0.41242	18	AXIN2	4.011781	0.445753	9
TBC1D16	5.663698	0.31465	18	CACNA2D4	3.763396	0.418155	9
ANKRD11	4.637601	0.257644	18	ASAP1	3.633912	0.403768	9
SEPTIN9	4.478314	0.248795	18	DLEU1	4.647124	0.58089	8
HOXA3	3.635087	0.201949	18	MSRA	4.295307	0.536913	8
OPCML	6.252435	0.36779	17	LHX4	4.246082	0.53076	8
PAX6-AS1	3.625755	0.21328	17	LINC00311	4.23156	0.528945	8
RCN1	3.625755	0.21328	17	SMAD3	4.093521	0.51169	8
FOXP1	5.479421	0.342464	16	RORA	3.917132	0.489642	8
NAV2	4.769675	0.298105	16	SHROOM3	3.593844	0.449231	8
EBF3	4.245607	0.26535	16	RGS20	3.52543	0.440679	8
GLI2	7.741287	0.516086	15	DUSP6	4.110106	0.587158	7
NFIX	6.705372	0.447025	15	RXRA	3.917573	0.559653	7
ZBTB20	4.563247	0.304216	15	LINC00461	3.617164	0.516738	7
SLX1B-SULT1A4	4.240652	0.28271	15	TSNAX-DISC1	4.095521	0.819104	5
SLX1A	4.240652	0.28271	15	BOC	4.393729	1.098432	4
LOC606724	4.240652	0.28271	15	TABLE 93: Cancer Type HGNET_PLAG			
EMX2OS	4.236075	0.282405	15	Gene site	imp_sum	imp_mean	n
LRMDA	3.883948	0.25893	15	PTPRN2	4.705472	0.057384	82
KIRREL3	3.505505	0.2337	15	PRDM16	4.475435	0.063034	71
RPS6KA2	5.780924	0.412923	14	PCDHGB1	1.291057	0.02436	53
ARHGEF10	4.310297	0.307878	14	PCDHGA4	1.291057	0.025315	51
MSI2	6.201837	0.477064	13	PCDHGB2	1.291057	0.026348	49
MYT1L	3.912213	0.300939	13	PCDHGA5	1.291057	0.027469	47
SPTBN4	3.634946	0.279611	13	HDAC4	3.756115	0.101517	37
CMIP	5.849535	0.487461	12	PAX6	3.421466	0.097756	35
ZC3H3	5.205313	0.433776	12	RBFOX3	1.806047	0.051601	35
MIRLET7BHG	5.070343	0.422529	12	DIP2C	2.46776	0.077117	32
TBX4	4.13671	0.344726	12	AGAP1	1.871741	0.07487	25
TNS3	4.118458	0.343205	12	RPTOR	2.933618	0.127549	23
RASA3	3.744375	0.312031	12	INPP5A	2.125246	0.092402	23
ADGRD1	3.661597	0.305133	12	NCOR2	1.764604	0.076722	23
ZC3H12D	5.857201	0.532473	11	SKI	6.178051	0.294193	21
FGFR2	4.244744	0.385886	11	SDK1	1.793089	0.089654	20
RAD51B	3.665567	0.333233	11	MAD1L1	5.540848	0.291624	19
SPON2	3.504301	0.318573	11	ZNF423	3.343331	0.175965	19
NR2F1-AS1	4.920196	0.49202	10	KCNQ1	1.373634	0.072297	19
TSPAN4	4.170382	0.417038	10	SEPTIN9	2.332394	0.129577	18
ACOT7	4.133986	0.413399	10	TBC1D16	1.768886	0.098271	18
AKAP13	4.130958	0.413096	10	PAX6-AS1	1.383236	0.081367	17
MAML2	3.920929	0.392093	10	RCN1	1.383236	0.081367	17
ANKS1B	3.577294	0.357729	10	EBF3	2.248947	0.140559	16
BCL11B	3.50077	0.350077	10	NFIX	2.486526	0.165768	15
ATP11A	5.634833	0.626093	9	KIRREL3	1.58193	0.105462	15
TRAPPC12	4.970254	0.55225	9	SLX1B-SULT1A4	1.49431	0.099621	15
SND1	4.610867	0.512319	9				
KCNH2	4.075902	0.452878	9				

SLX1A	1.49431	0.099621	15	BACH2	2.027731	0.405546	5
LOC606724	1.49431	0.099621	15	CADM1	1.951302	0.39026	5
KNDC1	1.392098	0.092807	15	CUEDC1	1.497338	0.299468	5
RPS6KA2	2.950333	0.210738	14	HHEX	1.373634	0.274727	5
C7orf50	2.75936	0.197097	14	VOPP1	2.346855	0.586714	4
ARHGEF10	1.396595	0.099757	14	SASH1	1.683054	0.420763	4
MSI2	2.710296	0.208484	13	CRB2	1.568691	0.392173	4
MYT1L	2.21453	0.170348	13	STAP2	1.464166	0.366042	4
RFX4	1.991563	0.153197	13	DSE	1.416996	0.354249	4
CLYBL	1.962564	0.150966	13	TET1	1.392098	0.348025	4
SPTBN4	1.393859	0.10722	13	CSRNP1	1.380255	0.345064	4
CMIP	1.761756	0.146813	12	PPM1H	1.346451	0.336613	4
MEIS2	1.58193	0.131827	12	GNAS	1.675009	0.558336	3
TBX4	1.477921	0.12316	12	SLC6A9	1.553944	0.517981	3
VGLL4	1.716353	0.156032	11	FAM83E	1.457047	0.485682	3
TSPAN4	2.233461	0.223346	10	FEZ1	1.428745	0.476248	3
AKAP13	1.799866	0.179987	10	HDAC7	2.043894	1.021947	2
KLHL29	1.653739	0.165374	10	SOX10	1.908056	0.954028	2
GAS7	1.456932	0.145693	10	CHTF18	1.6427	0.82135	2
AUTS2	1.444522	0.144452	10	EXT2	1.607093	0.803547	2
MAML2	1.387906	0.138791	10	ANKLE2	1.503659	0.75183	2
TSPAN9	3.080775	0.342308	9	TSC2	1.336326	0.668163	2
KCNH2	2.247511	0.249723	9	TTLL11	1.294769	0.647385	2
ATP11A	2.224048	0.247116	9	DDA1	1.729932	1.729932	1
EGFR	2.140931	0.237881	9	HMGCR	1.438004	1.438004	1
SND1	1.694061	0.188229	9				
TRAPPC12	1.641374	0.182375	9	TABLE 94:	Cancer Type HMB		
ADAMTS2	1.608443	0.178716	9	Gene site	imp_sum	imp_mean	n
KAZN	1.458536	0.16206	9	PTPRN2	26.46067	0.322691	82
ASAP1	1.416927	0.157436	9	PRDM16	24.26095	0.341704	71
CRISPLD2	2.200829	0.275104	8	PCDHGA1	14.03915	0.237952	59
DNMT3A	2.002498	0.250312	8	PCDHGA2	13.72276	0.24075	57
NR2E1	1.708484	0.213561	8	PCDHGA3	13.08999	0.242407	54
WWP2	1.690684	0.211335	8	PCDHGB1	12.7736	0.241011	53
GCSAML	1.58193	0.197741	8	PCDHGA4	12.7736	0.250463	51
DLEU1	1.363563	0.170445	8	PCDHGB2	12.45722	0.254229	49
C19orf25	1.875902	0.267986	7	PCDHGA5	11.75716	0.250152	47
RXRA	1.470451	0.210064	7	PCDHGB3	10.808	0.251349	43
SRGAP3	2.643332	0.440555	6	PCDHGA6	10.17523	0.254381	40
LYPD1	2.531618	0.421936	6	HDAC4	17.71129	0.478684	37
SLC22A18AS	2.126474	0.354412	6	PCDHGA7	9.858841	0.266455	37
NKD2	1.794592	0.299099	6	PAX6	9.923022	0.283515	35
LPIN1	1.712981	0.285497	6	PCDHGB4	9.106144	0.260176	35
CYBA	1.624883	0.270814	6	PCDHGA8	9.106144	0.260176	35
FBXL18	1.483841	0.247307	6	RBFOX3	6.361317	0.181752	35
CRACR2A	1.383259	0.230543	6	DIP2C	12.46961	0.389675	32
ROR1	1.368682	0.228114	6	PCDHGB5	8.473372	0.264793	32
RUNDC3A	2.833298	0.56666	5	PCDHGA9	8.026117	0.258907	31

SOX2-OT	9.70619	0.334696	29	IQSEC1	7.107435	0.507674	14
PCDHGB6	7.175401	0.247428	29	MIR548F5	6.86813	0.490581	14
PCDHGA10	6.859015	0.244965	28	CUX1	6.527938	0.466281	14
GALNT9	7.818675	0.289581	27	ARHGEF10	5.786339	0.41331	14
ADARB2	7.906132	0.304082	26	PRKAG2	5.056265	0.361162	14
SHANK2	7.070504	0.271942	26	PCDHGA12	5.014631	0.358188	14
AGAP1	11.75792	0.470317	25	MSI2	6.781856	0.521681	13
CAMTA1	9.840931	0.393637	25	MYT1L	5.974692	0.459592	13
PDGFRA	8.698086	0.347923	25	RFX4	5.591116	0.430086	13
MEIS1	7.999986	0.333333	24	ZC3H3	6.534405	0.544534	12
SATB2	7.40875	0.308698	24	CMIP	6.323173	0.526931	12
PCDHGB7	6.542629	0.27261	24	GNA12	6.002641	0.50022	12
RPTOR	13.45937	0.58519	23	TNS3	5.687364	0.473947	12
NCOR2	8.791106	0.382222	23	MAML3	5.634682	0.469557	12
INPP5A	7.765362	0.337624	23	RASA3	5.562932	0.463578	12
NXN	7.53317	0.327529	23	FBRSL1	5.349059	0.445755	12
RIMBP2	6.453255	0.280576	23	RAD51B	6.362292	0.57839	11
PCDHGA11	6.226243	0.270706	23	ANAPC16	5.819704	0.529064	11
PRKCZ	6.210195	0.282282	22	VGLL4	5.464586	0.496781	11
SKI	11.9245	0.567833	21	ACOT7	5.700837	0.570084	10
ZIC4	5.846935	0.278425	21	KLHL29	5.468208	0.546821	10
HOXA-AS3	5.081374	0.24197	21	SND1	6.468907	0.718767	9
FRMD4A	7.269919	0.363496	20	ATP11A	6.187374	0.687486	9
SDK1	7.083018	0.354151	20	ADAMTS2	5.936374	0.659597	9
MAD1L1	14.41389	0.758626	19	NOTCH1	5.540961	0.615662	9
ZNF423	10.48737	0.551967	19	ASAP1	5.087106	0.565234	9
CASZ1	9.066917	0.477206	19	LINC00311	5.411709	0.676464	8
SMG1P2	7.991465	0.420603	19	MCC	5.258706	0.657338	8
BOLA2	7.991465	0.420603	19	DLEU1	5.054179	0.631772	8
LOC613038	7.991465	0.420603	19	RXRA	5.195303	0.742186	7
KCNQ1	5.977189	0.314589	19	TSNAX-DISC1	5.815857	1.163171	5
FOKK1	8.730481	0.485027	18	ARHGEF7	5.557932	1.111586	5
TBC1D16	8.260186	0.458899	18				
ANKRD11	7.878235	0.43768	18	TABLE 95:	Cancer Type IDH_B		
SEPTIN9	7.040446	0.391136	18	Gene site	imp_sum	imp_mean	n
MCF2L	6.444229	0.358013	18	PTPRN2	17.16233	0.209297	82
OPCML	6.12059	0.360035	17	PRDM16	14.96187	0.210731	71
FOXP1	7.749369	0.484336	16	PCDHGA1	7.441341	0.126124	59
NAV2	7.034679	0.439667	16	PCDHGA2	6.8546	0.120256	57
SORBS2	6.588335	0.411771	16	PCDHGA3	6.407163	0.118651	54
GLI2	7.702327	0.513488	15	PCDHGB1	6.723549	0.126859	53
KIRREL3	7.493121	0.499541	15	PCDHGA4	6.723549	0.131834	51
ZBTB20	6.170748	0.411383	15	PCDHGB2	6.407163	0.130758	49
NFIX	6.062316	0.404154	15	PCDHGA5	6.661662	0.141737	47
NFATC1	5.634395	0.375626	15	PCDHGB3	6.249674	0.145341	43
BAIAP2	5.418057	0.361204	15	PCDHGA6	5.82758	0.14569	40
LRMDA	5.416243	0.361083	15	HDAC4	12.51746	0.33831	37
RPS6KA2	7.766361	0.55474	14	PCDHGA7	6.143966	0.166053	37

RBFOX3	10.87678	0.310765	35	LOC606724	5.138637	0.342576	15
PAX6	10.19727	0.291351	35	BAIAP2	4.870926	0.324728	15
PCDHGB4	6.326632	0.180761	35	RPS6KA2	5.921087	0.422935	14
PCDHGA8	6.326632	0.180761	35	IQSEC1	5.061376	0.361527	14
DIP2C	11.28103	0.352532	32	C7orf50	4.660564	0.332897	14
PCDHGB5	6.326632	0.197707	32	PRKAG2	4.396865	0.314062	14
PCDHGA9	6.326632	0.204085	31	MSI2	7.087188	0.545168	13
SOX2-OT	11.9739	0.412893	29	MYT1L	5.322932	0.409456	13
PCDHGB6	5.935454	0.204671	29	RFX4	4.816791	0.370522	13
PCDHGA10	5.619068	0.200681	28	KIF26B	4.55746	0.350574	13
SHANK2	4.728557	0.181868	26	SPTBN4	4.447745	0.342134	13
ADARB2	4.06952	0.15652	26	ZC3H3	5.713517	0.476126	12
AGAP1	8.657739	0.34631	25	CMIP	5.59996	0.466663	12
PDGFRA	6.586265	0.263451	25	MIRLET7BHG	4.177948	0.348162	12
CAMTA1	4.939632	0.197585	25	ADGRD1	4.159606	0.346634	12
MEIS1	9.504702	0.396029	24	FBRSL1	4.056428	0.338036	12
SATB2	7.120392	0.296683	24	VGLL4	4.973961	0.452178	11
PCDHGB7	5.944949	0.247706	24	FGFR2	4.888569	0.444415	11
RPTOR	10.58695	0.460302	23	RAD51B	4.783315	0.434847	11
NCOR2	6.324306	0.27497	23	ZC3H12D	4.146117	0.37692	11
PCDHGA11	5.280202	0.229574	23	NR2F1-AS1	4.866915	0.486691	10
HOXB3	5.139593	0.223461	23	TSPAN4	4.645856	0.464586	10
INPP5A	4.571725	0.198771	23	SH3RF3	4.417072	0.441707	10
RIMBP2	4.272317	0.185753	23	OTX1	4.083172	0.408317	10
PRKCZ	6.585171	0.299326	22	ATP11A	5.676572	0.63073	9
SKI	9.910396	0.471924	21	SND1	5.130784	0.570087	9
ZIC4	4.254706	0.202605	21	ADGRB1	5.066377	0.562931	9
FRMD4A	7.877648	0.393882	20	TSPAN9	5.020702	0.557856	9
ABR	6.512398	0.32562	20	TRAPPC12	4.9894	0.554378	9
MAD1L1	12.08799	0.63621	19	ASAP1	4.983764	0.553752	9
ZNF423	6.7748	0.356568	19	AXIN2	4.974147	0.552683	9
SMG1P2	5.607138	0.295113	19	RUNX1	4.191813	0.465757	9
BOLA2	5.607138	0.295113	19	ADAMTS2	4.02287	0.446986	9
LOC613038	5.607138	0.295113	19	LINC00311	4.643322	0.580415	8
CASZ1	4.524491	0.238131	19	NR2E1	4.551273	0.568909	8
FO XK1	6.358935	0.353274	18	DLEU1	4.506299	0.563287	8
ANKRD11	5.770334	0.320574	18	LINC00461	4.90227	0.700324	7
TBC1D16	4.557065	0.25317	18	FBXL18	4.159063	0.693177	6
OPCML	8.756938	0.515114	17	RUND C3A	5.22174	1.044348	5
PAX6-AS1	4.758871	0.279934	17	TSNAX-DISC1	4.071943	0.814389	5
RCN1	4.758871	0.279934	17				
FOXP1	5.7259	0.357869	16	TABLE 96: Cancer Type IHG			
NAV2	5.209677	0.325605	16	Gene site	imp_sum	imp_mean	n
GLI2	9.20778	0.613852	15	PTPRN2	21.98894	0.268158	82
ZBTB20	6.166419	0.411095	15	PRDM16	16.68139	0.234949	71
SLX1B-				PCDHGA1	6.820854	0.115608	59
SULT1A4	5.138637	0.342576	15	PCDHGA2	6.820854	0.119664	57
SLX1A	5.138637	0.342576	15	PCDHGA3	6.188082	0.114594	54

PCDHGB1	6.188082	0.116756	53	ZBTB20	6.714497	0.447633	15
PCDHGA4	5.871696	0.115131	51	BAIAP2	5.486625	0.365775	15
PCDHGB2	5.871696	0.119831	49	KIRREL3	5.185464	0.345698	15
PCDHGA5	6.318987	0.134447	47	SLX1B-			
PCDHGB3	5.369829	0.12488	43	SULT1A4	5.143539	0.342903	15
PCDHGA6	5.8623	0.146558	40	SLX1A	5.143539	0.342903	15
HDAC4	13.86379	0.374697	37	LOC606724	5.143539	0.342903	15
PCDHGA7	5.229528	0.141339	37	NFIX	4.968449	0.33123	15
PAX6	10.71551	0.306157	35	TBX5	6.484428	0.463173	14
RBFOX3	10.31778	0.294794	35	RPS6KA2	6.099945	0.43571	14
PCDHGB4	5.229528	0.149415	35	CUX1	5.931251	0.423661	14
PCDHGA8	5.229528	0.149415	35	IQSEC1	5.523478	0.394534	14
DIP2C	10.44121	0.326288	32	MIR548F5	5.231893	0.373707	14
PCDHGB5	4.596756	0.143649	32	ARHGEF10	4.882863	0.348776	14
PCDHGA9	4.913142	0.158488	31	PRKAG2	4.696947	0.335496	14
SOX2-OT	9.404015	0.324276	29	SPTBN4	9.679117	0.744547	13
SHANK2	5.97329	0.229742	26	MSI2	7.306432	0.562033	13
ADARB2	5.645742	0.217144	26	MYT1L	5.174987	0.398076	13
CAMTA1	8.361545	0.334462	25	KIF26B	5.16254	0.397118	13
AGAP1	8.047109	0.321884	25	RFX4	4.804251	0.369558	13
PDGFRA	6.74722	0.269889	25	ZC3H3	6.167031	0.513919	12
SATB2	7.958792	0.331616	24	MIRLET7BHG	5.276484	0.439707	12
MEIS1	7.797292	0.324887	24	CMIP	5.091453	0.424288	12
RPTOR	12.32278	0.535773	23	ZC3H12D	5.829639	0.529967	11
NCOR2	8.741034	0.380045	23	RAD51B	5.240653	0.476423	11
NXN	5.731381	0.24919	23	FGFR2	5.0712	0.461018	11
INPP5A	5.566191	0.242008	23	VGLL4	4.963901	0.451264	11
PRKCZ	7.299384	0.33179	22	NR2F1-AS1	4.662872	0.466287	10
SKI	9.972847	0.474897	21	AKAP13	4.618214	0.461821	10
SIM2	5.724523	0.272596	21	CHST11	4.535589	0.453559	10
FRMD4A	9.398365	0.469918	20	GAS7	4.521014	0.452101	10
ABR	6.182838	0.309142	20	ATP11A	7.610869	0.845652	9
SDK1	5.248318	0.262416	20	SND1	6.161357	0.684595	9
MAD1L1	11.70125	0.615855	19	KCNH2	5.738954	0.637662	9
ZNF423	7.967461	0.41934	19	AXIN2	4.982084	0.553565	9
CASZ1	7.888011	0.415158	19	ADAMTS2	4.935406	0.548378	9
SMG1P2	7.249408	0.381548	19	TRAPPC12	4.645836	0.516204	9
BOLA2	7.249408	0.381548	19	LINC00311	6.172338	0.771542	8
LOC613038	7.249408	0.381548	19	LHX4	5.191303	0.648913	8
FO XK1	7.589663	0.421648	18	DLEU1	4.549579	0.568697	8
ANKRD11	5.668737	0.31493	18	MSRA	4.495601	0.56195	8
SEPTIN9	4.595294	0.255294	18	RGS20	4.410543	0.551318	8
TBC1D16	4.550263	0.252792	18	DUSP6	6.409854	0.915693	7
OPCML	7.944399	0.467318	17	LINC00461	4.952709	0.70753	7
PAX6-AS1	5.215924	0.306819	17	RUNDC3A	5.680512	1.136102	5
RCN1	5.215924	0.306819	17	TSNAX-DISC1	4.566497	0.913299	5
FOXP1	6.734018	0.420876	16	ARHGEF7	4.427856	0.885571	5
GLI2	9.012125	0.600808	15	RBMS3	4.727666	1.181917	4

TABLE 97:	Cancer Type IO_MEPL			SLX1A	4.790424	0.319362	15
				LOC606724	4.790424	0.319362	15
Gene site	imp_sum	imp_mean	n	ZBTB20	4.784376	0.318958	15
PTPRN2	19.57579	0.238729	82	KNDC1	4.672532	0.311502	15
PRDM16	13.39836	0.188709	71	KIRREL3	4.620311	0.308021	15
PCDHGA2	4.149727	0.072802	57	RPS6KA2	8.189835	0.584988	14
PCDHGB2	4.003444	0.081703	49	MIR548F5	7.255671	0.518262	14
PCDHGA5	4.003444	0.08518	47	C7orf50	7.003642	0.50026	14
PCDHGB3	4.089625	0.095108	43	PRKAG2	5.365647	0.38326	14
HDAC4	16.86061	0.455692	37	IQSEC1	5.328487	0.380606	14
PAX6	7.205322	0.205866	35	CUX1	4.289627	0.306402	14
RBFOX3	4.407359	0.125925	35	MYT1L	6.437381	0.495183	13
DIP2C	10.45506	0.32672	32	MSI2	5.673086	0.436391	13
SOX2-OT	4.188497	0.144431	29	CLYBL	5.020663	0.386205	13
SHANK2	8.032537	0.308944	26	GSE1	4.968646	0.382204	13
AGAP1	13.61969	0.544788	25	KIF26B	4.768748	0.366827	13
CAMTA1	7.258327	0.290333	25	RFX4	4.112628	0.316356	13
PDGFRA	5.787904	0.231516	25	CMIP	5.445062	0.453755	12
MEIS1	6.160598	0.256692	24	ZC3H3	4.716954	0.39308	12
RPTOR	12.21252	0.530979	23	RASA3	4.708674	0.392389	12
INPP5A	6.643328	0.28884	23	ADGRD1	4.495558	0.37463	12
NCOR2	6.618779	0.287773	23	TNS3	4.396419	0.366368	12
NXN	6.500086	0.282612	23	FBRSL1	4.377279	0.364773	12
RIMBP2	4.707864	0.20469	23	MAML3	4.352462	0.362705	12
PRKCZ	5.144966	0.233862	22	MEIS2	4.249655	0.354138	12
SKI	8.219151	0.391388	21	GNA12	4.139511	0.344959	12
HOXA-AS3	4.440806	0.211467	21	RAD51B	5.524138	0.502194	11
ZIC4	4.366666	0.207936	21	COL4A1	4.950854	0.450078	11
SDK1	7.048012	0.352401	20	CTBP2	4.565877	0.41508	11
FRMD4A	6.156727	0.307836	20	ZC3H12D	4.337687	0.394335	11
MAD1L1	13.30588	0.70031	19	VGLL4	4.291892	0.390172	11
ZNF423	6.364884	0.334994	19	CCDC140	4.286443	0.389677	11
SMG1P2	6.161088	0.324268	19	TBCD	4.031543	0.366504	11
BOLA2	6.161088	0.324268	19	AKAP13	5.403911	0.540391	10
LOC613038	6.161088	0.324268	19	NBEA	5.17908	0.517908	10
CASZ1	5.576216	0.293485	19	ACOT7	4.447818	0.444782	10
TBC1D16	6.783411	0.376856	18	TSPAN4	4.277334	0.427733	10
FO XK1	6.461694	0.358983	18	KLHL29	4.146967	0.414697	10
ANKRD11	6.360361	0.353353	18	SND1	7.456092	0.828455	9
SEPTIN9	4.582259	0.25457	18	ATP11A	6.698008	0.744223	9
HOXA3	4.03831	0.224351	18	TRAPPC12	5.537784	0.615309	9
FOXP1	6.464623	0.404039	16	AXIN2	4.177251	0.464139	9
NAV2	4.301849	0.268866	16	ADAMTS2	4.05797	0.450886	9
GLI2	7.666491	0.511099	15	MGMT	4.00896	0.44544	9
LRMDA	5.004471	0.333631	15	MSRA	4.976348	0.622043	8
BAIAP2	4.945349	0.32969	15	DNMT3A	4.668408	0.583551	8
SLX1B-				SYNJ2	4.434465	0.554308	8
SULT1A4	4.790424	0.319362	15	DLEU1	4.089529	0.511191	8

PPP2R2B	3.981533	0.497692	8	NAV2	3.133991	0.195874	16
FBXL18	4.770152	0.795025	6	ZBTB20	4.881349	0.325423	15
CRADD	4.507778	0.751296	6	GLI2	3.960304	0.26402	15
SLC22A18AS	4.258436	0.709739	6	SLX1B-			
FMNL2	4.222057	0.703676	6	SULT1A4	3.591227	0.239415	15
TSNAX-DISC1	5.281229	1.056246	5	SLX1A	3.591227	0.239415	15
RUNDC3A	4.794213	0.958843	5	LOC606724	3.591227	0.239415	15
DAGLB	4.037646	1.345882	3	KIRREL3	3.000317	0.200021	15
				BAIAP2	2.97861	0.198574	15
				RPS6KA2	7.52999	0.537856	14
TABLE 98: Cancer Type LCH				CUX1	6.183826	0.441702	14
Gene site	imp_sum	imp_mean	n	IQSEC1	5.523366	0.394526	14
PTPRN2	11.90058	0.145129	82	C7orf50	4.021076	0.28722	14
PRDM16	6.340229	0.089299	71	ARHGEF10	3.337458	0.23839	14
PCDHGA1	3.009323	0.051005	59	PRKAG2	2.977514	0.21268	14
PCDHGA2	3.009323	0.052795	57	MYT1L	4.479703	0.344593	13
HDAC4	12.67247	0.342499	37	MSI2	3.719446	0.286111	13
PAX6	9.410904	0.268883	35	CMIP	6.420494	0.535041	12
RBFOX3	4.406468	0.125899	35	FBRSL1	4.962752	0.413563	12
DIP2C	7.492757	0.234149	32	GNA12	4.548846	0.379071	12
SHANK2	3.588698	0.138027	26	ZC3H3	4.072548	0.339379	12
AGAP1	7.359122	0.294365	25	TNS3	3.455477	0.287956	12
PDGFRA	5.737538	0.229502	25	RAD51B	3.854406	0.350401	11
CAMTA1	4.250446	0.170018	25	TBCD	3.40743	0.309766	11
RPTOR	10.60541	0.461105	23	VGLL4	3.205608	0.291419	11
NCOR2	7.527478	0.327282	23	SLC38A10	3.191701	0.290155	11
INPP5A	6.155063	0.267611	23	ZC3H12D	3.102792	0.282072	11
NXN	3.886534	0.16898	23	ACOT7	3.965729	0.396573	10
PRKCZ	3.531157	0.160507	22	OTX1	3.463251	0.346325	10
SKI	7.320851	0.348612	21	ATP11A	7.207192	0.800799	9
ZIC4	2.952765	0.140608	21	SND1	7.086397	0.787377	9
FRMD4A	3.211158	0.160558	20	ADAMTS2	4.230769	0.470085	9
SDK1	2.99271	0.149636	20	CACNA2D4	3.479424	0.386603	9
MAD1L1	10.71262	0.563822	19	AXIN2	3.428441	0.380938	9
CASZ1	4.302664	0.226456	19	MGMT	3.317762	0.36864	9
SMG1P2	4.101114	0.215848	19	ASAP1	3.281916	0.364657	9
BOLA2	4.101114	0.215848	19	TSPAN9	3.259625	0.362181	9
LOC613038	4.101114	0.215848	19	LINC00311	4.744947	0.593118	8
ZNF423	3.863493	0.203342	19	DLEU1	4.301357	0.53767	8
KCNQ1	3.067512	0.161448	19	DNMT3A	3.273543	0.409193	8
TBC1D16	5.600008	0.311112	18	MSRA	2.985396	0.373175	8
ANKRD11	4.708597	0.261589	18	MACROD1	2.949414	0.368677	8
FOXK1	4.345205	0.2414	18	C19orf25	5.014216	0.716317	7
SEPTIN9	3.964328	0.22024	18	NAV1	3.454065	0.493438	7
PAX6-AS1	3.90826	0.229898	17	VPS13D	3.358144	0.479735	7
RCN1	3.90826	0.229898	17	GAK	3.259103	0.465586	7
OPCML	3.510236	0.206484	17	MIR548H4	3.246832	0.463833	7
FOXP1	5.172432	0.323277	16	CXXC5	3.232364	0.461766	7
EBF3	3.530611	0.220663	16				

	RXRA	2.991782	0.427397	7	MEIS1	3.570653	0.148777	24	
	ITPK1	2.944881	0.420697	7	SATB2	3.25786	0.135744	24	
	RADIL	4.025201	0.670867	6	PCDHGB7	3.162728	0.13178	24	
	SLC22A18AS	3.415395	0.569233	6	RPTOR	10.27897	0.446912	23	
	FMNL2	3.35009	0.558348	6	NCOR2	7.796333	0.338971	23	
	FBXL18	3.110054	0.518342	6	INPP5A	5.31175	0.230946	23	
	CRADD	2.974569	0.495762	6	HOXB3	4.171853	0.181385	23	
	RUNDC3A	4.135282	0.827056	5	NXN	3.25688	0.141603	23	
	ARHGEF7	3.716845	0.743369	5	PCDHGA11	3.162728	0.13751	23	
	ARHGAP26	3.411236	0.682247	5	SKI	6.442682	0.306794	21	
	NHSL1	4.167055	1.041764	4	FRMD4A	5.439477	0.271974	20	
	NDST1	3.6207	0.905175	4	SDK1	3.382742	0.169137	20	
	DAGLB	4.221934	1.407311	3	MAD1L1	8.43267	0.443825	19	
	TBC1D7	3.805081	1.26836	3	CASZ1	5.143108	0.27069	19	
	DICER1	3.103681	1.03456	3	KCNQ1	4.759959	0.250524	19	
	SLC25A10	3.006057	1.503029	2	ZNF423	4.636213	0.244011	19	
TABLE 99:	Cancer Type LGG_DIG_DIA				SMG1P2	4.465582	0.235031	19	
					BOLA2	4.465582	0.235031	19	
					LOC613038	4.465582	0.235031	19	
		Gene site	imp_sum	imp_mean	n	ANKRD11	5.788786	0.321599	18
						TBC1D16	4.406929	0.244829	18
	PTPRN2	14.23623	0.173613	82					
	PRDM16	10.76981	0.151687	71					
	PCDHGA1	4.428272	0.075055	59		RBFOX1	3.568704	0.198261	18
	PCDHGA2	4.111886	0.072138	57		MCF2L	3.335676	0.185315	18
	PCDHGA3	4.111886	0.076146	54		OPCML	4.914005	0.289059	17
	PCDHGB1	4.111886	0.077583	53		PAX6-AS1	4.370298	0.257076	17
	PCDHGA4	4.111886	0.080625	51		RCN1	4.370298	0.257076	17
	PCDHGB2	4.111886	0.083916	49		FOXP1	5.151974	0.321998	16
	PCDHGA5	4.111886	0.087487	47		SORBS2	3.612279	0.225767	16
	PCDHGB3	3.7955	0.088267	43		GLI2	6.246745	0.41645	15
	PCDHGA6	3.7955	0.094888	40		BAIAP2	4.444424	0.296295	15
	HDAC4	12.09384	0.32686	37		ZBTB20	4.000898	0.266727	15
	PCDHGA7	3.7955	0.102581	37		KIRREL3	3.9588	0.26392	15
	RBFOX3	4.315354	0.123296	35		RPS6KA2	5.124608	0.366043	14
	PAX6	4.097637	0.117075	35		CUX1	4.211117	0.300794	14
	PCDHGB4	3.479114	0.099403	35		MIR548F5	3.791066	0.27079	14
	PCDHGA8	3.479114	0.099403	35		C7orf50	3.682449	0.263032	14
	DIP2C	9.29439	0.29045	32		IQSEC1	3.563053	0.254504	14
	PCDHGB5	3.162728	0.098835	32		PRKAG2	3.524436	0.251745	14
	SOX2-OT	4.772139	0.164557	29		MSI2	4.173561	0.321043	13
	PCDHGB6	3.162728	0.10906	29		CMIP	4.027842	0.335653	12
	PCDHGA10	3.162728	0.112955	28		TNS3	3.867169	0.322264	12
	GALNT9	5.318422	0.196979	27		FBRSL1	3.797234	0.316436	12
	SHANK2	4.310182	0.165776	26		MIRLET7BHG	3.723759	0.310313	12
	ADARB2	3.611297	0.138896	26		ZC3H3	3.464802	0.288733	12
	AGAP1	9.830515	0.393221	25		ADGRD1	3.416781	0.284732	12
	CAMTA1	6.399763	0.255991	25		FGFR2	3.448292	0.313481	11
	PDGFRA	4.316944	0.172678	25		ANAPC16	3.384766	0.307706	11
					SPON2	3.240691	0.294608	11	

ACOT7	4.742578	0.474258	10	SOX2-OT	10.59281	0.365269	29
OBI1-AS1	3.735848	0.373585	10	PCDHGB6	5.434719	0.187404	29
FMN1	3.643263	0.364326	10	PCDHGA10	5.118333	0.182798	28
NBEA	3.290281	0.329028	10	SHANK2	8.876006	0.341385	26
GAS7	3.287849	0.328785	10	ADARB2	7.537938	0.289921	26
RGS12	3.21931	0.321931	10	AGAP1	8.40558	0.336223	25
SND1	6.119553	0.67995	9	CAMTA1	7.763566	0.310543	25
ATP11A	4.62361	0.513734	9	PDGFRA	6.514455	0.260578	25
TRAPPC12	4.425617	0.491735	9	SATB2	6.728159	0.28034	24
ADAMTS2	4.14856	0.460951	9	PCDHGB7	5.118333	0.213264	24
RUNX1	3.551438	0.394604	9	RPTOR	10.82497	0.470651	23
DLEU1	4.021061	0.502633	8	NCOR2	10.41423	0.452793	23
SYNJ2	3.405088	0.425636	8	INPP5A	7.025501	0.305457	23
MSRA	3.27781	0.409726	8	HOXB3	6.240577	0.271329	23
RXRA	3.946638	0.563805	7	NXN	5.796623	0.252027	23
VPS13D	3.880843	0.554406	7	PCDHGA11	4.801947	0.20878	23
NAV1	3.73432	0.533474	7	PRKCZ	7.662516	0.348296	22
FBXL18	3.527527	0.587921	6	SKI	11.08687	0.527946	21
FMNL2	3.275497	0.545916	6	ABR	6.446972	0.322349	20
RUNDC3A	4.650154	0.930031	5	FRMD4A	5.1939	0.259695	20
ARHGEF7	3.309919	0.661984	5	SDK1	5.027435	0.251372	20
TSNAX-DISC1	3.267592	0.653518	5	ZNF423	11.04971	0.581564	19
KLHL25	3.181519	0.636304	5	MAD1L1	10.99	0.578421	19
ZAR1	3.916304	1.958152	2	CASZ1	8.386398	0.441389	19
				SMG1P2	5.578786	0.29362	19
				BOLA2	5.578786	0.29362	19
				LOC613038	5.578786	0.29362	19
				SEPTIN9	8.84043	0.491135	18
				FOXK1	6.569609	0.364978	18
				MCF2L	5.792536	0.321808	18
				TBC1D16	5.737236	0.318735	18
				ANKRD11	5.543978	0.307999	18
				OPCML	6.014814	0.353813	17
				PAX6-AS1	4.947244	0.291014	17
				RCN1	4.947244	0.291014	17
				NAV2	6.648902	0.415556	16
				FOXP1	6.374021	0.398376	16
				GLI2	8.757455	0.58383	15
				KIRREL3	6.571073	0.438072	15
				NFIX	6.394432	0.426295	15
				ZBTB20	6.005432	0.400362	15
				EMX2OS	5.739645	0.382643	15
				BAIAP2	4.842575	0.322838	15
				SLX1B-SULT1A4	4.676131	0.311742	15
				SLX1A	4.676131	0.311742	15
				CUX1	7.265301	0.51895	14
				RPS6KA2	7.2188	0.515629	14
				PRKAG2	4.906524	0.350466	14

TABLE 100:		Cancer Type	
		LGG_MYB_A	
Gene site	imp_sum	imp_mean	n
PTPRN2	26.29143	0.320627	82
PRDM16	21.21807	0.298846	71
PCDHGA1	8.16692	0.138422	59
PCDHGA2	7.850534	0.137729	57
PCDHGA3	7.534148	0.139521	54
PCDHGB1	7.534148	0.142154	53
PCDHGA4	7.217762	0.141525	51
PCDHGB2	6.80743	0.138927	49
PCDHGA5	6.857864	0.145912	47
PCDHGB3	6.446917	0.149928	43
PCDHGA6	6.130531	0.153263	40
HDAC4	15.14366	0.409288	37
PCDHGA7	5.814145	0.157139	37
PAX6	16.6925	0.476929	35
RBFOX3	9.111279	0.260322	35
PCDHGB4	6.130531	0.175158	35
PCDHGA8	6.130531	0.175158	35
DIP2C	11.70908	0.365909	32
PCDHGB5	6.130531	0.191579	32
PCDHGA9	5.814145	0.187553	31

MSI2	8.707651	0.669819	13	DIP2C	3.935759	0.122992	32
MYT1L	6.635139	0.510395	13	SOX2-OT	7.260823	0.250373	29
RFX4	6.006326	0.462025	13	SHANK2	2.749789	0.105761	26
GSE1	4.928383	0.379106	13	AGAP1	4.89778	0.195911	25
CLYBL	4.744826	0.364987	13	CAMTA1	3.840148	0.153606	25
ZC3H3	6.383408	0.531951	12	PDGFRA	2.344615	0.093785	25
CMIP	6.246763	0.520564	12	MEIS1	3.259669	0.13582	24
MIRLET7BHG	5.445528	0.453794	12	SATB2	2.465852	0.102744	24
MEGF6	5.170835	0.430903	12	RPTOR	3.341045	0.145263	23
CTNNA2	4.953259	0.412772	12	NCOR2	2.605574	0.113286	23
TBX4	4.845798	0.403817	12	PRKCZ	3.737433	0.169883	22
SPON2	5.815477	0.52868	11	SKI	6.522588	0.310599	21
RAD51B	5.263935	0.47854	11	FRMD4A	4.133611	0.206681	20
ZC3H12D	5.156671	0.468788	11	SDK1	2.531088	0.126554	20
SH3RF3	5.703608	0.570361	10	ABR	2.127596	0.10638	20
AKAP13	5.229688	0.522969	10	MAD1L1	6.182977	0.32542	19
IGF1R	4.676857	0.467686	10	ZNF423	4.378512	0.230448	19
ATP11A	6.235484	0.692832	9	SMG1P2	2.828645	0.148876	19
ASAP1	5.628994	0.625444	9	BOLA2	2.828645	0.148876	19
RUNX1	5.502947	0.611439	9	LOC613038	2.828645	0.148876	19
TSPAN9	5.099097	0.566566	9	CASZ1	2.304714	0.121301	19
ADAMTS2	4.897346	0.54415	9	FOXK1	4.758755	0.264375	18
SND1	4.870835	0.541204	9	RBFOX1	3.374229	0.187457	18
TRAPPC12	4.807277	0.534142	9	TBC1D16	3.083552	0.171308	18
NOTCH1	4.725715	0.525079	9	SEPTIN9	2.679801	0.148878	18
LHX4	5.078995	0.634874	8	MCF2L	2.166848	0.12038	18
MSRA	4.831149	0.603894	8	OPCML	3.863382	0.227258	17
NAV1	5.405609	0.77223	7	NAV2	2.84974	0.178109	16
RUNDC3A	4.967815	0.993563	5	FOXP1	2.480408	0.155026	16
TSNAX-DISC1	4.966489	0.993298	5	EBF3	2.3211	0.145069	16
RBMS3	5.011413	1.252853	4	GLI2	3.825441	0.255029	15
GRIN2B	4.981407	1.660469	3	EMX2OS	3.097589	0.206506	15
				ZBTB20	3.096569	0.206438	15
				KIRREL3	2.12156	0.141437	15
				CUX1	2.933436	0.209531	14
				RPS6KA2	2.791658	0.199404	14
				CACNA1H	2.648296	0.189164	14
				TBX5	2.51764	0.179831	14
				PRKAG2	2.319059	0.165647	14
				MSI2	4.075431	0.313495	13
				RFX4	2.98633	0.229718	13
				MYT1L	2.643675	0.20336	13
				TNS3	3.343622	0.278635	12
				CMIP	3.160924	0.26341	12
				ISLR2	3.052967	0.254414	12
				ADGRD1	2.769872	0.230823	12
				FBRSL1	2.016728	0.168061	12
				CCDC140	4.614115	0.419465	11

TABLE 101:		Cancer Type					
		LGG_MYB_B					
Gene site	imp_sum	imp_mean	n				
PTPRN2	9.894068	0.120659	82				
PRDM16	6.835973	0.096281	71				
PCDHGA1	2.924209	0.049563	59				
PCDHGA2	2.924209	0.051302	57				
PCDHGA3	2.291437	0.042434	54				
PCDHGB1	2.291437	0.043235	53				
PCDHGA4	2.291437	0.04493	51				
PCDHGB2	2.291437	0.046764	49				
PCDHGA5	2.291437	0.048754	47				
HDAC4	6.1271	0.165597	37				
PAX6	3.644378	0.104125	35				
RBFOX3	2.273223	0.064949	35				

ZC3H12D	3.119557	0.283596	11	PCDHGA3	4.60837	0.08534	54
RAD51B	2.623407	0.238492	11	PCDHGB1	4.60837	0.08695	53
SH3RF3	2.873823	0.287382	10	PCDHGA4	4.291984	0.084157	51
LBX1-AS1	2.521427	0.252143	10	PCDHGB2	3.975598	0.081135	49
OTX1	2.448407	0.244841	10	HDAC4	10.06805	0.272109	37
GRID1	2.340932	0.234093	10	PAX6	15.08031	0.430866	35
RGS12	2.322792	0.232279	10	RBFOX3	8.465599	0.241874	35
ANKS1B	2.208493	0.220849	10	DIP2C	10.80977	0.337805	32
MAML2	2.04004	0.204004	10	SOX2-OT	8.438282	0.290975	29
PAX3	3.636353	0.404039	9	GALNT9	4.570214	0.169267	27
ATP11A	2.872912	0.319212	9	SHANK2	5.741485	0.220826	26
RUNX1	2.672577	0.296953	9	ADARB2	3.994562	0.153637	26
NOTCH1	2.525311	0.28059	9	AGAP1	8.791625	0.351665	25
KCNH2	2.463535	0.273726	9	CAMTA1	6.88132	0.275253	25
SND1	2.355613	0.261735	9	PDGFRA	5.659159	0.226366	25
KCNMA1	2.183475	0.242608	9	SATB2	7.35095	0.30629	24
GRIK2	2.694068	0.336759	8	RPTOR	11.96567	0.520246	23
MSRA	2.68183	0.335229	8	NCOR2	8.201648	0.356593	23
RGS20	2.265403	0.283175	8	HOXB3	4.853942	0.211041	23
MACROD1	2.045585	0.255698	8	INPP5A	4.841783	0.210512	23
ASPCR1	2.018782	0.252348	8	RIMBP2	4.131433	0.179628	23
DUSP6	3.414944	0.487849	7	NXN	3.984332	0.173232	23
NAV1	2.56527	0.366467	7	PRKCZ	6.612622	0.300574	22
LINC00461	2.430513	0.347216	7	SKI	13.19454	0.628312	21
NRXN3	2.375256	0.339322	7	SDK1	6.583704	0.329185	20
RBMS1	2.336389	0.33377	7	ABR	4.146009	0.2073	20
FHIT	2.209925	0.315704	7	MAD1L1	11.45751	0.603027	19
VPS13D	2.080121	0.29716	7	ZNF423	9.218881	0.485204	19
COQ8A	2.607277	0.434546	6	CASZ1	8.599236	0.452591	19
FBXL18	2.406226	0.401038	6	SMG1P2	4.843875	0.254941	19
SLC22A18AS	2.041973	0.340329	6	BOLA2	4.843875	0.254941	19
RUNDC3A	2.474362	0.494872	5	LOC613038	4.843875	0.254941	19
ARHGEF7	2.035714	0.407143	5	FOXK1	7.433257	0.412959	18
OSBPL3	2.712546	0.678136	4	SEPTIN9	6.898671	0.383259	18
RBMS3	2.537584	0.634396	4	MCF2L	6.080352	0.337797	18
GRIN2B	3.514634	1.171545	3	RBFOX1	4.847449	0.269303	18
DAGLB	2.513521	0.83784	3	TBC1D16	4.803718	0.266873	18
SLC6A9	2.240435	0.746812	3	ANKRD11	4.704091	0.261338	18
PRDM2	2.140595	0.713532	3	OPCML	6.136104	0.360947	17
SOX10	2.748606	1.374303	2	PAX6-AS1	5.627414	0.331024	17
TABLE 102:	Cancer Type LGG_MYB_C		RCN1	5.627414	0.331024	17	
			TBX15	4.66374	0.274338	17	
			NAV2	5.587066	0.349192	16	
			EBF3	5.346808	0.334175	16	
			FOXP1	4.619708	0.288732	16	
			GLI2	9.468685	0.631246	15	
			ZBTB20	5.256564	0.350438	15	
			BAIAP2	4.249964	0.283331	15	
Gene site	imp_sum	imp_mean	n				
PTPRN2	20.20583	0.246413	82				
PRDM16	17.28914	0.243509	71				
PCDHGA1	4.924756	0.08347	59				
PCDHGA2	4.924756	0.086399	57				

RPS6KA2	6.945756	0.496125	14	TABLE 103:	Cancer Type		
TBX5	4.767199	0.340514	14		LGG_MYB_D		
CUX1	4.567314	0.326237	14	Gene site	imp_sum	imp_mean	n
IQSEC1	4.544448	0.324603	14	PTPRN2	23.27595	0.283853	82
C7orf50	4.426138	0.316153	14	PRDM16	16.21061	0.228318	71
MSI2	6.825236	0.525018	13	PCDHGA1	9.160539	0.155263	59
RFX4	5.374636	0.413434	13	PCDHGA2	9.160539	0.160711	57
MYT1L	5.10985	0.393065	13	PCDHGA3	7.852367	0.145414	54
GSE1	4.902216	0.377094	13	PCDHGB1	7.852367	0.148158	53
KIF26B	4.234824	0.325756	13	PCDHGA4	7.852367	0.153968	51
ZC3H3	5.958219	0.496518	12	PCDHGB2	7.405548	0.151134	49
CMIP	4.941409	0.411784	12	PCDHGA5	7.264056	0.154554	47
TNS3	4.795633	0.399636	12	PCDHGB3	5.979533	0.139059	43
FBRSL1	4.35464	0.362887	12	PCDHGA6	5.21626	0.130406	40
ADGRD1	3.98479	0.332066	12	HDAC4	16.02144	0.433012	37
ZC3H12D	6.127102	0.557009	11	PCDHGA7	5.21626	0.14098	37
RAD51B	5.338869	0.485352	11	PAX6	12.2992	0.351406	35
CACNA1C	4.235148	0.385013	11	RBFOX3	6.122396	0.174926	35
CCDC140	4.231694	0.384699	11	PCDHGB4	5.532646	0.158076	35
VGLL4	4.106819	0.373347	11	PCDHGA8	5.532646	0.158076	35
SPON2	4.059063	0.369006	11	DIP2C	9.983397	0.311981	32
ACOT7	4.827365	0.482737	10	PCDHGB5	5.349908	0.167185	32
SH3RF3	4.309594	0.430959	10	PCDHGA9	5.349908	0.172578	31
ANKS1B	4.241103	0.42411	10	SOX2-OT	9.671774	0.333509	29
SND1	6.994693	0.777188	9	PCDHGB6	4.458488	0.153741	29
CACNA2D4	5.266681	0.585187	9	ADARB2	5.588489	0.214942	26
ATP11A	4.720307	0.524479	9	AGAP1	9.213862	0.368554	25
GPC6	4.65542	0.517269	9	PDGFRA	7.30522	0.292209	25
RUNX1	4.628724	0.514303	9	CAMTA1	5.162567	0.206503	25
TRAPPC12	4.612695	0.512522	9	MEIS1	6.02547	0.251061	24
ADAMTS2	4.574137	0.508237	9	SATB2	5.621512	0.23423	24
SLC22A18	4.305448	0.478383	9	RPTOR	9.213192	0.400574	23
AXIN2	4.123233	0.458137	9	NCOR2	6.408949	0.27865	23
NOTCH1	3.941099	0.4379	9	HOXB3	6.227616	0.270766	23
LHX4	5.258583	0.657323	8	INPP5A	5.694734	0.247597	23
LINC00311	4.611648	0.576456	8	PRKCZ	6.459749	0.293625	22
DLEU1	4.375936	0.546992	8	SKI	12.18697	0.580332	21
ASPCR1	4.105064	0.513133	8	FRMD4A	6.85308	0.342654	20
MSRA	4.098997	0.512375	8	ABR	4.623305	0.231165	20
DUSP6	8.13263	1.161804	7	MAD1L1	10.44305	0.549634	19
NAV1	4.915243	0.702178	7	SMG1P2	6.689881	0.352099	19
LINC00461	4.07618	0.582311	7	BOLA2	6.689881	0.352099	19
FBXL18	4.502532	0.750422	6	LOC613038	6.689881	0.352099	19
FAM181A	4.098243	0.683041	6	CASZ1	5.910579	0.311083	19
RUNDC3A	5.333783	1.066757	5	ZNF423	5.371146	0.282692	19
TSNAX-DISC1	5.037322	1.007464	5	FO XK1	6.442305	0.357906	18
RBMS3	4.399929	1.099982	4	TBC1D16	6.239467	0.346637	18
GRIN2B	4.044385	1.348128	3				

SEPTIN9	5.949188	0.33051	18	MSRA	4.107945	0.513493	8
RBFOX1	4.629235	0.25718	18	DUSP6	6.069555	0.867079	7
MCF2L	4.384944	0.243608	18	VPS13D	4.62615	0.660879	7
OPCML	8.442759	0.496633	17	GAK	4.356915	0.622416	7
TBX15	4.712791	0.277223	17	NAV1	4.354487	0.62207	7
NAV2	6.350364	0.396898	16	FAM181A	4.252081	0.70868	6
SORBS2	5.402963	0.337685	16	RUNDC3A	4.698262	0.939652	5
FOXP1	4.987706	0.311732	16	SOX10	4.990034	2.495017	2
GLI2	10.69003	0.712669	15				
EMX2OS	6.133218	0.408881	15	TABLE 104:	Cancer Type LIPN		
ZBTB20	5.331774	0.355452	15	Gene site	imp_sum	imp_mean	n
LRMDA	4.22455	0.281637	15	PTPRN2	6.731022	0.082086	82
TBX5	7.168475	0.512034	14	PRDM16	9.056435	0.127555	71
RPS6KA2	6.102015	0.435858	14	HDAC4	6.920459	0.187039	37
IQSEC1	5.481145	0.39151	14	RBFOX3	4.482568	0.128073	35
CUX1	5.281736	0.377267	14	PAX6	3.647653	0.104219	35
C7orf50	4.578078	0.327006	14	DIP2C	6.348889	0.198403	32
PRKAG2	4.47899	0.319928	14	SOX2-OT	3.711222	0.127973	29
MSI2	6.722419	0.517109	13	ADARB2	6.182806	0.2378	26
RFX4	6.635387	0.510414	13	SHANK2	3.204426	0.123247	26
MYT1L	6.108125	0.469856	13	CAMTA1	6.741431	0.269657	25
KIF26B	4.407831	0.339064	13	AGAP1	4.874396	0.194976	25
CMIP	6.108514	0.509043	12	PDGFRA	3.166753	0.12667	25
MIRLET7BHG	5.178592	0.431549	12	SATB2	2.720432	0.113351	24
TBX4	5.011236	0.417603	12	RPTOR	10.67932	0.464318	23
ADGRD1	4.376792	0.364733	12	INPP5A	5.333496	0.231891	23
CCDC140	5.725205	0.520473	11	NCOR2	4.784433	0.208019	23
RAD51B	4.883983	0.443998	11	RIMBP2	3.878209	0.168618	23
ZC3H12D	4.397805	0.3998	11	PRKCZ	5.076408	0.230746	22
ANAPC16	4.3899	0.399082	11	SKI	11.38324	0.542059	21
GLUD1P2	4.13606	0.376005	11	ZIC4	2.675222	0.127392	21
TSPAN4	4.482039	0.448204	10	ABR	3.659858	0.182993	20
ACOT7	4.480182	0.448018	10	FRMD4A	3.233023	0.161651	20
NR2F1-AS1	4.411228	0.441123	10	MAD1L1	8.907459	0.468814	19
AKAP13	4.391567	0.439157	10	ZNF423	6.517334	0.343018	19
SH3RF3	4.192477	0.419248	10	SMG1P2	6.286146	0.33085	19
SND1	6.302178	0.700242	9	BOLA2	6.286146	0.33085	19
ATP11A	5.52456	0.61384	9	LOC613038	6.286146	0.33085	19
NOTCH1	5.406527	0.600725	9	CASZ1	3.545162	0.186587	19
ADAMTS2	5.093618	0.565958	9	KCNQ1	2.803672	0.147562	19
ASAP1	4.613364	0.512596	9	ANKRD11	3.883679	0.21576	18
PACS2	4.499113	0.499901	9	FO XK1	3.581042	0.198947	18
RUNX1	4.160767	0.462307	9	TBC1D16	3.291546	0.182864	18
TRAPPC12	4.153276	0.461475	9	SEPTIN9	3.145068	0.174726	18
KCNMA1	4.103531	0.455948	9	OPCML	3.807395	0.223964	17
LINC00311	4.754081	0.59426	8	TBX15	3.227398	0.189847	17
ESRRG	4.166404	0.520801	8	GLI2	6.244295	0.416286	15
PPP2R2B	4.13858	0.517322	8	NFIX	3.842107	0.25614	15

SLX1B-SULT1A4	3.508078	0.233872	15	PRR5L	4.743315	0.948663	5
SLX1A	3.508078	0.233872	15	ARHGEF7	4.358366	0.871673	5
LOC606724	3.508078	0.233872	15	RUNDC3A	4.230101	0.84602	5
ZBTB20	3.393498	0.226233	15	TSNAX-DISC1	3.971266	0.794253	5
C7orf50	4.232753	0.302339	14	TK1	3.759883	0.751977	5
PRKAG2	3.853803	0.275272	14	BCAR1	2.967733	0.593547	5
MIR548F5	3.550057	0.253575	14	AP2A2	2.928493	0.585699	5
CUX1	3.514123	0.251009	14	TTLL10	2.856842	0.571368	5
GSE1	5.333509	0.41027	13	TOLLIP	2.67497	0.534994	5
MSI2	5.045792	0.388138	13	RBMS3	3.938709	0.984677	4
CLYBL	3.955888	0.304299	13	SLC25A22	3.14499	1.04833	3
MYT1L	3.641557	0.28012	13	ANKLE2	4.355455	2.177728	2
KIF26B	3.115991	0.239692	13	SLC25A10	3.758294	1.879147	2
MIR9-3HG	2.847369	0.219028	13	CHTF18	2.700933	1.350466	2
MAML3	4.351798	0.36265	12	ACMSD	2.670176	2.670176	1
ZC3H3	4.308123	0.35901	12				
FBRSL1	3.596014	0.299668	12	TABLE 105:	Cancer Type MB_G34_I		
CMIP	3.053446	0.254454	12	Gene site	imp_sum	imp_mean	n
MEIS2	3.037518	0.253126	12	PTPRN2	15.21477	0.185546	82
RASA3	2.849411	0.237451	12	PRDM16	13.99515	0.197115	71
MIRLET7BHG	2.720116	0.226676	12	HDAC4	15.05659	0.406935	37
ZC3H12D	5.705381	0.518671	11	PAX6	10.99121	0.314035	35
CACNA1C	3.106977	0.282452	11	RBFOX3	9.720497	0.277728	35
TBCD	2.993291	0.272117	11	DIP2C	5.267308	0.164603	32
ACOT7	4.5126	0.45126	10	GALNT9	11.235	0.416111	27
NR2F1-AS1	3.941043	0.394104	10	SHANK2	6.139225	0.236124	26
LMF1	2.876585	0.287659	10	ADARB2	4.713313	0.181281	26
RGS12	2.712554	0.271255	10	CAMTA1	8.61843	0.344737	25
ATP11A	5.393156	0.59924	9	AGAP1	8.576106	0.343044	25
ADAMTS2	5.08888	0.565431	9	PDGFRA	3.561496	0.14246	25
TRAPPC12	3.099343	0.344371	9	MEIS1	3.752097	0.156337	24
SND1	3.000188	0.333354	9	RPTOR	9.10743	0.395975	23
KAZN	2.994854	0.332762	9	RIMBP2	8.129395	0.353452	23
SLC22A18	2.898108	0.322012	9	INPP5A	7.378585	0.320808	23
SPECC1	2.848229	0.31647	9	NCOR2	7.302389	0.317495	23
BAHCC1	4.507579	0.563447	8	NXN	6.254104	0.271918	23
MSRA	3.594303	0.449288	8	PRKCZ	6.210744	0.282307	22
LINC00311	3.134488	0.391811	8	SKI	6.826888	0.32509	21
RORA	2.807937	0.350992	8	ABR	6.348683	0.317434	20
PPP2R2B	2.79953	0.349941	8	MAD1L1	15.24947	0.802603	19
MCC	2.725199	0.34065	8	CASZ1	7.148909	0.376258	19
GAK	4.535148	0.647878	7	SMG1P2	6.024295	0.317068	19
RXRA	3.758968	0.536995	7	BOLA2	6.024295	0.317068	19
DUSP6	3.5019	0.500271	7	LOC613038	6.024295	0.317068	19
ITPK1	2.882647	0.411807	7	ZNF423	5.916425	0.311391	19
COQ8A	3.96694	0.661157	6	KCNQ1	4.662981	0.24542	19
CRADD	3.5242	0.587367	6	CFAP46	3.287552	0.173029	19
FBXL18	3.099236	0.516539	6	RBFOX1	5.193119	0.288507	18

SEPTIN9	4.630468	0.257248	18	CACNA2D4	4.219973	0.468886	9
FO XK1	4.379068	0.243282	18	TSPAN9	4.196219	0.466247	9
ANKRD11	4.039479	0.224415	18	VRK2	9.809346	1.226168	8
SIM1	5.337274	0.313957	17	PPP2R2B	4.7627	0.595338	8
PAX6-AS1	5.125289	0.301488	17	DNMT3A	4.54865	0.568581	8
RCN1	5.125289	0.301488	17	MSRA	4.300761	0.537595	8
OPCML	4.841857	0.284815	17	TRAPPC9	3.895066	0.486883	8
TBX15	4.156233	0.244484	17	ASPSCR1	3.587117	0.44839	8
HBG2	3.582301	0.210724	17	AFF3	3.463264	0.432908	8
FOXP1	7.656811	0.478551	16	PLEC	3.469843	0.495692	7
NAV2	5.590731	0.349421	16	PITPNC1	3.27975	0.468536	7
KNDC1	5.127187	0.341812	15	TRAK1	3.699044	0.616507	6
ZBTB20	4.614327	0.307622	15	CRADD	3.603323	0.600554	6
NFIX	4.566382	0.304425	15	KDM4B	3.299808	0.549968	6
GLI2	4.154642	0.276976	15	ARHGEF7	4.059958	0.811992	5
BAIAP2	4.089022	0.272601	15	TSNAX-DISC1	4.032988	0.806598	5
C7orf50	5.987317	0.427665	14	SNX29	3.323028	0.664606	5
IQSEC1	5.521955	0.394425	14	TK1	3.266153	0.653231	5
CUX1	4.926357	0.351883	14	EXT1	3.723467	0.930867	4
PRKAG2	4.728344	0.337739	14	SOGA1	3.214915	1.071638	3
RPS6KA2	4.723242	0.337374	14	CHTF18	4.254009	2.127004	2
MOB2	3.873649	0.276689	14	ANKLE2	4.207152	2.103576	2
ARHGEF10	3.870515	0.276465	14				
MSI2	6.361069	0.489313	13	TABLE 106: Cancer Type MB_G34_II			
MYT1L	4.843261	0.372559	13	Gene site	imp_sum	imp_mean	n
RFX4	4.65499	0.358076	13	PTPRN2	12.74639	0.155444	82
CLYBL	3.8267	0.294362	13	PRDM16	13.53703	0.190662	71
FBRSL1	5.87314	0.489428	12	PCDHGA1	5.680155	0.096274	59
ZC3H3	3.999881	0.333323	12	PCDHGA2	6.101345	0.107041	57
CSMD1	3.899739	0.324978	12	PCDHGA3	5.346211	0.099004	54
CMIP	3.871864	0.322655	12	PCDHGB1	5.346211	0.100872	53
LRBA	3.42567	0.285473	12	PCDHGA4	5.662597	0.111031	51
ADGRD1	3.385211	0.282101	12	PCDHGB2	5.662597	0.115563	49
COL4A1	4.603563	0.418506	11	PCDHGA5	5.662597	0.120481	47
TBCD	3.949157	0.359014	11	PCDHGB3	5.346211	0.12433	43
RAD51B	3.597217	0.32702	11	PCDHGA6	5.029825	0.125746	40
AUTS2	4.614624	0.461462	10	HDAC4	13.47601	0.364216	37
AKAP13	4.399463	0.439946	10	PCDHGA7	5.029825	0.135941	37
SNTG2	4.025889	0.402589	10	RBFOX3	5.762697	0.164648	35
STK32C	3.914647	0.391465	10	PCDHGB4	4.397053	0.12563	35
CHST11	3.564208	0.356421	10	PCDHGA8	4.397053	0.12563	35
NBEA	3.471319	0.347132	10	DIP2C	5.296077	0.165502	32
LMF1	3.252013	0.325201	10	PCDHGB5	4.397053	0.137408	32
AXIN2	5.679917	0.631102	9	PCDHGA9	3.849052	0.124163	31
ADAMTS2	5.592358	0.621373	9	SOX2-OT	4.564477	0.157396	29
SND1	5.569503	0.618834	9	PCDHGB6	3.849052	0.132726	29
ATP11A	4.782212	0.531357	9	PCDHGA10	3.849052	0.137466	28
GPC6	4.612468	0.512496	9	GALNT9	12.32559	0.456503	27

ADARB2	5.603404	0.215516	26	GSE1	4.289678	0.329975	13
SHANK2	5.402806	0.2078	26	FBRSL1	5.542824	0.461902	12
AGAP1	7.424954	0.296998	25	ZC3H3	5.160154	0.430013	12
CAMTA1	6.513135	0.260525	25	CSMD1	3.343871	0.278656	12
MEIS1	4.4845	0.186854	24	GNA12	3.269859	0.272488	12
PCDHGB7	3.849052	0.160377	24	AKAP13	4.584297	0.45843	10
RPTOR	8.737766	0.379903	23	LBX1-AS1	3.278201	0.32782	10
INPP5A	6.413009	0.278826	23	ATP11A	5.039492	0.559944	9
RIMBP2	4.94583	0.215036	23	ADAMTS2	4.637422	0.515269	9
NCOR2	4.636315	0.201579	23	GPC6	4.451665	0.494629	9
NXN	4.272086	0.185743	23	AXIN2	4.177111	0.464123	9
PCDHGA11	3.532666	0.153594	23	SND1	4.06486	0.451651	9
PRKCZ	7.474125	0.339733	22	SSBP3	3.706025	0.411781	9
SKI	7.30758	0.34798	21	PDE6B	3.491528	0.387948	9
SDK1	4.802333	0.240117	20	KAZN	3.397258	0.377473	9
FRMD4A	4.44969	0.222485	20	CACNA2D4	3.344224	0.37158	9
MAD1L1	14.57738	0.767231	19	ASAP1	3.281443	0.364605	9
CASZ1	6.899549	0.363134	19	PPP2R2B	4.157437	0.51968	8
ZNF423	5.180383	0.272652	19	TRAPPC9	4.044266	0.505533	8
SMG1P2	4.077975	0.21463	19	MSRA	3.725977	0.465747	8
BOLA2	4.077975	0.21463	19	GAK	3.32362	0.474803	7
LOC613038	4.077975	0.21463	19	PITPNC1	3.300358	0.47148	7
ANKRD11	5.335731	0.29643	18	COLEC11	3.730471	0.621745	6
RBFOX1	4.681435	0.26008	18	ARHGEF7	3.733163	0.746633	5
MCF2L	4.295341	0.23863	18	TSNAX-DISC1	3.660898	0.73218	5
FOKK1	4.236444	0.235358	18	CPEB1-AS1	3.41389	0.682778	5
SEPTIN9	3.476701	0.19315	18	EML1	3.313764	0.828441	4
SIM1	6.314996	0.37147	17	LOC339874	3.749811	1.249937	3
TBX15	4.392645	0.258391	17	CHTF18	4.105874	2.052937	2
OPCML	3.71019	0.218246	17				
FOXP1	7.802048	0.487628	16	TABLE 107:	Cancer Type	MB_G34_III	
NAV2	3.845894	0.240368	16	Gene site	imp_sum	imp_mean	n
KNDC1	6.151625	0.410108	15	PTPRN2	14.7975	0.180457	82
GLI2	5.423438	0.361563	15	PRDM16	17.7935	0.250613	71
ZBTB20	5.123853	0.34159	15	PCDHGA4	3.301688	0.064739	51
EMX2OS	4.663506	0.3109	15	PCDHGB2	3.301688	0.067381	49
KIRREL3	3.868391	0.257893	15	HDAC4	15.89626	0.429629	37
BAIAP2	3.340001	0.222667	15	RBFOX3	9.015163	0.257576	35
NFATC1	3.316835	0.221122	15	PAX6	6.048704	0.17282	35
NFIX	3.292725	0.219515	15	DIP2C	7.277516	0.227422	32
IQSEC1	5.181107	0.370079	14	PCDHGB5	3.618074	0.113065	32
C7orf50	4.968043	0.35486	14	PCDHGA9	3.217874	0.103802	31
CUX1	4.661009	0.332929	14	GALNT9	13.00801	0.481778	27
MOB2	4.283801	0.305986	14	SHANK2	3.631955	0.139691	26
CACNA1H	3.670581	0.262184	14	ADARB2	3.273835	0.125917	26
GNG7	3.388734	0.242052	14	AGAP1	10.3121	0.412484	25
MSI2	5.854141	0.450319	13	CAMTA1	7.452654	0.298106	25
MYT1L	5.022727	0.386364	13	PDGFRA	4.596988	0.18388	25

SATB2	3.175686	0.13232	24	ANAPC16	3.40214	0.309285	11
RPTOR	7.891204	0.343096	23	TBCD	3.146873	0.286079	11
NCOR2	6.955156	0.302398	23	AKAP13	3.858257	0.385826	10
INPP5A	6.462027	0.280958	23	LBX1-AS1	3.738787	0.373879	10
RIMBP2	6.059287	0.263447	23	AUTS2	3.589948	0.358995	10
NXN	5.423888	0.235821	23	SPPL2B	3.508733	0.350873	10
PRKCZ	4.474655	0.203393	22	FMN1	3.484234	0.348423	10
SKI	5.782114	0.275339	21	STK32C	3.35421	0.335421	10
ABR	6.255236	0.312762	20	AXIN2	5.46599	0.607332	9
SDK1	4.515301	0.225765	20	ATP11A	4.793503	0.532611	9
MAD1L1	15.11224	0.795381	19	SND1	4.675186	0.519465	9
ZNF423	5.857209	0.308274	19	ADAMTS2	4.119619	0.457735	9
SMG1P2	5.796451	0.305076	19	ASAP1	4.117795	0.457533	9
BOLA2	5.796451	0.305076	19	GPC6	4.069688	0.452188	9
LOC613038	5.796451	0.305076	19	TSPAN9	3.990656	0.443406	9
CASZ1	5.064561	0.266556	19	CACNA2D4	3.902544	0.433616	9
FOXK1	4.875026	0.270835	18	SSBP3	3.601051	0.400117	9
ANKRD11	4.659964	0.258887	18	VRK2	7.800481	0.97506	8
TBC1D16	3.530374	0.196132	18	PPP2R2B	4.310545	0.538818	8
HBG2	4.828729	0.284043	17	DNMT3A	3.937105	0.492138	8
OPCML	4.282999	0.251941	17	TRAPPC9	3.643122	0.45539	8
TBX15	3.693365	0.217257	17	DLEU1	3.586537	0.448317	8
FOXP1	7.819508	0.488719	16	ASPSCR1	3.52984	0.44123	8
NAV2	4.755238	0.297202	16	MSRA	3.365206	0.420651	8
KNDC1	6.627559	0.441837	15	GAK	4.133953	0.590565	7
KIRREL3	5.070696	0.338046	15	PITPNC1	4.01956	0.574223	7
BAIAP2	4.656342	0.310423	15	TRAK1	4.188055	0.698009	6
ZBTB20	4.388692	0.292579	15	CRADD	3.633965	0.605661	6
C7orf50	5.919713	0.422837	14	MYO16	3.490851	0.581809	6
RPS6KA2	5.695952	0.406854	14	TSNAX-DISC1	4.541564	0.908313	5
MOB2	4.067668	0.290548	14	CPEB1-AS1	3.981913	0.796383	5
PRKAG2	4.057194	0.2898	14	ARHGEF7	3.487939	0.697588	5
IQSEC1	3.935264	0.28109	14	CASP8	3.234689	0.646938	5
CUX1	3.910719	0.279337	14	LOC339874	3.535577	1.178526	3
ARHGEF10	3.843161	0.274512	14	CHTF18	4.356605	2.178303	2
MIR548F5	3.551018	0.253644	14	ANKLE2	3.982797	1.991399	2
GNG7	3.269011	0.233501	14				
MSI2	7.8038	0.600292	13	TABLE 108:	Cancer Type	MB_G34_IV	
GSE1	5.661925	0.435533	13	Gene site	imp_sum	imp_mean	n
MYT1L	4.991771	0.383982	13	PTPRN2	10.83321	0.132112	82
RFX4	3.282977	0.252537	13	PRDM16	11.50299	0.162014	71
FBRSL1	5.460206	0.455017	12	PCDHGA1	4.072054	0.069018	59
MAML3	4.796059	0.399672	12	PCDHGA2	3.755668	0.065889	57
ZC3H3	4.548573	0.379048	12	PCDHGA3	3.755668	0.069549	54
CMIP	4.470874	0.372573	12	PCDHGB1	3.755668	0.070862	53
ADGRD1	4.190215	0.349185	12	PCDHGA4	3.755668	0.073641	51
TNS3	3.750401	0.312533	12	PCDHGB2	3.755668	0.076646	49
RAD51B	4.047182	0.367926	11	PCDHGA5	3.755668	0.079908	47

PCDHGB3	3.755668	0.087341	43	BAIAP2	4.480791	0.298719	15
HDAC4	16.18352	0.437393	37	IQSEC1	6.483397	0.4631	14
PCDHGA7	3.755668	0.101505	37	CUX1	5.545862	0.396133	14
RBFOX3	10.2518	0.292908	35	PRKAG2	5.327675	0.380548	14
PAX6	7.480697	0.213734	35	C7orf50	4.800099	0.342864	14
PCDHGB4	3.755668	0.107305	35	ARHGEF10	4.360194	0.311442	14
PCDHGA8	3.755668	0.107305	35	MOB2	3.909447	0.279246	14
DIP2C	6.618094	0.206815	32	MSI2	6.564374	0.504952	13
PCDHGB5	3.755668	0.117365	32	MYT1L	5.843539	0.449503	13
SOX2-OT	10.14846	0.349947	29	GSE1	4.535568	0.34889	13
GALNT9	12.59928	0.46664	27	RFX4	3.880353	0.298489	13
ADARB2	6.984609	0.268639	26	CLYBL	3.800938	0.29238	13
SHANK2	3.576848	0.137571	26	ZC3H3	6.596127	0.549677	12
CAMTA1	10.48882	0.419553	25	FBRSL1	4.890676	0.407556	12
AGAP1	8.930669	0.357227	25	CMIP	4.778508	0.398209	12
SATB2	4.666845	0.194452	24	MAML3	4.161716	0.34681	12
MEIS1	4.566273	0.190261	24	RAD51B	4.162748	0.378432	11
RPTOR	9.535014	0.414566	23	SLC38A10	4.026507	0.366046	11
NCOR2	7.285519	0.316762	23	AKAP13	5.211785	0.521178	10
NXN	6.055428	0.263279	23	AUTS2	4.624032	0.462403	10
RIMBP2	5.965647	0.259376	23	TSPAN4	3.669455	0.366946	10
INPP5A	5.795189	0.251965	23	ATP11A	5.709846	0.634427	9
PRKCZ	9.59318	0.436054	22	AXIN2	5.384306	0.598256	9
SKI	8.127488	0.387023	21	SND1	5.220556	0.580062	9
FRMD4A	5.105498	0.255275	20	ADAMTS2	5.121794	0.569088	9
ABR	4.470979	0.223549	20	TSPAN9	4.387251	0.487472	9
SDK1	3.740007	0.187	20	ASAP1	4.383918	0.487102	9
MAD1L1	14.70789	0.774099	19	CACNA2D4	4.234207	0.470467	9
SMG1P2	6.317952	0.332524	19	GPC6	3.728289	0.414254	9
BOLA2	6.317952	0.332524	19	VRK2	11.87504	1.484379	8
LOC613038	6.317952	0.332524	19	PPP2R2B	5.757154	0.719644	8
CASZ1	5.713871	0.30073	19	POU6F2	4.305534	0.538192	8
ZNF423	4.570964	0.240577	19	DNMT3A	3.872041	0.484005	8
KCNQ1	4.169022	0.219422	19	DGKG	5.205547	0.74365	7
RBFOX1	5.531657	0.307314	18	TRAK1	4.530712	0.755119	6
ANKRD11	4.37895	0.243275	18	CRADD	4.031996	0.671999	6
TBC1D16	4.136146	0.229786	18	FBXL18	3.823593	0.637265	6
FO XK1	3.841966	0.213443	18	PBX1	3.588716	0.598119	6
PAX6-AS1	5.58225	0.328368	17	DNAJC17	3.582465	0.597078	6
RCN1	5.58225	0.328368	17	TSNAX-DISC1	4.381651	0.87633	5
OPCML	4.51488	0.265581	17	CPEB1-AS1	3.876459	0.775292	5
FOXP1	7.148465	0.446779	16	GSG1	3.838918	0.95973	4
NAV2	4.558608	0.284913	16	CHTF18	4.578998	2.289499	2
SORBS2	3.795118	0.237195	16				
NFIX	5.333722	0.355581	15	TABLE 109:	Cancer Type	MB_G34_V	
ZBTB20	5.109232	0.340615	15	Gene site	imp_sum	imp_mean	n
KNDC1	5.067394	0.337826	15	PTPRN2	15.02368	0.183216	82
GLI2	4.87772	0.325181	15	PRDM16	13.41886	0.188998	71

PCDHGA1	3.065898	0.051964	59	ZBTB20	3.68549	0.245699	15
PCDHGA2	3.065898	0.053788	57	BAIAP2	3.120851	0.208057	15
PCDHGA3	3.065898	0.056776	54	C7orf50	5.481035	0.391503	14
PCDHGB1	3.065898	0.057847	53	IQSEC1	4.496178	0.321156	14
PCDHGA4	3.16386	0.062036	51	PRKAG2	4.202065	0.300148	14
PCDHGB2	3.16386	0.064569	49	MIR548F5	3.680712	0.262908	14
PCDHGA5	3.16386	0.067316	47	ARHGEF10	3.628172	0.259155	14
HDAC4	17.31966	0.468099	37	CACNA1H	3.292159	0.235154	14
PAX6	8.428562	0.240816	35	RPS6KA2	2.986116	0.213294	14
RBFOX3	3.922926	0.112084	35	CUX1	2.968351	0.212025	14
DIP2C	2.991318	0.093479	32	MSI2	6.420698	0.4939	13
SOX2-OT	5.144005	0.177379	29	MYT1L	5.041558	0.387812	13
GALNT9	10.38172	0.384508	27	KIF26B	3.1165	0.239731	13
SHANK2	4.511083	0.173503	26	FBRSL1	5.282675	0.440223	12
ADARB2	3.52234	0.135475	26	CMIP	3.938958	0.328246	12
CAMTA1	8.519389	0.340776	25	GNAI2	3.670793	0.305899	12
AGAP1	6.689657	0.267586	25	ADGRD1	3.100876	0.258406	12
PDGFRA	4.069607	0.162784	25	RAD51B	3.753865	0.34126	11
RPTOR	8.105897	0.35243	23	TBCD	3.148106	0.286191	11
NCOR2	6.317118	0.274657	23	AUTS2	5.178221	0.517822	10
RIMBP2	6.002695	0.260987	23	LMF1	3.745211	0.374521	10
INPP5A	5.458839	0.237341	23	KCNIP4	3.594265	0.359426	10
NXN	4.695211	0.20414	23	AKAP13	3.474133	0.347413	10
PRKCZ	4.592679	0.208758	22	STK32C	3.223752	0.322375	10
SKI	6.257065	0.297955	21	SNTG2	3.181238	0.318124	10
ZIC4	3.985685	0.189795	21	SND1	5.78745	0.64305	9
ABR	4.831867	0.241593	20	ATP11A	5.549079	0.616564	9
SDK1	4.369185	0.218459	20	ADAMTS2	5.070177	0.563353	9
MAD1L1	15.70623	0.826644	19	AXIN2	4.408033	0.489781	9
CASZ1	6.481234	0.341118	19	CACNA2D4	3.86314	0.429238	9
ZNF423	5.926592	0.311926	19	GPC6	3.508593	0.389844	9
SMG1P2	5.729856	0.301571	19	TRAPPC12	3.361639	0.373515	9
BOLA2	5.729856	0.301571	19	PACS2	3.019137	0.33546	9
LOC613038	5.729856	0.301571	19	APBA2	2.968133	0.329793	9
ANKRD11	4.661094	0.25895	18	VRK2	6.038017	0.754752	8
FO XK1	4.579725	0.254429	18	PPP2R2B	4.733325	0.591666	8
SEPTIN9	3.983606	0.221311	18	MSRA	3.190686	0.398836	8
RBFOX1	3.736773	0.207599	18	LHX4	3.165907	0.395738	8
SIM1	6.169379	0.362905	17	CACHD1	3.077802	0.384725	8
OPCML	6.068681	0.356981	17	PITPNC1	4.553902	0.650557	7
TBX15	3.817539	0.224561	17	TRAK1	3.987901	0.66465	6
PAX6-AS1	3.360435	0.197673	17	FBXL18	3.290669	0.548445	6
RCN1	3.360435	0.197673	17	TSNAX-DISC1	4.152699	0.83054	5
FOXP1	7.540532	0.471283	16	ARHGEF7	4.077908	0.815582	5
NAV2	3.306268	0.206642	16	RUNDC3A	3.27271	0.654542	5
GLI2	4.726612	0.315107	15	NPHP4	3.018238	0.603648	5
KIRREL3	4.323392	0.288226	15	EXT1	3.188407	0.797102	4
KNDC1	4.300115	0.286674	15	TUBA1C	3.059964	0.764991	4

SLC25A22	3.133245	1.044415	3	OPCML	4.070115	0.239419	17
ANKLE2	4.199293	2.099646	2	FOXP1	6.653114	0.41582	16
TABLE 110:	Cancer Type	MB_G34_VI	n	NAV2	3.306215	0.206638	16
				KNDC1	4.03037	0.268691	15
Gene site	imp_sum	imp_mean	n	BAIAP2	3.990254	0.266017	15
PTPRN2	10.17979	0.124144	82	GLI2	3.975502	0.265033	15
PRDM16	11.67227	0.164398	71	NFIX	3.914943	0.260996	15
PCDHGA1	3.480246	0.058987	59	COL23A1	3.42571	0.228381	15
PCDHGA2	3.480246	0.061057	57	ZBTB20	3.248796	0.216586	15
PCDHGA3	3.16386	0.05859	54	RPS6KA2	5.475875	0.391134	14
PCDHGB1	3.16386	0.059695	53	ARHGEF10	5.037701	0.359836	14
PCDHGA4	3.16386	0.062036	51	CUX1	4.752663	0.339476	14
PCDHGB2	3.16386	0.064569	49	IQSEC1	4.448833	0.317774	14
PCDHGB3	3.16386	0.073578	43	CACNA1H	4.134716	0.295337	14
HDAC4	9.744729	0.263371	37	PRKAG2	3.83548	0.273963	14
PAX6	8.568253	0.244807	35	C7orf50	3.718669	0.265619	14
RBFOX3	8.19285	0.234081	35	MSI2	5.875307	0.451947	13
DIP2C	6.787527	0.21211	32	MYT1L	4.451341	0.342411	13
SOX2-OT	4.234859	0.14603	29	RFX4	3.148192	0.242169	13
GALNT9	5.760336	0.213346	27	FBRSL1	4.537368	0.378114	12
SHANK2	3.358318	0.129166	26	ZC3H3	4.41386	0.367822	12
CAMTA1	9.053347	0.362134	25	CMIP	3.487553	0.290629	12
AGAP1	7.179943	0.287198	25	GNA12	3.230051	0.269171	12
PDGFRA	3.471099	0.138844	25	CSMD1	3.219359	0.26828	12
RPTOR	8.284353	0.360189	23	RAD51B	3.769786	0.342708	11
NXN	5.924414	0.257583	23	ANAPC16	3.663236	0.333021	11
NCOR2	5.889471	0.256064	23	AUTS2	5.381906	0.538191	10
INPP5A	5.523952	0.240172	23	FMN1	3.894166	0.389417	10
PRKCZ	5.805273	0.263876	22	AKAP13	3.674493	0.367449	10
SKI	8.221779	0.391513	21	SPPL2B	3.110089	0.311009	10
SIM2	3.126904	0.1489	21	ADAMTS2	5.97969	0.66441	9
FRMD4A	5.072868	0.253643	20	AXIN2	4.644633	0.51607	9
ABR	4.938759	0.246938	20	CACNA2D4	4.153062	0.461451	9
SDK1	3.616258	0.180813	20	TSPAN9	4.120196	0.4578	9
MAD1L1	15.08777	0.794093	19	ATP11A	3.821801	0.424645	9
CASZ1	7.558691	0.397826	19	SND1	3.648233	0.405359	9
SMG1P2	5.981934	0.314839	19	GPC6	3.634651	0.40385	9
BOLA2	5.981934	0.314839	19	ASAP1	3.191981	0.354665	9
LOC613038	5.981934	0.314839	19	SSBP3	3.112073	0.345786	9
ZNF423	3.774906	0.198679	19	VRK2	7.861226	0.982653	8
ANKRD11	5.977816	0.332101	18	PPP2R2B	4.859435	0.607429	8
FO XK1	5.126775	0.284821	18	CACHD1	3.485521	0.43569	8
RBFOX1	4.580482	0.254471	18	DLEU1	3.438064	0.429758	8
TBC1D16	4.244049	0.235781	18	SYNJ2	3.288412	0.411051	8
SEPTIN9	3.720862	0.206715	18	PITPNC1	4.366461	0.62378	7
HOXA3	3.192502	0.177361	18	MIR124-2HG	3.521223	0.503032	7
SIM1	4.398925	0.25876	17	NAV1	3.352132	0.478876	7
TBX15	4.300947	0.252997	17	TRAK1	4.023501	0.670584	6

FBXL18	3.697156	0.616193	6	SEPTIN9	4.576042	0.254225	18
MYO16	3.325326	0.554221	6	FOXK1	4.219129	0.234396	18
KDM4B	3.154782	0.525797	6	SIM1	5.678352	0.334021	17
TSNAX-DISC1	4.513548	0.90271	5	PAX6-AS1	4.920365	0.289433	17
ARHGEF7	3.418039	0.683608	5	RCN1	4.920365	0.289433	17
PRR5L	3.178152	0.63563	5	OPCML	4.643683	0.273158	17
DAGLB	3.126133	1.042044	3	FOXP1	4.504852	0.281553	16
ANKLE2	4.27943	2.139715	2	NAV2	4.067416	0.254213	16
CHTF18	3.98205	1.991025	2	BAIAP2	4.327026	0.288468	15
				KNDC1	4.062649	0.270843	15
TABLE 111:	Cancer Type MB_G34_VII			GLI2	3.871486	0.258099	15
Gene site	imp_sum	imp_mean	n	NFIX	3.67403	0.244935	15
PTPRN2	17.04639	0.207883	82	ZBTB20	3.399125	0.226608	15
PRDM16	11.53801	0.162507	71	RPS6KA2	6.006307	0.429022	14
PCDHGA4	3.418749	0.067034	51	MIR548F5	5.164099	0.368864	14
PCDHGB2	3.418749	0.06977	49	C7orf50	4.769793	0.340699	14
PCDHGA5	3.418749	0.072739	47	CUX1	4.451564	0.317969	14
PCDHGB3	3.418749	0.079506	43	PRKAG2	4.423848	0.315989	14
PCDHGA6	3.304608	0.082615	40	ARHGEF10	3.474581	0.248184	14
HDAC4	10.74833	0.290495	37	MOB2	3.466234	0.247588	14
PAX6	12.88611	0.368175	35	MSI2	6.747519	0.51904	13
RBFOX3	7.249014	0.207115	35	MYT1L	5.256997	0.404384	13
DIP2C	4.86296	0.151968	32	GSE1	3.864862	0.297297	13
SOX2-OT	4.555504	0.157086	29	RFX4	3.106126	0.238933	13
GALNT9	8.297959	0.307332	27	FBRSL1	6.470299	0.539192	12
SHANK2	6.660721	0.256182	26	ZC3H3	4.847501	0.403958	12
CAMTA1	8.372982	0.334919	25	CMIP	4.417143	0.368095	12
AGAP1	7.769507	0.31078	25	GNA12	3.368387	0.280699	12
SATB2	3.540531	0.147522	24	ADGRD1	3.31883	0.276569	12
RPTOR	8.809254	0.383011	23	COL4A1	3.846087	0.349644	11
NCOR2	6.919265	0.300838	23	TBCD	3.438012	0.312547	11
NXN	5.018761	0.218207	23	SLC38A10	3.411534	0.310139	11
INPP5A	4.405626	0.191549	23	AUTS2	5.079352	0.507935	10
RIMBP2	3.938363	0.171233	23	AKAP13	4.669508	0.466951	10
PRKCZ	6.917698	0.314441	22	CHST11	3.239795	0.323979	10
SKI	5.83892	0.278044	21	FMN1	3.198852	0.319885	10
ABR	5.347094	0.267355	20	ADAMTS2	6.019738	0.66886	9
FRMD4A	4.905347	0.245267	20	ASAP1	5.521091	0.613455	9
SDK1	4.260924	0.213046	20	SND1	4.862382	0.540265	9
MAD1L1	16.30223	0.858012	19	ATP11A	4.324377	0.480486	9
CASZ1	7.001381	0.368494	19	CACNA2D4	4.292604	0.476956	9
SMG1P2	6.849276	0.360488	19	AXIN2	4.107988	0.456443	9
BOLA2	6.849276	0.360488	19	TRAPPC12	3.656299	0.406255	9
LOC613038	6.849276	0.360488	19	TSPAN9	3.573777	0.397086	9
ZNF423	4.929504	0.259448	19	GPC6	3.34619	0.371799	9
KCNQ1	3.717288	0.195647	19	VRK2	9.410478	1.17631	8
ANKRD11	6.106655	0.339259	18	PPP2R2B	5.123059	0.640382	8
TBC1D16	4.832975	0.268499	18	AFF3	3.560936	0.445117	8

DNMT3A	3.505303	0.438163	8	CASZ1	4.483706	0.235985	19
MSRA	3.282092	0.410261	8	SEPTIN9	6.234626	0.346368	18
MACROD1	3.237537	0.404692	8	ANKRD11	5.754369	0.319687	18
GAK	5.338333	0.762619	7	TBC1D16	2.862671	0.159037	18
PITPNC1	4.266097	0.609442	7	PAX6-AS1	4.611682	0.271275	17
KDM4B	3.779773	0.629962	6	RCN1	4.611682	0.271275	17
TRAK1	3.520526	0.586754	6	OPCML	4.231436	0.248908	17
FBXL18	3.426544	0.571091	6	FOXP1	5.111416	0.319464	16
COLEC11	3.399725	0.566621	6	NAV2	3.395159	0.212197	16
MYO16	3.249272	0.541545	6	GLI2	3.746676	0.249778	15
TSNAX-DISC1	4.644008	0.928802	5	BAIAP2	3.302877	0.220192	15
VAV2	3.821501	0.7643	5	RPS6KA2	5.857572	0.418398	14
ARHGEF7	3.681206	0.736241	5	C7orf50	5.496564	0.392612	14
EXT1	3.487271	0.871818	4	CACNA1H	5.012177	0.358013	14
ANKLE2	4.23297	2.116485	2	CUX1	4.071116	0.290794	14
CHTF18	4.140574	2.070287	2	IQSEC1	3.653357	0.260954	14
				ARHGEF10	3.255632	0.232545	14
				MIR548F5	3.212982	0.229499	14
				PPP2R2A	3.103164	0.221655	14
				PRKAG2	2.953235	0.210945	14
				MSI2	5.642549	0.434042	13
				GSE1	4.189249	0.32225	13
				MYT1L	3.556903	0.273608	13
				FBRSL1	5.232895	0.436075	12
				ZC3H3	4.260363	0.35503	12
				TNS3	3.420782	0.285065	12
				CMIP	3.288465	0.274039	12
				RASA3	3.00796	0.250663	12
				ADGRD1	2.850136	0.237511	12
				LMF1	3.80437	0.380437	10
				AUTS2	3.525084	0.352508	10
				KCNIP4	3.505412	0.350541	10
				AKAP13	3.444648	0.344465	10
				SPPL2B	2.931918	0.293192	10
				NBEA	2.856603	0.28566	10
				ADAMTS2	5.84082	0.64898	9
				ATP11A	5.816007	0.646223	9
				SND1	4.531475	0.503497	9
				ASAP1	4.478279	0.497587	9
				TSPAN9	3.791592	0.421288	9
				TRAPPC12	3.668458	0.407606	9
				AXIN2	3.446436	0.382937	9
				CACNA2D4	3.32849	0.369832	9
				MGMT	3.227272	0.358586	9
				GPC6	3.028942	0.336549	9
				KCNMA1	2.827183	0.314131	9
				VRK2	6.931173	0.866397	8
				PPP2R2B	4.915064	0.614383	8

TABLE 112: Cancer Type MB_G34_VIII			
Gene site	imp_sum	imp_mean	n
PTPRN2	12.41194	0.151365	82
PRDM16	9.171053	0.12917	71
PCDHGA5	2.847474	0.060585	47
HDAC4	19.15223	0.517628	37
RBFOX3	7.021825	0.200624	35
PAX6	5.771277	0.164894	35
DIP2C	7.083844	0.22137	32
GALNT9	8.220999	0.304481	27
SHANK2	5.171992	0.198923	26
ADARB2	3.869727	0.148836	26
AGAP1	7.03262	0.281305	25
CAMTA1	6.648568	0.265943	25
PDGFRA	3.818061	0.152722	25
RPTOR	8.99687	0.391168	23
NCOR2	5.77417	0.251051	23
INPP5A	5.710913	0.248301	23
NXN	4.916837	0.213776	23
RIMBP2	3.734723	0.162379	23
PRKCZ	4.604762	0.209307	22
SKI	8.27076	0.393846	21
ABR	3.627221	0.181361	20
FRMD4A	3.288809	0.16444	20
MAD1L1	14.58326	0.76754	19
SMG1P2	6.073956	0.319682	19
BOLA2	6.073956	0.319682	19
LOC613038	6.073956	0.319682	19
ZNF423	5.20503	0.273949	19
KCNQ1	4.682545	0.24645	19

MSRA	3.678484	0.459811	8	NXN	3.259735	0.141728	23
DNMT3A	3.518789	0.439849	8	INPP5A	2.909853	0.126515	23
DLEU1	2.818785	0.352348	8	PRKCZ	2.154902	0.09795	22
GAK	3.810517	0.54436	7	SKI	4.584725	0.21832	21
PLEC	2.924521	0.417789	7	MAD1L1	8.264018	0.434948	19
COLEC11	3.272893	0.545482	6	CASZ1	4.00511	0.210795	19
FBXL18	2.993867	0.498978	6	SMG1P2	3.599582	0.189452	19
TRAK1	2.924649	0.487442	6	BOLA2	3.599582	0.189452	19
TSNAX-DISC1	5.124489	1.024898	5	LOC613038	3.599582	0.189452	19
EXPH5	3.453852	0.69077	5	ZNF423	2.44059	0.128452	19
ARHGEF7	3.007099	0.60142	5	FOXK1	2.97292	0.165162	18
NPHP4	2.860235	0.572047	5	TBC1D16	2.75853	0.153252	18
KIAA1522	3.621688	0.905422	4	SEPTIN9	2.343916	0.130218	18
SLC25A22	3.098151	1.032717	3	TBX15	3.458112	0.203418	17
DAGLB	2.998599	0.999533	3	HBG2	2.126484	0.125087	17
RASGRP3	2.837226	0.945742	3	FOXP1	5.347217	0.334201	16
ANKLE2	4.310693	2.155347	2	NAV2	2.471203	0.15445	16
CHTF18	3.302048	1.651024	2	EBF3	1.916364	0.119773	16
UHRF1	3.16184	1.58092	2	KNDC1	3.930209	0.262014	15
KIF21B	2.987182	1.493591	2	BAIAP2	3.588691	0.239246	15
SLC25A10	2.855353	1.427677	2	ZBTB20	3.235695	0.215713	15
KCNV2	2.984463	2.984463	1	SYCP2L	5.723577	0.408827	14
DDT	2.922807	2.922807	1	IQSEC1	3.736916	0.266923	14
ARL6IP6	2.877777	2.877777	1	CUX1	3.402324	0.243023	14
				C7orf50	3.341656	0.23869	14
TABLE 113:	Cancer Type MB_MYO			PRKAG2	2.335498	0.166821	14
Gene site	imp_sum	imp_mean	n	CACNA1H	2.27144	0.162246	14
PTPRN2	3.785764	0.046168	82	ARHGEF10	2.023279	0.14452	14
PRDM16	8.662869	0.122012	71	RPS6KA2	1.898316	0.135594	14
PCDHGA1	2.905979	0.049254	59	MYT1L	3.01092	0.231609	13
PCDHGA2	2.589593	0.045431	57	GSE1	2.81954	0.216888	13
PCDHGA3	2.273207	0.042096	54	RFX4	2.068167	0.15909	13
PCDHGB1	2.273207	0.042891	53	MEGF6	2.437108	0.203092	12
PCDHGA4	2.273207	0.044573	51	FBRSL1	2.331273	0.194273	12
PCDHGB2	2.273207	0.046392	49	GNA12	2.069569	0.172464	12
PCDHGA5	2.273207	0.048366	47	TFAP2B	3.312113	0.331211	10
PCDHGB3	1.956821	0.045507	43	AKAP13	3.253774	0.325377	10
HDAC4	8.08646	0.218553	37	NBEA	2.197763	0.219776	10
PAX6	3.196964	0.091342	35	FMN1	2.093129	0.209313	10
DIP2C	2.964181	0.092631	32	SND1	4.095694	0.455077	9
SOX2-OT	3.704058	0.127726	29	TSPAN9	3.126332	0.34737	9
AGAP1	4.754946	0.190198	25	CACNA2D4	3.069865	0.341096	9
CAMTA1	3.193667	0.127747	25	ADAMTS2	2.8411	0.315678	9
MEIS1	3.63319	0.151383	24	ATP11A	2.667221	0.296358	9
SATB2	1.996545	0.083189	24	AXIN2	2.122505	0.235834	9
RPTOR	6.711731	0.291814	23	DNMT3A	2.986323	0.37329	8
RIMBP2	4.09283	0.177949	23	PPP2R2B	2.506865	0.313358	8
NCOR2	3.267564	0.142068	23	RORA	2.125144	0.265643	8

LINC00311	2.025461	0.253183	8	PCDHGA2	8.916148	0.156424	57
ASPSR1	2.025297	0.253162	8	PCDHGA3	7.587891	0.140517	54
SMAD3	1.887128	0.235891	8	PCDHGA3	7.51521	0.139171	54
RXRA	2.000038	0.28572	7	PCDHGA3	8.916148	0.165114	54
EBF2	1.964235	0.280605	7	PCDHGB1	7.587891	0.143168	53
ARHGAP18	3.172124	0.528687	6	PCDHGB1	7.51521	0.141796	53
MYO16	2.570597	0.428433	6	PCDHGB1	8.916148	0.168229	53
COLEC11	2.317683	0.386281	6	PCDHGA4	7.587891	0.148782	51
MIR548G	2.237624	0.372937	6	PCDHGA4	7.51521	0.147357	51
CRADD	2.050473	0.341746	6	PCDHGA4	8.916148	0.174826	51
CCDC177	1.921631	0.320272	6	PCDHGB2	7.503957	0.153142	49
TSNAX-DISC1	2.117145	0.423429	5	PCDHGB2	6.882438	0.140458	49
VAV2	1.991836	0.398367	5	PCDHGB2	8.283376	0.169048	49
SHOX2	1.910358	0.382072	5	PCDHGA5	6.543723	0.139228	47
CPE	2.202064	0.550516	4	PCDHGA5	5.867063	0.124831	47
IGSF21	1.982063	0.495516	4	PCDHGA5	7.370543	0.15682	47
LOC339874	2.815089	0.938363	3	PCDHGB3	6.227337	0.144822	43
WNT16	2.546151	0.848717	3	PCDHGB3	5.452341	0.126799	43
DICER1	2.539719	0.846573	3	PCDHGB3	6.251393	0.145381	43
CHID1	2.469217	0.823072	3	PCDHGA6	6.543723	0.163593	40
SLC1A7	2.178243	0.726081	3	PCDHGA6	5.321472	0.133037	40
BFSP2	1.97466	0.65822	3	PCDHGA6	5.935007	0.148375	40
ANKLE2	3.431389	1.715695	2	HDAC4	11.44288	0.309267	37
CHTF18	2.845109	1.422554	2	PCDHGA7	5.49864	0.148612	37
UTRN	2.535066	1.267533	2	HDAC4	9.878771	0.266994	37
DISC1	1.968634	0.984317	2	PCDHGA7	4.899938	0.132431	37
KIF21B	1.874384	0.937192	2	HDAC4	7.008804	0.189427	37
ARL6IP6	2.61283	2.61283	1	HDAC4	9.624697	0.260127	37
DDT	2.59893	2.59893	1	PCDHGA7	5.302235	0.143304	37
DNAJC27	2.220019	2.220019	1	RBFOX3	8.400886	0.240025	35
DLG4	1.974717	1.974717	1	PAX6	5.800011	0.165715	35
				PCDHGB4	5.182254	0.148064	35
				PCDHGA8	5.182254	0.148064	35
				RBFOX3	8.114223	0.231835	35
				PAX6	6.09272	0.174078	35
				PCDHGB4	4.583552	0.130959	35
				PCDHGA8	4.583552	0.130959	35
				RBFOX3	9.113563	0.260388	35
				PAX6	3.406611	0.097332	35
				RBFOX3	6.680933	0.190884	35
				PCDHGB4	5.618621	0.160532	35
				PCDHGA8	5.618621	0.160532	35
				DIP2C	8.48953	0.265298	32
				PCDHGB5	4.95066	0.154708	32
				DIP2C	10.05901	0.314344	32
				PCDHGB5	4.509287	0.140915	32
				DIP2C	6.27013	0.195942	32
				DIP2C	9.408016	0.294001	32

TABLE 114:

Cancer Type
MB_SHH_AD

Gene site	imp_sum	imp_mean	n
PTPRN2	15.1265	0.18447	82
PTPRN2	17.35912	0.211697	82
PTPRN2	12.58685	0.153498	82
PTPRN2	12.13645	0.148005	82
PRDM16	7.907722	0.111376	71
PRDM16	11.0177	0.155179	71
PRDM16	8.809374	0.124076	71
PRDM16	7.679804	0.108166	71
PCDHGA1	7.892189	0.133766	59
PCDHGA1	7.831596	0.132739	59
PCDHGA1	8.916148	0.151121	59
PCDHGA2	7.904277	0.138672	57
PCDHGA2	7.831596	0.137396	57

PCDHGB5	4.717386	0.147418	32	NXN	6.050887	0.263082	23
PCDHGA9	4.634274	0.149493	31	RPTOR	6.854974	0.298042	23
PCDHGA9	4.509287	0.145461	31	NCOR2	6.23076	0.270903	23
PCDHGA9	4.717386	0.152174	31	INPP5A	5.522711	0.240118	23
SOX2-OT	6.737024	0.232311	29	NXN	5.108222	0.222097	23
PCDHGB6	3.660059	0.126209	29	RIMBP2	4.095477	0.178064	23
SOX2-OT	8.048747	0.277543	29	RPTOR	10.69073	0.464814	23
SOX2-OT	5.334916	0.183963	29	RIMBP2	8.17955	0.355633	23
SOX2-OT	9.085177	0.313282	29	NCOR2	5.678988	0.246913	23
PCDHGB6	3.662255	0.126285	29	PCDHA3	4.270382	0.185669	23
PCDHGA10	3.660059	0.130716	28	PRKCZ	5.399293	0.245422	22
PCDHGA10	3.662255	0.130795	28	PRKCZ	6.940502	0.315477	22
GALNT9	2.999202	0.111082	27	PRKCZ	3.781779	0.171899	22
PCDHA2	4.903154	0.181598	27	PRKCZ	5.777631	0.26262	22
PCDHA1	4.903154	0.181598	27	SKI	8.213644	0.391126	21
SHANK2	4.211899	0.161996	26	ZIC4	4.004628	0.190697	21
ADARB2	3.815923	0.146766	26	SKI	8.808682	0.419461	21
ADARB2	6.355375	0.244438	26	ZIC4	5.049453	0.24045	21
SHANK2	5.581315	0.214666	26	SIM2	4.200894	0.200043	21
ADARB2	4.42342	0.170132	26	SKI	6.37787	0.303708	21
SHANK2	4.141465	0.159287	26	ZIC4	5.926099	0.282195	21
ADARB2	4.612131	0.17739	26	SKI	6.428761	0.306131	21
SHANK2	3.884978	0.149422	26	PCDHA4	3.953996	0.188286	21
CAMTA1	7.940562	0.317622	25	ZIC4	3.611484	0.171975	21
AGAP1	7.763085	0.310523	25	ABR	3.90796	0.195398	20
PDGFRA	3.817616	0.152705	25	SDK1	6.719232	0.335962	20
AGAP1	8.738619	0.349545	25	ABR	4.43783	0.221892	20
CAMTA1	8.134202	0.325368	25	FRMD4A	4.326176	0.216309	20
PDGFRA	5.017886	0.200715	25	ABR	3.132036	0.156602	20
CAMTA1	7.419743	0.29679	25	ABR	5.060822	0.253041	20
AGAP1	6.302105	0.252084	25	FRMD4A	4.066681	0.203334	20
PDGFRA	3.972671	0.158907	25	SMG1P2	8.884298	0.467595	19
CAMTA1	6.810666	0.272427	25	BOLA2	8.884298	0.467595	19
AGAP1	5.913963	0.236559	25	LOC613038	8.884298	0.467595	19
PDGFRA	4.733582	0.189343	25	ZNF423	7.177879	0.377783	19
SATB2	3.738509	0.155771	24	MAD1L1	6.614525	0.348133	19
MEIS1	6.011862	0.250494	24	KCNQ1	4.692295	0.246963	19
SATB2	5.746239	0.239427	24	CASZ1	3.789958	0.199471	19
SATB2	4.43271	0.184696	24	SMG1P2	8.900718	0.468459	19
RPTOR	11.98578	0.521121	23	BOLA2	8.900718	0.468459	19
NCOR2	6.236985	0.271173	23	LOC613038	8.900718	0.468459	19
RIMBP2	5.323145	0.231441	23	MAD1L1	7.943356	0.418071	19
NXN	4.909253	0.213446	23	ZNF423	6.41927	0.337856	19
INPP5A	4.781912	0.207909	23	CASZ1	4.631459	0.243761	19
RPTOR	11.83216	0.514442	23	KCNQ1	4.348355	0.228861	19
INPP5A	7.120684	0.309595	23	SMG1P2	7.982796	0.420147	19
NCOR2	6.749041	0.293437	23	BOLA2	7.982796	0.420147	19
RIMBP2	6.364259	0.276707	23	LOC613038	7.982796	0.420147	19

MAD1L1	5.93073	0.312144	19	LOC606724	4.431234	0.295416	15
ZNF423	5.242571	0.275925	19	NFIX	4.404545	0.293636	15
CASZ1	4.876325	0.256649	19	ZBTB20	3.903113	0.260208	15
CFAP46	3.280592	0.172663	19	GLI2	6.532372	0.435491	15
MAD1L1	9.665857	0.508729	19	ZBTB20	3.220659	0.214711	15
SMG1P2	8.480735	0.446354	19	BAIAP2	3.082184	0.205479	15
BOLA2	8.480735	0.446354	19	GLI2	3.915004	0.261	15
LOC613038	8.480735	0.446354	19	DLX6-AS1	3.904856	0.260324	15
ZNF423	7.52162	0.395875	19	PRKAG2	5.408447	0.386318	14
CASZ1	5.039069	0.265214	19	IQSEC1	5.405558	0.386111	14
FOKK1	5.681706	0.31565	18	CUX1	5.352775	0.382341	14
TBC1D16	4.757733	0.264319	18	RPS6KA2	5.138169	0.367012	14
MCF2L	3.771779	0.209543	18	C7orf50	4.980817	0.355773	14
ANKRD11	6.6446	0.369144	18	RPS6KA2	5.705567	0.40754	14
FOKK1	5.729092	0.318283	18	PRKAG2	5.346347	0.381882	14
TBC1D16	5.363412	0.297967	18	C7orf50	4.971	0.355071	14
MCF2L	4.485611	0.249201	18	IQSEC1	4.690514	0.335037	14
FOKK1	3.633137	0.201841	18	CUX1	4.036515	0.288323	14
SEPTIN9	3.042159	0.169009	18	ARHGEF10	3.838387	0.274171	14
ANKRD11	4.928495	0.273805	18	RPS6KA2	4.231365	0.30224	14
TBC1D16	4.497394	0.249855	18	CUX1	4.051786	0.289413	14
FOKK1	3.924434	0.218024	18	PPP2R2A	4.002789	0.285914	14
OPCML	7.221906	0.424818	17	MIR548F5	3.630739	0.259338	14
TBX15	3.633948	0.213762	17	PRKAG2	3.54061	0.252901	14
OPCML	6.749132	0.397008	17	ARHGEF10	3.300672	0.235762	14
SIM1	4.667199	0.274541	17	CACNA1H	3.191626	0.227973	14
TBX15	5.971427	0.35126	17	C7orf50	2.963868	0.211705	14
OPCML	5.473333	0.321961	17	GNG7	2.94343	0.210245	14
TBX15	5.575745	0.327985	17	CUX1	5.722125	0.408723	14
OPCML	5.455402	0.320906	17	RPS6KA2	4.713006	0.336643	14
SIM1	3.704432	0.217908	17	TBX5	3.899536	0.278538	14
EBF3	5.790181	0.361886	16	C7orf50	3.651625	0.26083	14
FOXP1	4.298654	0.268666	16	MSI2	6.083076	0.467929	13
NAV2	3.50322	0.218951	16	CLYBL	4.973501	0.382577	13
EBF3	5.106376	0.319148	16	MYT1L	4.916223	0.378171	13
NAV2	4.965713	0.310357	16	MSI2	6.966227	0.535864	13
FOXP1	4.89795	0.306122	16	CLYBL	5.077306	0.390562	13
NAV2	3.925816	0.245363	16	GSE1	4.599659	0.35382	13
EBF3	4.010135	0.250633	16	MSI2	4.272438	0.328649	13
GLI2	7.440531	0.496035	15	MYT1L	3.438404	0.264493	13
ZBTB20	4.040587	0.269372	15	GSE1	3.425092	0.263469	13
SLX1B-SULT1A4	3.79633	0.253089	15	RFX4	3.082134	0.237087	13
SLX1A	3.79633	0.253089	15	MSI2	5.990683	0.460822	13
LOC606724	3.79633	0.253089	15	CLYBL	4.587194	0.352861	13
GLI2	7.602239	0.506816	15	MYT1L	4.512123	0.347086	13
BAIAP2	4.846091	0.323073	15	MEIS2	4.900008	0.408334	12
SLX1B-SULT1A4	4.431234	0.295416	15	ADGRD1	4.681714	0.390143	12
SLX1A	4.431234	0.295416	15	CMIP	4.430408	0.369201	12

TNS3	4.377581	0.364798	12	RGS12	3.022987	0.302299	10
ZC3H3	4.046952	0.337246	12	SKOR1	4.887111	0.488711	10
MAML3	3.846496	0.320541	12	ACOT7	4.533972	0.453397	10
LRBA	3.637413	0.303118	12	LBX1-AS1	4.171722	0.417172	10
FBRSL1	3.636163	0.303014	12	SH3RF3	3.5777	0.35777	10
FBRSL1	5.48669	0.457224	12	SND1	5.70304	0.633671	9
ZC3H3	4.948896	0.412408	12	ATP11A	5.622162	0.624685	9
MAML3	4.671648	0.389304	12	TRAPPC12	4.436276	0.49292	9
CMIP	4.629361	0.38578	12	TSPAN9	4.162421	0.462491	9
RASA3	4.196058	0.349671	12	ADAMTS2	3.952429	0.439159	9
ADGRD1	4.121606	0.343467	12	SND1	6.390561	0.710062	9
MIRLET7BHG	3.85566	0.321305	12	ATP11A	5.643567	0.627063	9
LRBA	5.184367	0.432031	12	ADAMTS2	4.303716	0.478191	9
ADGRD1	3.957863	0.329822	12	ASAP1	4.066582	0.451842	9
TBX4	3.821608	0.318467	12	TRAPPC12	3.825479	0.425053	9
MIRLET7BHG	3.206211	0.267184	12	TSPAN9	4.932572	0.548064	9
MEIS2	2.957049	0.246421	12	SND1	4.695963	0.521774	9
ZC3H3	4.634894	0.386241	12	ATP11A	4.336107	0.48179	9
FBRSL1	4.454571	0.371214	12	ADAMTS2	3.89938	0.433264	9
RASA3	4.441187	0.370099	12	PAX3	3.546297	0.394033	9
ADGRD1	4.350455	0.362538	12	PACS2	3.341665	0.371296	9
CMIP	3.988099	0.332342	12	RUNX1	3.203476	0.355942	9
TBX4	3.801473	0.316789	12	AXIN2	3.123528	0.347059	9
LRBA	3.722755	0.31023	12	ADAMTS2	5.603878	0.622653	9
MAML3	3.668841	0.305737	12	ATP11A	5.593948	0.62155	9
TNS3	3.624613	0.302051	12	SND1	5.04309	0.560343	9
VGLL4	4.623824	0.420348	11	SLC22A18	3.945131	0.438348	9
CCDC140	4.304976	0.391361	11	TXNRD1	3.837119	0.426347	9
RAD51B	3.648926	0.331721	11	KCNH2	3.78563	0.420626	9
TBCD	3.622455	0.329314	11	TSPAN9	3.637798	0.4042	9
VGLL4	5.236927	0.476084	11	APBA2	3.61274	0.401416	9
CCDC140	4.820168	0.438197	11	SYNJ2	4.734921	0.591865	8
ZC3H12D	3.196704	0.290609	11	LINC00311	4.473012	0.559127	8
CCDC140	4.61614	0.419649	11	PPP2R2B	4.083048	0.510381	8
RAD51B	3.946997	0.358818	11	MCC	3.52537	0.440671	8
ZC3H12D	3.675656	0.334151	11	DLEU1	3.520617	0.440077	8
TSPAN4	4.461114	0.446111	10	MSRA	4.278226	0.534778	8
KLHL29	4.385021	0.438502	10	DNMT3A	4.024289	0.503036	8
AKAP13	4.079004	0.4079	10	NR2E1	4.112219	0.514027	8
TSPAN4	4.902196	0.49022	10	SYNJ2	3.515851	0.439481	8
ACOT7	4.816818	0.481682	10	DLEU1	3.334536	0.416817	8
NR2F1-AS1	4.147053	0.414705	10	LINC00311	3.12969	0.391211	8
SKOR1	4.068187	0.406819	10	MSRA	3.019324	0.377415	8
ACOT7	4.47878	0.447878	10	SYNJ2	4.360336	0.545042	8
NR2F1-AS1	3.503822	0.350382	10	TENM2	3.872294	0.484037	8
TSPAN4	3.394916	0.339492	10	PPP2R2B	3.630106	0.453763	8
GRID1	3.282706	0.328271	10	NAV1	3.829699	0.5471	7
AKAP13	3.113864	0.311386	10	GAK	3.817429	0.545347	7

GAK	4.006282	0.572326	7	CYTH1	3.061654	1.530827	2
NAV1	3.778695	0.539814	7	ANKLE2	6.031201	3.0156	2
EBF2	3.898516	0.556931	7	SLC25A10	3.800057	1.900028	2
NAV1	3.151697	0.450242	7				
NAV1	4.116692	0.588099	7	TABLE 115:	Cancer Type		
FBXL18	3.818437	0.636406	6	Gene site	MB_SHH_IDH		
CRADD	3.713185	0.618864	6	imp_sum	imp_mean	n	
COQ8A	4.501953	0.750325	6	PTPRN2	4.186386	0.051053	82
COQ8A	4.638227	0.773038	6	PRDM16	2.531088	0.035649	71
CRADD	3.676599	0.612767	6	PCDHGA1	6.521723	0.110538	59
FBXL18	3.413187	0.568865	6	PCDHGA2	6.521723	0.114416	57
IRF6	3.056409	0.509402	6	PCDHGA3	6.521723	0.120773	54
COQ8A	4.801492	0.800249	6	PCDHGB1	6.521723	0.123051	53
FBXL18	3.744823	0.624137	6	PCDHGA4	6.521723	0.127877	51
TK1	4.81045	0.96209	5	PCDHGB2	6.205337	0.12664	49
ARHGEF7	4.225031	0.845006	5	PCDHGA5	5.572565	0.118565	47
TSNAX-DISC1	3.942396	0.788479	5	PCDHGB3	5.256179	0.122237	43
TK1	5.723311	1.144662	5	PCDHGA6	5.256179	0.131404	40
AP2A2	5.165172	1.033034	5	PCDHGA7	4.623407	0.124957	37
ARHGEF7	5.051048	1.01021	5	HDAC4	3.15463	0.08526	37
TSNAX-DISC1	4.917045	0.983409	5	PCDHGB4	4.307021	0.123058	35
PRR5L	3.826285	0.765257	5	PCDHGA8	4.307021	0.123058	35
TK1	5.058368	1.011674	5	RBFOX3	3.185196	0.091006	35
TSNAX-DISC1	4.717782	0.943556	5	DIP2C	4.089401	0.127794	32
RUNDC3A	4.234243	0.846849	5	PCDHGB5	3.990635	0.124707	32
AP2A2	3.591004	0.718201	5	PCDHGA9	3.990635	0.12873	31
MRC2	3.551757	0.710351	5	SOX2-OT	8.014506	0.276362	29
ARHGAP27P1	3.505253	0.701051	5	PCDHGB6	3.674249	0.126698	29
PLEKHM1P1	3.505253	0.701051	5	PCDHGA10	3.357863	0.119924	28
ARHGEF7	3.352543	0.670509	5	AGAP1	3.776256	0.15105	25
BTBD9	3.303687	0.660737	5	CAMTA1	3.045261	0.12181	25
TK1	5.499776	1.099955	5	PCDHGB7	3.041477	0.126728	24
TSNAX-DISC1	4.941693	0.988339	5	RIMBP2	3.827594	0.166417	23
AP2A2	4.107508	0.821502	5	PCDHGA11	3.041477	0.132238	23
RUNDC3A	3.708473	0.741695	5	NCOR2	2.477374	0.107712	23
TUBA1C	3.897376	0.974344	4	PRKCZ	2.170949	0.098679	22
DAGLB	3.951956	1.317319	3	SKI	2.502695	0.119176	21
SLC25A22	3.541157	1.180386	3	SIM2	1.927917	0.091806	21
CHID1	3.035271	1.011757	3	ABR	1.811715	0.090586	20
SLC25A22	3.689941	1.22998	3	MAD1L1	4.648104	0.244637	19
ANKLE2	5.964983	2.982492	2	SMG1P2	3.141926	0.165365	19
ANKLE2	6.397189	3.198595	2	BOLA2	3.141926	0.165365	19
DISC1	3.796866	1.898433	2	LOC613038	3.141926	0.165365	19
SLC25A10	3.781775	1.890887	2	CASZ1	1.844257	0.097066	19
ANKLE2	6.209738	3.104869	2	FO XK1	2.800405	0.155578	18
DDX31	3.308125	1.654063	2	TBC1D16	1.770802	0.098378	18
DISC1	3.234475	1.617238	2	HBG2	4.870262	0.286486	17
SLC25A10	3.131187	1.565593	2	SIM1	2.993498	0.176088	17

OPCML	1.755075	0.10324	17	DICER1	2.188384	0.729461	3
TBX15	1.66968	0.098216	17	SRRM3	1.94638	0.648793	3
FOXP1	1.670958	0.104435	16	IGFBPL1	1.873898	0.624633	3
EBF3	1.572011	0.098251	16	LIN28A	1.680143	0.560048	3
GLI2	3.276761	0.218451	15	DERL3	1.619892	0.539964	3
ZBTB20	1.562454	0.104164	15	ANKLE2	5.371886	2.685943	2
PRKAG2	3.090339	0.220739	14	REXO1	1.950061	0.97503	2
PCDHGA12	2.725091	0.194649	14	DDX31	1.909347	0.954674	2
CUX1	2.351194	0.167942	14	SLC25A10	1.732353	0.866176	2
IQSEC1	1.946442	0.139032	14	TBC1D9	1.858811	1.858811	1
SYCP2L	1.889476	0.134963	14	TNRC18P1	1.858811	1.858811	1
SPTBN4	1.707594	0.131353	13				
CTNNA2	2.642407	0.220201	12	TABLE 116:	Cancer Type	MB_WNT	
TBX4	2.423594	0.201966	12	Gene site	imp_sum	imp_mean	n
ISLR2	2.327659	0.193972	12	PTPRN2	10.8371	0.13216	82
FBRSL1	1.630753	0.135896	12	PRDM16	7.265933	0.102337	71
PCDHGC3	2.408705	0.218973	11	HDAC4	17.01119	0.459762	37
NR2F1-AS1	2.429421	0.242942	10	RBFOX3	9.054346	0.258696	35
SLC22A18	3.285046	0.365005	9	PAX6	7.817762	0.223365	35
TXNRD1	2.762601	0.306956	9	DIP2C	6.105956	0.190811	32
ADAMTS2	2.498552	0.277617	9	SOX2-OT	3.383323	0.116666	29
SND1	2.072379	0.230264	9	GALNT9	4.666088	0.172818	27
TRAPPC12	1.727633	0.191959	9	SHANK2	4.975523	0.191366	26
RUNX1	1.620398	0.180044	9	ADARB2	3.712105	0.142773	26
LHX4	3.362207	0.420276	8	CAMTA1	10.199	0.40796	25
DLX5	3.307152	0.413394	8	AGAP1	7.697982	0.307919	25
NR2E1	2.426585	0.303323	8	PDGFRA	3.015656	0.120626	25
SYNJ2	1.978768	0.247346	8	NCOR2	6.786393	0.295061	23
DNMT3A	1.844033	0.230504	8	NXN	6.120921	0.266127	23
NXPH1	1.677876	0.209734	8	RPTOR	5.335037	0.231958	23
AFF3	1.665786	0.208223	8	RIMBP2	4.418345	0.192102	23
TRIM6-TRIM34	2.409658	0.344237	7	INPP5A	4.096703	0.178118	23
DUSP6	2.367342	0.338192	7	PRKCZ	6.825763	0.310262	22
EBF2	1.834614	0.262088	7	SKI	6.771276	0.322442	21
TRIM34	2.409658	0.40161	6	ABR	4.717846	0.235892	20
FBXL18	1.900496	0.316749	6	FRMD4A	3.249455	0.162473	20
EPHA10	1.866265	0.311044	6	MAD1L1	14.32428	0.75391	19
SRCIN1	1.838764	0.306461	6	SMG1P2	6.724541	0.353923	19
RUNDC3A	2.635708	0.527142	5	BOLA2	6.724541	0.353923	19
ARHGEF7	2.408727	0.481745	5	LOC613038	6.724541	0.353923	19
GNAO1	1.918317	0.383663	5	CASZ1	4.353618	0.229138	19
ATP2B4	1.669945	0.333989	5	ZNF423	4.227003	0.222474	19
TSNAX-DISC1	1.66602	0.333204	5	KCNQ1	3.560444	0.187392	19
TK1	1.580119	0.316024	5	ANKRD11	5.201042	0.288947	18
TUBA1C	2.900214	0.725053	4	FOXK1	5.148867	0.286048	18
MLC1	1.992379	0.498095	4	TBC1D16	4.107056	0.22817	18
PPM1H	1.623709	0.405927	4	SEPTIN9	3.389096	0.188283	18
SLC25A22	2.547072	0.849024	3	OPCML	6.012083	0.353652	17

PAX6-AS1	3.072803	0.180753	17	DNMT3A	3.10049	0.387561	8
RCN1	3.072803	0.180753	17	MSRA	3.05823	0.382279	8
NAV2	5.489458	0.343091	16	GAK	4.58643	0.655204	7
BAIAP2	5.041965	0.336131	15	AGO2	3.723265	0.531895	7
GLI2	4.504027	0.300268	15	PLEC	3.578589	0.511227	7
NFIX	3.66554	0.244369	15	PCCA	3.024493	0.43207	7
KNDC1	3.550985	0.236732	15	PITPNC1	3.007431	0.429633	7
ZBTB20	3.330934	0.222062	15	CRADD	4.274558	0.712426	6
KIRREL3	2.97936	0.198624	15	ROR1	3.09436	0.515727	6
SLX1B-SULT1A4	2.966254	0.19775	15	FBXL18	3.034703	0.505784	6
SLX1A	2.966254	0.19775	15	COLEC11	3.00026	0.500043	6
CUX1	6.497046	0.464075	14	TSNAX-DISC1	3.3902	0.67804	5
IQSEC1	5.309558	0.379254	14	NPHP4	2.99828	0.599656	5
PRKAG2	4.103524	0.293109	14	EXT1	2.976673	0.744168	4
RPS6KA2	3.719359	0.265668	14	SLC25A22	3.201603	1.067201	3
CACNA1H	3.524163	0.251726	14	ANKLE2	4.340864	2.170432	2
C7orf50	3.282155	0.23444	14	CHTF18	4.334141	2.16707	2
MOB2	3.113394	0.222385	14	KIF21B	3.020143	1.510072	2
MIR548F5	3.068117	0.219151	14				
GNG7	2.981215	0.212944	14	TABLE 117: Cancer Type MELN			
MYT1L	5.53196	0.425535	13	Gene site	imp_sum	imp_mean	n
MSI2	5.384966	0.414228	13	PTPRN2	20.07972	0.244875	82
CLYBL	3.963235	0.304864	13	PRDM16	11.87507	0.167254	71
RFX4	3.398564	0.261428	13	PCDHGA1	3.96148	0.067144	59
FBRSL1	4.406138	0.367178	12	PCDHGA2	3.96148	0.0695	57
ADGRD1	3.655516	0.304626	12	PCDHGA3	3.960003	0.073333	54
MEGF6	3.627383	0.302282	12	PCDHGB1	3.960003	0.074717	53
ZC3H3	3.613021	0.301085	12	PCDHGA4	3.960003	0.077647	51
CMIP	3.606883	0.300574	12	PCDHGB2	3.960003	0.080816	49
CTNNA2	3.234056	0.269505	12	HDAC4	18.18092	0.491376	37
CTBP2	3.962087	0.36019	11	RBFOX3	5.033948	0.143827	35
COL4A1	3.499449	0.318132	11	PAX6	4.40364	0.125818	35
VGLL4	3.209159	0.291742	11	DIP2C	10.80042	0.337513	32
FMN1	4.202709	0.420271	10	SHANK2	5.242768	0.201645	26
AKAP13	3.692004	0.3692	10	AGAP1	12.02566	0.481026	25
AXIN2	6.344218	0.704913	9	CAMTA1	5.565815	0.222633	25
TSPAN9	6.202349	0.68915	9	PDGFRA	4.404613	0.176185	25
ATP11A	5.78398	0.642664	9	MEIS1	4.675042	0.194793	24
ADAMTS2	5.710575	0.634508	9	RPTOR	10.88275	0.473163	23
SND1	5.235502	0.581722	9	NCOR2	6.702184	0.291399	23
GPC6	3.336133	0.370681	9	INPP5A	5.909184	0.256921	23
SLC22A18	3.32686	0.369651	9	PRKCZ	4.100656	0.186393	22
VRK2	6.942704	0.867838	8	SKI	10.42127	0.496251	21
PPP2R2B	4.533826	0.566728	8	FRMD4A	6.386336	0.319317	20
RORA	4.217902	0.527238	8	SDK1	5.100932	0.255047	20
ASPSCR1	3.717924	0.46474	8	ABR	4.102454	0.205123	20
DLEU1	3.459904	0.432488	8	MAD1L1	11.59755	0.610397	19
LINC00311	3.311936	0.413992	8	CASZ1	5.539392	0.291547	19

KCNQ1	5.170629	0.272138	19	MSRA	4.226066	0.528258	8
SMG1P2	4.905835	0.258202	19	SMAD3	4.156583	0.519573	8
BOLA2	4.905835	0.258202	19	AFF3	4.068188	0.508523	8
LOC613038	4.905835	0.258202	19	LHX4	3.799541	0.474943	8
TBC1D16	8.824067	0.490226	18	MACROD1	3.773525	0.471691	8
ANKRD11	5.752647	0.319591	18	C19orf25	5.557351	0.793907	7
SEPTIN9	5.209593	0.289422	18	ITPK1	4.294166	0.613452	7
FOXK1	5.117212	0.28429	18	VPS13D	3.978662	0.56838	7
OPCML	4.359006	0.256412	17	GAK	3.899819	0.557117	7
FOXP1	5.82112	0.36382	16	MIR548H4	3.870347	0.552907	7
EBF3	5.292018	0.330751	16	NAV1	3.868259	0.552608	7
GLI2	7.458051	0.497203	15	RXRA	3.867873	0.552553	7
ZBTB20	4.374324	0.291622	15	FBXL18	5.400368	0.900061	6
KIRREL3	4.342944	0.28953	15	FMNL2	4.109786	0.684964	6
RPS6KA2	6.474401	0.462457	14	SLC22A18AS	4.041922	0.673654	6
CUX1	6.042582	0.431613	14	RADIL	3.89196	0.64866	6
IQSEC1	5.9396	0.424257	14	KDM4B	3.77629	0.629382	6
C7orf50	5.879431	0.419959	14	TSNAX-DISC1	5.541611	1.108322	5
PRKAG2	5.215217	0.372516	14	RUNDC3A	5.352348	1.07047	5
ARHGEF10	4.90525	0.350375	14	ARHGEF7	4.019536	0.803907	5
GNG7	4.302019	0.307287	14	BCAR1	3.752209	0.750442	5
MSI2	6.601134	0.50778	13	DAGLB	3.877602	1.292534	3
MYT1L	4.80067	0.369282	13	TBC1D7	3.795514	1.265171	3
GSE1	4.797274	0.369021	13	SOX10	4.35304	2.17652	2
RFX4	4.172827	0.320987	13	SLC25A10	3.769522	1.884761	2
CMIP	7.044486	0.58704	12				
FBRSL1	5.539667	0.461639	12	TABLE 118:	Cancer Type	MET_MEL	
TNS3	5.362109	0.446842	12	Gene site	imp_sum	imp_mean	n
GNA12	3.84182	0.320152	12	PTPRN2	23.28815	0.284002	82
MAML3	3.836794	0.319733	12	PRDM16	14.10422	0.198651	71
ZC3H3	3.806348	0.317196	12	PCDHGA1	5.198538	0.088111	59
COL4A1	3.977189	0.361563	11	PCDHGA2	4.775169	0.083775	57
RAD51B	3.939323	0.35812	11	PCDHGA3	4.775169	0.088429	54
TSPAN4	5.621388	0.562139	10	PCDHGB1	4.775169	0.090098	53
RGS12	4.168971	0.416897	10	PCDHGA4	4.458783	0.087427	51
ANKS1B	3.869659	0.386966	10	PCDHGB2	4.458783	0.090996	49
ACOT7	3.84659	0.384659	10	PCDHGA5	4.775169	0.101599	47
FMN1	3.754881	0.375488	10	PCDHGB3	4.799988	0.111628	43
ATP11A	7.987864	0.88754	9	PCDHGA6	4.483602	0.11209	40
SND1	7.076724	0.786303	9	HDAC4	15.6732	0.4236	37
ADAMTS2	5.238921	0.582102	9	PCDHGA7	4.799988	0.129729	37
TSPAN9	4.794222	0.532691	9	PAX6	7.001312	0.200037	35
AXIN2	4.740056	0.526673	9	RBFOX3	6.523178	0.186377	35
TRAPPC12	4.546979	0.50522	9	PCDHGB4	4.799988	0.137143	35
PAX3	3.868641	0.429849	9	PCDHGA8	4.799988	0.137143	35
NOTCH1	3.794656	0.421628	9	DIP2C	8.736887	0.273028	32
SYNJ2	5.876355	0.734544	8	PCDHGB5	4.799988	0.15	32
DLEU1	4.325624	0.540703	8	PCDHGA9	4.799988	0.154838	31

SOX2-OT	6.186026	0.213311	29	TNS3	3.906238	0.32552	12
PCDHGB6	4.799988	0.165517	29	TBX4	3.896038	0.32467	12
PCDHGA10	4.799988	0.171428	28	GNA12	3.760847	0.313404	12
GALNT9	4.480326	0.165938	27	ADGRD1	3.737897	0.311491	12
AGAP1	11.55531	0.462212	25	CCDC140	4.946652	0.449696	11
PDGFRA	5.857961	0.234318	25	COL4A1	4.646674	0.422425	11
MEIS1	4.887093	0.203629	24	RAD51B	3.97844	0.361676	11
PCDHGB7	4.483602	0.186817	24	SPON2	3.963238	0.360294	11
RPTOR	10.90653	0.474197	23	AKAP13	4.293365	0.429336	10
NCOR2	7.582035	0.329654	23	IGF1R	3.950148	0.395015	10
INPP5A	5.808428	0.25254	23	ATP11A	6.829316	0.758813	9
NXN	5.799721	0.252162	23	NOTCH1	4.594711	0.510523	9
RIMBP2	5.085832	0.221123	23	TRAPPC12	4.392991	0.48811	9
PCDHGA11	4.483602	0.194939	23	SND1	4.228188	0.469799	9
SKI	8.010844	0.381469	21	ASAP1	4.089509	0.45439	9
FRMD4A	4.993953	0.249698	20	AXIN2	4.088872	0.454319	9
ABR	4.685585	0.234279	20	SMAD3	4.429079	0.553635	8
MAD1L1	10.65961	0.561032	19	RGS20	4.200273	0.525034	8
ZNF423	5.576102	0.293479	19	VRK2	4.133411	0.516676	8
CASZ1	4.063253	0.213855	19	DLEU1	4.086511	0.510814	8
FO XK1	7.808541	0.433808	18	MSRA	3.881242	0.485155	8
TBC1D16	5.840426	0.324468	18	ASPSCR1	3.834464	0.479308	8
ANKRD11	5.655526	0.314196	18	NAV1	5.274058	0.753437	7
HOXA3	5.018438	0.278802	18	MIR548H4	4.091968	0.584567	7
RBFOX1	3.797883	0.210994	18	GAK	4.045485	0.577926	7
TBX15	4.119351	0.242315	17	ITPK1	3.91298	0.558997	7
OPCML	3.844648	0.226156	17	ANK2	4.362606	0.727101	6
SORBS2	4.419792	0.276237	16	SLC22A18AS	4.105502	0.68425	6
NFIX	4.959722	0.330648	15	RUNDC3A	5.207004	1.041401	5
GLI2	4.953296	0.33022	15	TSNAX-DISC1	4.928417	0.985683	5
BAIAP2	4.818579	0.321239	15	TBC1D7	5.407551	1.802517	3
LRMDA	4.401163	0.293411	15	SOX10	3.859623	1.929812	2
ZBTB20	4.342012	0.289467	15				
KIRREL3	3.914596	0.260973	15				
ARHGEF10	6.140654	0.438618	14	TABLE 119:	Cancer Type	MMNST	
CUX1	5.918096	0.422721	14	Gene site	imp_sum	imp_mean	n
MIR548F5	5.793953	0.413854	14	PRDM16	6.47284	0.091167	71
PRKAG2	5.082395	0.363028	14	PCDHGA1	4.946677	0.083842	59
IQSEC1	4.546697	0.324764	14	PCDHGA2	4.512407	0.079165	57
C7orf50	3.84999	0.274999	14	PCDHGA3	4.424657	0.081938	54
MSI2	5.84468	0.449591	13	PCDHGB1	4.424657	0.083484	53
RFX4	4.729256	0.363789	13	PCDHGA4	4.424657	0.086758	51
MYT1L	4.557003	0.350539	13	PCDHGB2	4.424657	0.090299	49
CMIP	6.193215	0.516101	12	PCDHGA5	4.424657	0.094142	47
FBRSL1	4.591671	0.382639	12	PCDHGB3	4.108271	0.095541	43
ZC3H3	4.200662	0.350055	12	PCDHGA6	4.424657	0.110616	40
LRBA	4.18372	0.348643	12	HDAC4	8.717707	0.235614	37
MIRLET7BHG	4.086926	0.340577	12	PCDHGA7	4.741043	0.128136	37

PAX6	8.339197	0.238263	35	RPS6KA2	3.335163	0.238226	14
PCDHGB4	4.741043	0.135458	35	IQSEC1	3.07831	0.219879	14
PCDHGA8	4.741043	0.135458	35	MIR548F5	2.78253	0.198752	14
RBFOX3	3.738019	0.106801	35	PCDHGA12	2.585121	0.184652	14
DIP2C	5.333114	0.16666	32	C7orf50	2.36413	0.168866	14
PCDHGB5	4.108271	0.128383	32	RFX4	2.46895	0.189919	13
PCDHGA9	4.108271	0.132525	31	CMIP	5.48478	0.457065	12
PCDHGB6	4.108271	0.141665	29	LRBA	3.462573	0.288548	12
SOX2-OT	4.06689	0.140238	29	RASA3	2.827938	0.235661	12
PCDHGA10	3.665331	0.130905	28	ADGRD1	2.730173	0.227514	12
AGAP1	6.318014	0.252721	25	TNS3	2.419795	0.20165	12
CAMTA1	5.243006	0.20972	25	RAD51B	3.190738	0.290067	11
PDGFRA	3.660136	0.146405	25	SORCS2	2.80278	0.254798	11
PCDHGB7	3.665331	0.152722	24	RGS12	3.619502	0.36195	10
RPTOR	6.879654	0.299115	23	ACOT7	3.153595	0.31536	10
NCOR2	3.752568	0.163155	23	KLHL29	2.635382	0.263538	10
PCDHGA11	3.348945	0.145606	23	SH3RF3	2.47046	0.247046	10
INPP5A	3.273184	0.142312	23	FMN1	2.381283	0.238128	10
NXN	3.203231	0.139271	23	ADAMTS2	3.842903	0.426989	9
PRKCZ	3.058926	0.139042	22	AXIN2	3.621175	0.402353	9
SKI	5.061311	0.241015	21	SND1	2.303007	0.25589	9
SIM2	2.404562	0.114503	21	SMAD3	4.347245	0.543406	8
SDK1	3.56718	0.178359	20	DNMT3A	3.593892	0.449237	8
ABR	2.758593	0.13793	20	DLEU1	2.484178	0.310522	8
FRMD4A	2.733413	0.136671	20	MACROD1	2.316054	0.289507	8
MAD1L1	5.8859	0.309784	19	ITPKB	2.876351	0.410907	7
ZNF423	3.740023	0.196843	19	LINC00461	2.545239	0.363606	7
SMG1P2	3.218867	0.169414	19	CCDC177	3.109625	0.518271	6
BOLA2	3.218867	0.169414	19	PBX1	2.471809	0.411968	6
LOC613038	3.218867	0.169414	19	MIR100HG	2.463133	0.410522	6
CASZ1	3.080883	0.162152	19	SLC22A18AS	2.347513	0.391252	6
FO XK1	6.262441	0.347913	18	FBXL18	2.345463	0.39091	6
TBC1D16	4.226576	0.23481	18	RUNDC3A	4.46828	0.893656	5
ANKRD11	3.09493	0.171941	18	CYREN	3.126123	0.625225	5
SEPTIN9	2.591572	0.143976	18	TSNAX-DISC1	3.086616	0.617323	5
PAX6-AS1	4.46816	0.262833	17	KLHL25	2.601482	0.520296	5
RCN1	4.46816	0.262833	17	TBC1D7	2.550573	0.850191	3
FOXP1	3.819536	0.238721	16	RTEL1-			
SORBS2	2.963446	0.185215	16	TNFRSF6B	2.916835	1.458418	2
KIRREL3	3.418558	0.227904	15	RTEL1	2.916835	1.458418	2
GLI2	2.992747	0.199516	15				
NFIX	2.916915	0.194461	15	TABLE 120:	Cancer Type	MNG_ben-1	
SLX1B-SULT1A4	2.708597	0.180573	15	Gene site	imp_sum	imp_mean	n
SLX1A	2.708597	0.180573	15	PTPRN2	13.82051	0.168543	82
LOC606724	2.708597	0.180573	15	PRDM16	11.89894	0.167591	71
CUX1	4.698023	0.335573	14	PCDHGA1	6.849261	0.116089	59
CACNA1H	3.842483	0.274463	14	PCDHGA2	6.849261	0.120162	57
PRKAG2	3.418302	0.244164	14	PCDHGA3	6.532875	0.120979	54

PCDHGB1	6.532875	0.123262	53	GLI2	5.663911	0.377594	15
PCDHGA4	6.849261	0.134299	51	KIRREL3	5.414844	0.36099	15
PCDHGB2	6.849261	0.139781	49	BAIAP2	5.169657	0.344644	15
PCDHGA5	6.849261	0.145729	47	NFIX	4.969003	0.331267	15
PCDHGB3	6.574277	0.15289	43	SLX1B-SULT1A4	4.72077	0.314718	15
PCDHGA6	6.574277	0.164357	40	SLX1A	4.72077	0.314718	15
HDAC4	18.90875	0.511047	37	LOC606724	4.72077	0.314718	15
PCDHGA7	6.257891	0.169132	37	KNDC1	4.688957	0.312597	15
RBFOX3	7.710426	0.220298	35	LRMDA	4.292951	0.286197	15
PCDHGB4	6.257891	0.178797	35	RPS6KA2	8.370342	0.597882	14
PCDHGA8	6.257891	0.178797	35	CUX1	6.066803	0.433343	14
PAX6	5.857744	0.167364	35	IQSEC1	5.85587	0.418276	14
DIP2C	10.83243	0.338514	32	MIR548F5	5.695434	0.406817	14
PCDHGB5	5.625119	0.175785	32	C7orf50	5.470546	0.390753	14
PCDHGA9	5.625119	0.181455	31	PRKAG2	4.775703	0.341122	14
PCDHGB6	4.808758	0.165819	29	ARHGEF10	4.659786	0.332842	14
SOX2-OT	4.578854	0.157892	29	MSI2	6.755835	0.51968	13
PCDHGA10	4.808758	0.171741	28	MYT1L	5.168853	0.397604	13
GALNT9	4.679084	0.173299	27	CMIP	7.54371	0.628643	12
SHANK2	6.49194	0.24969	26	ZC3H3	5.654797	0.471233	12
AGAP1	13.00458	0.520183	25	FBRSL1	5.433467	0.452789	12
CAMTA1	7.461963	0.298479	25	MIRLET7BHG	5.316198	0.443017	12
PDGFRA	5.74881	0.229952	25	TNS3	4.843598	0.403633	12
PCDHGB7	4.422271	0.184261	24	GNA12	4.74899	0.395749	12
RPTOR	12.87515	0.559789	23	CTBP2	4.902419	0.445674	11
NXN	8.33912	0.36257	23	TSPAN4	5.826729	0.582673	10
NCOR2	7.104845	0.308906	23	ACOT7	4.817172	0.481717	10
RIMBP2	6.980383	0.303495	23	AKAP13	4.554964	0.455496	10
INPP5A	6.449253	0.280402	23	ATP11A	8.56874	0.952082	9
SKI	11.38974	0.542368	21	SND1	8.150821	0.905647	9
FRMD4A	6.895792	0.34479	20	ADAMTS2	6.501277	0.722364	9
ABR	5.14037	0.257019	20	NOTCH1	4.88438	0.542709	9
SDK1	4.958414	0.247921	20	AXIN2	4.332555	0.481395	9
MAD1L1	13.22295	0.695945	19	DNMT3A	6.086909	0.760864	8
CASZ1	6.12576	0.322408	19	LINC00311	5.472052	0.684007	8
SMG1P2	5.844299	0.307595	19	MSRA	4.427701	0.553463	8
BOLA2	5.844299	0.307595	19	C19orf25	5.998215	0.856888	7
LOC613038	5.844299	0.307595	19	MIR548H4	5.819089	0.831298	7
KCNQ1	5.469755	0.287882	19	VPS13D	5.39522	0.770746	7
ZNF423	5.039602	0.265242	19	NAV1	5.274197	0.753457	7
FO XK1	10.05902	0.558835	18	STRA6	5.817815	0.969636	6
TBC1D16	7.904142	0.439119	18	FMNL2	5.378446	0.896408	6
MCF2L	6.214789	0.345266	18	FBXL18	4.926141	0.821024	6
SEPTIN9	6.02498	0.334721	18	RUNDC3A	4.808672	0.961734	5
ANKRD11	4.350671	0.241704	18	ARHGEF7	4.74985	0.94997	5
FOXP1	7.817105	0.488569	16	TSNAX-DISC1	4.324226	0.864845	5
NAV2	6.435163	0.402198	16	USP20	4.814654	1.604885	3
ZBTB20	6.143446	0.409563	15				

TABLE 121:	Cancer Type MNG_ben-2			SEPTIN9	6.654283	0.369682	18
				ANKRD11	4.890269	0.271682	18
Gene site	imp_sum	imp_mean	n	MCF2L	4.862958	0.270164	18
PTPRN2	13.45409	0.164074	82	FOXP1	6.013375	0.375836	16
PRDM16	12.3714	0.174245	71	NAV2	5.478894	0.342431	16
PCDHGA1	5.613835	0.09515	59	EBF3	4.702232	0.29389	16
PCDHGA2	5.613835	0.098488	57	NFIX	5.97872	0.398581	15
PCDHGA3	5.575012	0.103241	54	SLX1B-			
PCDHGB1	5.575012	0.105189	53	SULT1A4	5.381892	0.358793	15
PCDHGA4	5.575012	0.109314	51	SLX1A	5.381892	0.358793	15
PCDHGB2	5.575012	0.113776	49	LOC606724	5.381892	0.358793	15
PCDHGA5	5.575012	0.118617	47	KIRREL3	4.943827	0.329588	15
PCDHGB3	4.900676	0.113969	43	ZBTB20	4.615239	0.307683	15
PCDHGA6	4.267904	0.106698	40	BAIAP2	4.598236	0.306549	15
HDAC4	20.05845	0.54212	37	RPS6KA2	9.649029	0.689216	14
PCDHGA7	4.267904	0.115349	37	IQSEC1	6.291758	0.449411	14
PAX6	7.562683	0.216077	35	C7orf50	6.014972	0.429641	14
RBFOX3	7.013312	0.20038	35	PRKAG2	5.576157	0.398297	14
PCDHGB4	4.267904	0.12194	35	MIR548F5	4.577077	0.326934	14
PCDHGA8	4.267904	0.12194	35	CUX1	4.429173	0.316369	14
DIP2C	11.17988	0.349371	32	ARHGEF10	4.400306	0.314308	14
PCDHGB5	4.267904	0.133372	32	GSE1	7.665565	0.589659	13
PCDHGA9	4.267904	0.137674	31	MSI2	5.419438	0.41688	13
SHANK2	6.742333	0.259321	26	MYT1L	4.303207	0.331016	13
ADARB2	4.171369	0.160437	26	CMIP	7.426731	0.618894	12
AGAP1	13.829	0.55316	25	ZC3H3	6.74163	0.561802	12
CAMTA1	6.527083	0.261083	25	GNA12	5.848317	0.48736	12
PDGFRA	5.479023	0.219161	25	RASA3	5.406658	0.450555	12
RPTOR	12.86316	0.559268	23	FBRSL1	5.397095	0.449758	12
NXN	8.208397	0.356887	23	TBX4	5.026797	0.4189	12
NCOR2	7.86704	0.342045	23	ADGRD1	4.534801	0.3779	12
INPP5A	6.254527	0.271936	23	ACOT7	5.775309	0.577531	10
RIMBP2	5.449726	0.236945	23	TSPAN4	5.19165	0.519165	10
PRKCZ	6.528564	0.296753	22	SH3RF3	4.652618	0.465262	10
SKI	11.00161	0.523886	21	AKAP13	4.486244	0.448624	10
FRMD4A	6.074896	0.303745	20	ATP11A	8.379338	0.931038	9
ABR	4.863719	0.243186	20	SND1	8.193473	0.910386	9
SDK1	4.582411	0.229121	20	TSPAN9	6.169591	0.68551	9
MAD1L1	12.37047	0.651078	19	ADAMTS2	4.257765	0.473085	9
CASZ1	6.339035	0.333633	19	AXIN2	4.167995	0.463111	9
ZNF423	5.561251	0.292697	19	DNMT3A	5.873956	0.734245	8
KCNQ1	5.297414	0.278811	19	MSRA	4.879587	0.609948	8
SMG1P2	5.2427	0.275932	19	LINC00311	4.791788	0.598973	8
BOLA2	5.2427	0.275932	19	AFF3	4.572348	0.571543	8
LOC613038	5.2427	0.275932	19	C19orf25	5.705311	0.815044	7
FO XK1	7.706177	0.428121	18	NAV1	5.457155	0.779594	7
TBC1D16	6.940259	0.38557	18	MIR548H4	5.03525	0.719321	7
				VPS13D	4.517048	0.645293	7

CXXC5	4.440766	0.634395	7	SDK1	4.606377	0.230319	20
STRA6	5.02413	0.837355	6	MAD1L1	13.63544	0.717655	19
RADIL	4.864294	0.810716	6	CASZ1	6.490032	0.341581	19
FBXL18	4.811372	0.801895	6	SMG1P2	6.468926	0.34047	19
FMNL2	4.58933	0.764888	6	BOLA2	6.468926	0.34047	19
CRADD	4.280388	0.713398	6	LOC613038	6.468926	0.34047	19
TSNAX-DISC1	5.346518	1.069304	5	KCNQ1	6.287567	0.330925	19
RUNDC3A	4.676827	0.935365	5	ZNF423	5.828266	0.306751	19
ARHGEF7	4.428799	0.88576	5	TBC1D16	8.725799	0.484767	18
				FOXK1	8.629545	0.479419	18
				MCF2L	6.375049	0.354169	18
TABLE 122:	Cancer Type MNG_ben-3						
Gene site	imp_sum	imp_mean	n	SEPTIN9	5.866236	0.325902	18
PTPRN2	20.68387	0.252242	82	FOXP1	7.901613	0.493851	16
PRDM16	15.67589	0.220787	71	EBF3	5.143972	0.321498	16
PCDHGA1	6.053782	0.102606	59	NAV2	4.154127	0.259633	16
PCDHGA2	6.053782	0.106207	57	GLI2	6.306125	0.420408	15
PCDHGA3	6.370168	0.117966	54	KIRREL3	6.113129	0.407542	15
PCDHGB1	6.370168	0.120192	53	ZBTB20	5.936453	0.395764	15
PCDHGA4	6.370168	0.124905	51	BAIAP2	4.920905	0.32806	15
PCDHGB2	5.853512	0.119459	49	NFIX	4.920802	0.328053	15
PCDHGA5	5.853512	0.124543	47	SLX1B-			
PCDHGB3	5.537126	0.12877	43	SULT1A4	4.25033	0.283355	15
PCDHGA6	5.22074	0.130519	40	SLX1A	4.25033	0.283355	15
HDAC4	20.47131	0.553279	37	LOC606724	4.25033	0.283355	15
PCDHGA7	5.22074	0.141101	37	RPS6KA2	9.58383	0.684559	14
RBFOX3	7.450315	0.212866	35	GNG7	5.548519	0.396323	14
PAX6	6.806875	0.194482	35	IQSEC1	5.331153	0.380797	14
PCDHGB4	4.904354	0.140124	35	C7orf50	5.028188	0.359156	14
PCDHGA8	4.904354	0.140124	35	PRKAG2	5.008809	0.357772	14
DIP2C	10.59089	0.330965	32	MIR548F5	4.352643	0.310903	14
PCDHGB5	4.587968	0.143374	32	MSI2	7.327424	0.563648	13
PCDHGA9	4.587968	0.147999	31	GSE1	7.256201	0.558169	13
SHANK2	4.876093	0.187542	26	MYT1L	4.3416	0.333969	13
AGAP1	13.06947	0.522779	25	CMIP	7.483342	0.623612	12
CAMTA1	7.897581	0.315903	25	ZC3H3	6.132744	0.511062	12
PDGFRA	6.972754	0.27891	25	GNA12	5.702648	0.475221	12
MEIS1	6.104129	0.254339	24	FBRSL1	5.368661	0.447388	12
SATB2	4.776486	0.19902	24	MAML3	5.175135	0.431261	12
RPTOR	12.81574	0.557206	23	MIRLET7BHG	4.929492	0.410791	12
NXN	8.906232	0.387227	23	ADGRD1	4.570833	0.380903	12
NCOR2	8.168088	0.355134	23	GLUD1P2	4.151601	0.377418	11
INPP5A	7.309307	0.317796	23	TBCD	4.149873	0.377261	11
HOXB3	5.36647	0.233325	23	ACOT7	5.285428	0.528543	10
RIMBP2	4.571507	0.198761	23	TSPAN4	5.22317	0.522317	10
PRKCZ	6.534716	0.297033	22	FMN1	4.161922	0.416192	10
SKI	10.2754	0.489305	21	SND1	8.359196	0.9288	9
FRMD4A	8.19508	0.409754	20	ATP11A	7.898134	0.87757	9
ABR	4.632685	0.231634	20	ADAMTS2	6.192204	0.688023	9

AXIN2	4.836435	0.537382	9	FRMD4A	6.034431	0.301722	20
CACNA2D4	4.640282	0.515587	9	ABR	5.825177	0.291259	20
LINC00311	4.776345	0.597043	8	MAD1L1	11.00779	0.579357	19
SYNJ2	4.629386	0.578673	8	SMG1P2	6.451549	0.339555	19
DNMT3A	4.550418	0.568802	8	BOLA2	6.451549	0.339555	19
VRK2	4.391817	0.548977	8	LOC613038	6.451549	0.339555	19
MSRA	4.391373	0.548922	8	KCNQ1	6.01296	0.316472	19
C19orf25	6.125387	0.875055	7	CASZ1	5.531977	0.291157	19
NAV1	5.887576	0.841082	7	ZNF423	5.186152	0.272955	19
CXXC5	4.602583	0.657512	7	FOXK1	8.350727	0.463929	18
GAK	4.365581	0.623654	7	SEPTIN9	6.99831	0.388795	18
STRA6	4.980778	0.83013	6	MCF2L	6.022257	0.33457	18
FBXL18	4.916689	0.819448	6	TBC1D16	5.64135	0.313408	18
CRADD	4.235191	0.705865	6	FOXP1	6.280391	0.392524	16
TSNAX-DISC1	5.959609	1.191922	5	NAV2	5.462	0.341375	16
RUNDC3A	4.568501	0.9137	5	EBF3	3.907012	0.244188	16
ARHGEF7	4.229516	0.845903	5	NFIX	6.747804	0.449854	15
				GLI2	6.071155	0.404744	15
TABLE 123:	Cancer Type MNG_int-A			ZBTB20	5.817437	0.387829	15
Gene site	imp_sum	imp_mean	n	KIRREL3	5.119068	0.341271	15
PTPRN2	12.70906	0.154989	82	KNDC1	4.725142	0.315009	15
PRDM16	11.63816	0.163918	71	SLX1B-			
PCDHGA1	5.103482	0.0865	59	SULT1A4	4.604287	0.306952	15
PCDHGA2	5.103482	0.089535	57	SLX1A	4.604287	0.306952	15
PCDHGA3	4.787096	0.08865	54	LOC606724	4.604287	0.306952	15
PCDHGB1	4.787096	0.090323	53	BAIAP2	4.299045	0.286603	15
PCDHGA4	4.47071	0.087661	51	RPS6KA2	8.388311	0.599165	14
PCDHGB2	4.47071	0.091239	49	PRKAG2	5.969594	0.4264	14
PCDHGA5	4.154324	0.08839	47	ARHGEF10	5.511199	0.393657	14
PCDHGB3	3.837938	0.089254	43	C7orf50	5.16093	0.368638	14
HDAC4	18.83304	0.509001	37	IQSEC1	4.830224	0.345016	14
RBFOX3	7.4952	0.214149	35	CUX1	4.348677	0.31062	14
PAX6	6.917716	0.197649	35	GNG7	3.996251	0.285446	14
DIP2C	9.266203	0.289569	32	MSI2	5.972012	0.459386	13
PCDHGB5	3.837938	0.119936	32	GSE1	5.837919	0.449071	13
PCDHGA9	3.837938	0.123804	31	CMIP	7.304481	0.608707	12
GALNT9	6.076149	0.225043	27	FBRSL1	5.400748	0.450062	12
SHANK2	7.525851	0.289456	26	ISLR2	4.337054	0.361421	12
AGAP1	12.5019	0.500076	25	ZC3H3	4.310919	0.359243	12
CAMTA1	5.854312	0.234172	25	GNA12	4.165423	0.347119	12
PDGFRA	5.588541	0.223542	25	MIRLET7BHG	3.974034	0.331169	12
MEIS1	3.891259	0.162136	24	TNS3	3.872449	0.322704	12
RPTOR	14.11158	0.613547	23	TBCD	3.872749	0.352068	11
NXN	9.413313	0.409274	23	VGLL4	3.823593	0.347599	11
INPP5A	7.284435	0.316715	23	CTBP2	3.812363	0.346578	11
NCOR2	6.839873	0.297386	23	ACOT7	4.898796	0.48988	10
PRKCZ	5.423639	0.246529	22	TSPAN4	4.506346	0.450635	10
SKI	10.53312	0.501577	21	SH3RF3	4.276021	0.427602	10

AKAP13	4.268271	0.426827	10	SOX2-OT	3.6476	0.125779	29
CHST11	4.217964	0.421796	10	PCDHGA10	3.863568	0.137985	28
SND1	7.821647	0.869072	9	GALNT9	4.52022	0.167416	27
ATP11A	6.425911	0.71399	9	SHANK2	4.557056	0.175271	26
ADAMTS2	5.261391	0.584599	9	AGAP1	11.67976	0.46719	25
NOTCH1	5.148668	0.572074	9	PDGFRA	6.689215	0.267569	25
TSPAN9	4.710569	0.523397	9	CAMTA1	4.055465	0.162219	25
LINC00311	4.665631	0.583204	8	MEIS1	3.916639	0.163193	24
MACROD1	3.916449	0.489556	8	RPTOR	11.11178	0.483121	23
MSRA	3.844343	0.480543	8	NCOR2	6.268918	0.272562	23
NAV1	5.309092	0.758442	7	RIMBP2	6.09139	0.264843	23
C19orf25	4.837513	0.691073	7	NXN	5.381697	0.233987	23
MIR548H4	4.474154	0.639165	7	INPP5A	4.981406	0.216583	23
VPS13D	4.415997	0.630857	7	HOXB3	4.55696	0.198129	23
CXXC5	3.911578	0.558797	7	PRKCZ	4.330653	0.196848	22
PCCA	3.903166	0.557595	7	SKI	9.446678	0.449842	21
STRA6	5.093259	0.848877	6	SIM2	4.017456	0.191307	21
RADIL	4.962304	0.827051	6	HOXA-AS3	3.580392	0.170495	21
FBXL18	4.351839	0.725306	6	FRMD4A	5.566009	0.2783	20
SLC22A18AS	3.926613	0.654436	6	ABR	3.899798	0.19499	20
GRK5	3.770511	0.628419	6	MAD1L1	11.63535	0.612387	19
TSNAX-DISC1	5.623399	1.12468	5	SMG1P2	6.677326	0.351438	19
ARHGEF7	4.661456	0.932291	5	BOLA2	6.677326	0.351438	19
RUNDC3A	4.656096	0.931219	5	LOC613038	6.677326	0.351438	19
NDST1	3.786943	0.946736	4	CASZ1	5.756259	0.302961	19
TABLE 124: Cancer Type MNG_int-B				KCNQ1	4.439789	0.233673	19
				ZNF423	4.205795	0.221358	19
Gene site	imp_sum	imp_mean	n	FO XK1	7.534776	0.418599	18
PTPRN2	13.88466	0.169325	82	MCF2L	6.120838	0.340047	18
PRDM16	8.173372	0.115118	71	TBC1D16	5.90075	0.327819	18
PCDHGA1	5.065148	0.08585	59	SEPTIN9	4.89401	0.271889	18
PCDHGA2	5.065148	0.088862	57	HOXA3	4.728806	0.262711	18
PCDHGA3	5.511897	0.102072	54	FOXP1	6.315857	0.394741	16
PCDHGB1	5.828283	0.109968	53	NAV2	4.609604	0.2881	16
PCDHGA4	5.511897	0.108076	51	GLI2	4.915242	0.327683	15
PCDHGB2	5.511897	0.112488	49	ZBTB20	4.755149	0.31701	15
PCDHGA5	5.511897	0.117274	47	KIRREL3	4.620703	0.308047	15
PCDHGB3	5.195511	0.120826	43	SLX1B-			
PCDHGA6	4.562739	0.114068	40	SULT1A4	4.161771	0.277451	15
HDAC4	15.7932	0.426843	37	SLX1A	4.161771	0.277451	15
PCDHGA7	4.562739	0.123317	37	LOC606724	4.161771	0.277451	15
PAX6	6.438263	0.18395	35	BAIAP2	3.744433	0.249629	15
PCDHGB4	4.562739	0.130364	35	RPS6KA2	6.906835	0.493345	14
PCDHGA8	4.562739	0.130364	35	PRKAG2	5.427565	0.387683	14
DIP2C	7.867118	0.245847	32	C7orf50	5.391732	0.385124	14
PCDHGB5	4.562739	0.142586	32	IQSEC1	4.600055	0.328575	14
PCDHGA9	4.562739	0.147185	31	GNG7	3.6835	0.263107	14
PCDHGB6	3.863568	0.133226	29	GSE1	5.549748	0.426904	13

MIR548F5	4.155173	0.296798	14	PCDHGA3	3.210092	0.059446	54
GNG7	3.580244	0.255732	14	PCDHGB1	3.210092	0.060568	53
MSI2	5.133305	0.39487	13	PCDHGB2	2.893706	0.059055	49
MYT1L	3.815554	0.293504	13	PCDHGA5	2.893706	0.061568	47
CMIP	6.809888	0.567491	12	HDAC4	16.10253	0.435203	37
ZC3H3	4.398193	0.366516	12	RBFOX3	4.992208	0.142635	35
GNA12	4.310731	0.359228	12	DIP2C	7.020543	0.219392	32
FBRSL1	4.034154	0.33618	12	GALNT9	3.837148	0.142117	27
CTNNA2	3.687655	0.307305	12	SHANK2	4.458318	0.171474	26
ADGRD1	3.647518	0.30396	12	AGAP1	9.868271	0.394731	25
FGFR2	4.0546	0.3686	11	PDGFRA	3.890312	0.155612	25
CTBP2	3.601913	0.327447	11	CAMTA1	3.737071	0.149483	25
ACOT7	5.255968	0.525597	10	RPTOR	8.560527	0.372197	23
TSPAN4	4.289444	0.428944	10	NXN	5.377517	0.233805	23
SH3RF3	3.83336	0.383336	10	NCOR2	4.435836	0.192862	23
IGF1R	3.476465	0.347647	10	INPP5A	4.025097	0.175004	23
OTX1	3.449022	0.344902	10	PRKCZ	3.311051	0.150502	22
ATP11A	7.824007	0.869334	9	SKI	8.789183	0.418533	21
SND1	7.442588	0.826954	9	FRMD4A	4.962322	0.248116	20
ADAMTS2	5.027489	0.55861	9	SDK1	3.806423	0.190321	20
CACNA2D4	3.628826	0.403203	9	ABR	3.53343	0.176672	20
SMAD3	4.239672	0.529959	8	MAD1L1	9.944865	0.523414	19
DNMT3A	3.946081	0.49326	8	CASZ1	5.357683	0.281983	19
VEPH1	3.88798	0.485998	8	SMG1P2	5.102141	0.268534	19
VRK2	3.825472	0.478184	8	BOLA2	5.102141	0.268534	19
DLEU1	3.764402	0.47055	8	LOC613038	5.102141	0.268534	19
LINC00311	3.678141	0.459768	8	KCNQ1	3.579382	0.188389	19
MIR548H4	5.581196	0.797314	7	FO XK1	6.658177	0.369899	18
NAV1	5.02652	0.718074	7	MCF2L	4.412204	0.245122	18
VPS13D	4.911104	0.701586	7	TBC1D16	4.185513	0.232528	18
C19orf25	4.766988	0.680998	7	TBX15	2.980007	0.175295	17
RXRA	3.926521	0.560932	7	FOXP1	6.048305	0.378019	16
FBXL18	3.935586	0.655931	6	EBF3	3.478604	0.217413	16
RADIL	3.842419	0.640403	6	GLI2	5.692075	0.379472	15
STRA6	3.640968	0.606828	6	BAIAP2	4.493922	0.299595	15
TSNAX-DISC1	4.753472	0.950694	5	KIRREL3	4.378257	0.291884	15
RUNDC3A	4.748996	0.949799	5	SLX1B-			
ARHGEF7	3.710766	0.742153	5	SULT1A4	4.125981	0.275065	15
STAP2	3.497874	0.874469	4	SLX1A	4.125981	0.275065	15
NDST1	3.352395	0.838099	4	LOC606724	4.125981	0.275065	15
RALGAPA2	3.456247	1.728124	2	ZBTB20	3.943137	0.262876	15
				NFIX	3.623907	0.241594	15
				RPS6KA2	6.025742	0.43041	14
				IQSEC1	5.110088	0.365006	14
				ARHGEF10	4.474738	0.319624	14
				PRKAG2	3.804304	0.271736	14
				C7orf50	3.55488	0.25392	14
				CUX1	3.121578	0.22297	14

TABLE 126:	Cancer Type MNG_SMARCE1			
Gene site	imp_sum	imp_mean	n	
PTPRN2	12.6468	0.154229	82	
PRDM16	7.651707	0.107771	71	
PCDHGA1	3.526478	0.059771	59	
PCDHGA2	3.526478	0.061868	57	

MSI2	4.770678	0.366975	13	CHTF18	2.949343	1.474671	2
MYT1L	4.076914	0.313609	13				
GSE1	4.001949	0.307842	13	TABLE 127:	Cancer Type	MPNST_Atyp	
CMIP	6.030674	0.502556	12	Gene site	imp_sum	imp_mean	n
FBRSL1	4.65505	0.387921	12	PTPRN2	10.49688	0.128011	82
ZC3H3	3.719253	0.309938	12	PRDM16	9.331638	0.131432	71
ADGRD1	3.181569	0.265131	12	PCDHGA1	4.610238	0.07814	59
CTBP2	3.630217	0.33002	11	PCDHGA2	4.926624	0.086432	57
COL4A1	2.990737	0.271885	11	PCDHGA3	4.926624	0.091234	54
ACOT7	5.373632	0.537363	10	PCDHGB1	4.926624	0.092955	53
GAS7	3.731548	0.373155	10	PCDHGA4	4.926624	0.0966	51
TSPAN4	3.550146	0.355015	10	PCDHGB2	4.926624	0.100543	49
AKAP13	3.401954	0.340195	10	PCDHGA5	4.926624	0.104822	47
ATP11A	6.644252	0.73825	9	PCDHGB3	4.077744	0.094831	43
SND1	5.700985	0.633443	9	PCDHGA6	3.761358	0.094034	40
ADAMTS2	5.450143	0.605571	9	HDAC4	11.4268	0.308832	37
KCNH2	3.652449	0.405828	9	PCDHGA7	3.761358	0.101658	37
TSPAN9	3.398288	0.377588	9	RBFOX3	3.763689	0.107534	35
CACNA2D4	3.264015	0.362668	9	PCDHGB4	3.761358	0.107467	35
TRAPPC12	2.944589	0.327177	9	PCDHGA8	3.761358	0.107467	35
LINC00311	4.435695	0.554462	8	DIP2C	4.329398	0.135294	32
DNMT3A	4.416558	0.55207	8	PCDHGB5	4.077744	0.127429	32
DLEU1	3.361173	0.420147	8	PCDHGA9	4.077744	0.13154	31
MSRA	3.294925	0.411866	8	PCDHGB6	4.077744	0.140612	29
SYNJ2	2.961715	0.370214	8	PCDHGA10	3.761358	0.134334	28
ASPSR1	2.915682	0.36446	8	ADARB2	5.230539	0.201175	26
CXXC5	5.650038	0.807148	7	AGAP1	10.77193	0.430877	25
RXRA	4.165872	0.595125	7	PDGFRA	4.667772	0.186711	25
VPS13D	4.089338	0.584191	7	PCDHGB7	3.761358	0.156723	24
MIR548H4	3.961827	0.565975	7	MEIS1	2.611056	0.108794	24
NAV1	3.792954	0.541851	7	RPTOR	8.23786	0.358168	23
GAK	3.696837	0.52812	7	NCOR2	7.734358	0.336276	23
C19orf25	3.252634	0.464662	7	HOXB3	4.665346	0.202841	23
FBXL18	4.26533	0.710888	6	RIMBP2	3.795662	0.165029	23
RADIL	3.421879	0.570313	6	PCDHGA11	3.761358	0.163537	23
COQ8A	3.189345	0.531558	6	NXN	3.212903	0.139691	23
SLC22A18AS	3.068701	0.51145	6	HOXA-AS3	8.000536	0.380978	21
CRADD	2.919457	0.486576	6	SKI	7.268894	0.346138	21
RUNDC3A	4.524519	0.904904	5	ZIC4	2.892044	0.137716	21
ARHGEF7	4.430204	0.886041	5	FRMD4A	5.721777	0.286089	20
TSNAX-DISC1	3.723805	0.744761	5	ABR	3.043403	0.15217	20
SDK2	2.924278	0.584856	5	SDK1	3.002207	0.15011	20
GSG1	3.483081	0.87077	4	MAD1L1	6.504966	0.342367	19
STAP2	3.222442	0.80561	4	SMG1P2	5.137537	0.270397	19
DAGLB	2.962308	0.987436	3	BOLA2	5.137537	0.270397	19
SLC6A9	2.929569	0.976523	3	LOC613038	5.137537	0.270397	19
RALGAPA2	3.938003	1.969001	2	ZNF423	4.51416	0.237587	19
SLC25A10	2.971607	1.485803	2	CASZ1	2.803664	0.147561	19

KCNQ1	2.551606	0.134295	19	ARHGEF7	3.716752	0.74335	5
SEPTIN9	3.752735	0.208485	18	TSNAX-DISC1	3.313869	0.662774	5
TBC1D16	3.662815	0.20349	18	RUNDC3A	2.954544	0.590909	5
RBFOX1	3.58725	0.199292	18	ARHGAP25	2.753627	0.550725	5
FOXK1	3.086634	0.17148	18	VAV2	2.665216	0.533043	5
TBX15	3.045215	0.17913	17	TK1	2.58289	0.516578	5
EBF3	2.79486	0.174679	16	DICER1	2.564388	0.854796	3
NAV2	2.583868	0.161492	16	WDR81	2.558472	1.279236	2
GLI2	4.238032	0.282535	15				
ZBTB20	3.214638	0.214309	15	TABLE 128:	Cancer Type	MPNST_Typ	
BAIAP2	3.051758	0.203451	15	Gene site	imp_sum	imp_mean	n
PCDHGA12	3.761358	0.268668	14	PTPRN2	11.40859	0.139129	82
C7orf50	3.23462	0.231044	14	PRDM16	16.35938	0.230414	71
PRKAG2	3.066192	0.219014	14	PCDHGA1	7.813541	0.132433	59
CUX1	3.004756	0.214625	14	PCDHGA2	7.497155	0.131529	57
MSI2	3.521666	0.270897	13	PCDHGA3	7.813541	0.144695	54
HOXC4	2.965225	0.228094	13	PCDHGB1	8.129927	0.153395	53
CMIP	4.557839	0.37982	12	PCDHGA4	7.682672	0.150641	51
FBRSL1	4.0272	0.3356	12	PCDHGB2	7.682672	0.156789	49
ADGRD1	2.847644	0.237304	12	PCDHGA5	7.366286	0.156729	47
CSMD1	2.623068	0.218589	12	PCDHGB3	7.006468	0.162941	43
SPON2	3.904574	0.354961	11	PCDHGA6	7.006468	0.175162	40
PCDHGC3	3.761358	0.341942	11	HDAC4	18.57195	0.501945	37
TBCD	3.554525	0.323139	11	PCDHGA7	6.243333	0.168739	37
SLC9A3	2.948527	0.268048	11	RBFOX3	7.251853	0.207196	35
CACNA1C	2.885609	0.262328	11	PCDHGB4	6.243333	0.178381	35
SLC38A10	2.782131	0.252921	11	PCDHGA8	6.243333	0.178381	35
AKAP13	3.296816	0.329682	10	PAX6	5.878477	0.167956	35
TSPAN4	2.826546	0.282655	10	DIP2C	8.558231	0.267445	32
OTX1	2.726245	0.272625	10	PCDHGB5	6.559719	0.204991	32
SND1	6.561738	0.729082	9	PCDHGA9	6.559719	0.211604	31
ATP11A	5.144064	0.571563	9	SOX2-OT	7.031322	0.242459	29
TSPAN9	4.146995	0.460777	9	PCDHGB6	5.793022	0.199759	29
ADAMTS2	3.609916	0.401102	9	PCDHGA10	5.793022	0.206894	28
CACNA2D4	3.200749	0.355639	9	GALNT9	5.65269	0.209359	27
NOTCH1	2.66549	0.296166	9	SHANK2	5.418389	0.2084	26
MGMT	2.65052	0.294502	9	AGAP1	13.66331	0.546533	25
MSRA	3.799832	0.474979	8	CAMTA1	7.369768	0.294791	25
DLEU1	3.293788	0.411723	8	PDGFRA	5.680583	0.227223	25
LINC00311	3.188449	0.398556	8	SATB2	6.052462	0.252186	24
MACROD1	2.626244	0.32828	8	PCDHGB7	6.005152	0.250215	24
GAK	3.474309	0.49633	7	MEIS1	5.069165	0.211215	24
NAV1	2.733392	0.390485	7	RPTOR	11.28283	0.490558	23
MIR548H4	2.627448	0.37535	7	INPP5A	6.336466	0.275499	23
VPS13D	2.601164	0.371595	7	PCDHGA11	5.688766	0.247338	23
CCDC177	3.719957	0.619993	6	NCOR2	4.059225	0.176488	23
FBXL18	3.461798	0.576966	6	RIMBP2	4.055906	0.176344	23
FMNL2	2.888892	0.481482	6	PRKCZ	4.788565	0.217662	22

SKI	7.873089	0.374909	21	ATP11A	6.044255	0.671584	9
HOXA-AS3	6.084415	0.289734	21	TRAPPC12	4.67812	0.519791	9
SIM2	5.226048	0.248859	21	MGMT	4.059266	0.45103	9
ZIC4	4.034207	0.192105	21	DLEU1	5.18969	0.648711	8
FRMD4A	6.957362	0.347868	20	MSRA	4.894293	0.611787	8
SDK1	4.378271	0.218914	20	GATA4	4.400518	0.550065	8
MAD1L1	12.12049	0.637921	19	DNMT3A	3.983243	0.497905	8
CASZ1	7.28862	0.383612	19	NAV1	4.498508	0.642644	7
ZNF423	6.088723	0.320459	19	GAK	4.268656	0.609808	7
SMG1P2	5.066878	0.266678	19	FBXL18	4.842362	0.80706	6
BOLA2	5.066878	0.266678	19	CRADD	4.395121	0.73252	6
LOC613038	5.066878	0.266678	19	PAX1	4.032237	0.672039	6
KCNQ1	4.118846	0.216781	19	RUNDC3A	5.089872	1.017974	5
FO XK1	6.011675	0.333982	18	TSNAX-DISC1	4.853614	0.970723	5
TBC1D16	5.491063	0.305059	18	ARHGEF7	4.292926	0.858585	5
ANKRD11	4.830669	0.268371	18				
MCF2L	3.893409	0.216301	18	TABLE 129:	Cancer Type MYXGNT		
PAX6-AS1	5.287482	0.311028	17	Gene site	imp_sum	imp_mean	n
RCN1	5.287482	0.311028	17	PTPRN2	8.063995	0.098341	82
FOXP1	6.513298	0.407081	16	PRDM16	6.015023	0.084719	71
EBF3	5.517271	0.344829	16	PCDHGA1	2.438596	0.041332	59
GLI2	6.64064	0.442709	15	PCDHGA2	2.438596	0.042782	57
BAIAP2	5.555953	0.370397	15	PCDHGA3	2.438596	0.045159	54
KIRREL3	4.728594	0.31524	15	PCDHGB1	2.438596	0.046011	53
IQSEC1	5.990637	0.427903	14	PCDHGA4	2.438596	0.047816	51
RPS6KA2	5.431633	0.387974	14	PCDHGB2	2.438596	0.049767	49
PCDHGA12	4.608739	0.329196	14	PCDHGA5	2.438596	0.051885	47
TBX5	4.533789	0.323842	14	PCDHGB3	2.12221	0.049354	43
CACNA1H	4.164851	0.297489	14	PCDHGA6	2.12221	0.053055	40
PRKAG2	4.033154	0.288082	14	HDAC4	5.344795	0.144454	37
ARHGEF10	4.013836	0.286703	14	PCDHGA7	2.12221	0.057357	37
MIR548F5	3.912287	0.279449	14	PAX6	5.957941	0.170227	35
GSE1	5.106679	0.392821	13	RBFOX3	2.249688	0.064277	35
MSI2	4.801108	0.369316	13	PCDHGB4	2.12221	0.060635	35
SPTBN4	4.123586	0.317199	13	PCDHGA8	2.12221	0.060635	35
CMIP	5.474613	0.456218	12	DIP2C	4.667771	0.145868	32
ZC3H3	5.183168	0.431931	12	PCDHGB5	2.12221	0.066319	32
FBRSL1	4.300782	0.358398	12	PCDHGA9	2.12221	0.068458	31
TNS3	4.118537	0.343211	12	SOX2-OT	4.654458	0.160499	29
CCDC140	5.431056	0.493732	11	PDGFRA	4.560928	0.182437	25
COL4A1	4.814247	0.437659	11	CAMTA1	2.86826	0.11473	25
PCDHGC3	4.292353	0.390214	11	AGAP1	2.62551	0.10502	25
AKAP13	4.837756	0.483776	10	SATB2	4.23038	0.176266	24
FMN1	4.308091	0.430809	10	RPTOR	5.827061	0.25335	23
KLHL29	4.18457	0.418457	10	INPP5A	2.986581	0.129851	23
ACOT7	3.897802	0.38978	10	NXN	2.618838	0.113863	23
SND1	7.906603	0.878511	9	NCOR2	2.359705	0.102596	23
ADAMTS2	6.07413	0.674903	9	PRKCZ	2.771693	0.125986	22

SKI	4.88071	0.232415	21	KCNH2	2.23091	0.247879	9
SIM2	2.403596	0.114457	21	ADGRB1	2.222378	0.246931	9
FRMD4A	4.809888	0.240494	20	LINC00311	2.238754	0.279844	8
ZNF423	5.127221	0.269854	19	MSRA	2.182144	0.272768	8
MAD1L1	5.063347	0.266492	19	NXPH1	2.151276	0.268909	8
SMG1P2	3.051539	0.160607	19	DUSP6	4.271224	0.610175	7
BOLA2	3.051539	0.160607	19	FHIT	2.833737	0.40482	7
LOC613038	3.051539	0.160607	19	NAV1	2.786186	0.398027	7
MCF2L	3.682952	0.204608	18	LINC00461	2.366798	0.338114	7
SEPTIN9	3.483625	0.193535	18	LHPP	2.10422	0.300603	7
TBC1D16	3.38681	0.188156	18	FBXL18	2.190535	0.365089	6
FOXK1	3.374784	0.187488	18	CRADD	2.179627	0.363271	6
RBFOX1	2.248114	0.124895	18	CACNA2D3	2.129801	0.354967	6
OPCML	4.650709	0.273571	17	FAM181A	2.11702	0.352837	6
TBX15	3.241245	0.190661	17	RUNDC3A	3.425236	0.685047	5
SORBS2	2.949142	0.184321	16	LIPE-AS1	2.290428	0.572607	4
FOXP1	2.733394	0.170837	16	RBMS3	2.287928	0.571982	4
GLI2	7.012457	0.467497	15	GRIN2B	3.005057	1.001686	3
EMX2OS	2.535671	0.169045	15	BFSP2	2.545119	0.848373	3
CUX1	2.623715	0.187408	14	DAGLB	2.260342	0.753447	3
C7orf50	2.108388	0.150599	14	LOXL3	2.084867	0.694956	3
MSI2	3.427545	0.263657	13	SOX10	4.027447	2.013724	2
MYT1L	2.912141	0.224011	13				
SPTBN4	2.214702	0.170362	13	TABLE 130:	Cancer Type	NB_MYCN	
CMIP	3.717364	0.30978	12	Gene site	imp_sum	imp_mean	n
FBRSL1	2.420882	0.20174	12	PTPRN2	13.77349	0.167969	82
MEIS2	2.311873	0.192656	12	PRDM16	9.137531	0.128698	71
MIRLET7BHG	2.110346	0.175862	12	HDAC4	14.90914	0.40295	37
CCDC140	2.680388	0.243672	11	PAX6	10.20883	0.291681	35
RAD51B	2.510789	0.228254	11	RBFOX3	5.604467	0.160128	35
VGLL4	2.298538	0.208958	11	DIP2C	12.68854	0.396517	32
FGFR2	2.241963	0.203815	11	SHANK2	4.94307	0.190118	26
GLUD1P2	2.212583	0.201144	11	ADARB2	3.879706	0.149219	26
ZC3H12D	2.073195	0.188472	11	AGAP1	8.455554	0.338222	25
LBX1-AS1	3.409043	0.340904	10	CAMTA1	4.880188	0.195208	25
ACOT7	2.570845	0.257085	10	RPTOR	8.818478	0.383412	23
RGS12	2.401681	0.240168	10	NXN	7.999339	0.347797	23
TP73	2.363542	0.236354	10	NCOR2	5.498296	0.239056	23
GRID1	2.214702	0.22147	10	INPP5A	4.389074	0.190829	23
MAML2	2.119074	0.211907	10	RIMBP2	3.857062	0.167698	23
ATP11A	3.768101	0.418678	9	HOXB3	3.516834	0.152906	23
TRAPPC12	3.431857	0.381317	9	PRKCZ	4.116492	0.187113	22
SND1	3.356011	0.37289	9	SKI	7.34881	0.349943	21
NOTCH1	3.323558	0.369284	9	SIM2	4.031072	0.191956	21
ASAP1	3.018533	0.335393	9	FRMD4A	5.693082	0.284654	20
KAZN	2.509768	0.278863	9	SDK1	3.987692	0.199385	20
KCNMA1	2.356243	0.261805	9	ABR	3.501392	0.17507	20
AXIN2	2.329512	0.258835	9	MAD1L1	11.2606	0.592663	19

ZNF423	6.710876	0.353204	19	CACNA2D4	4.211872	0.467986	9
SMG1P2	6.20605	0.326634	19	KAZN	3.950567	0.438952	9
BOLA2	6.20605	0.326634	19	AXIN2	3.512069	0.39023	9
LOC613038	6.20605	0.326634	19	GPC6	3.439569	0.382174	9
CASZ1	5.513095	0.290163	19	KCNH2	3.396482	0.377387	9
KCNQ1	3.348152	0.176219	19	EGFR	3.281196	0.364577	9
SEPTIN9	4.875206	0.270845	18	MSRA	4.251822	0.531478	8
FOXK1	4.738861	0.26327	18	SYNJ2	3.507904	0.438488	8
ANKRD11	4.444749	0.246931	18	TENM2	3.360203	0.420025	8
MCF2L	3.973541	0.220752	18	NXPH1	3.272993	0.409124	8
TBC1D16	3.477985	0.193221	18	LINC00311	3.247338	0.405917	8
PAX6-AS1	6.095823	0.358578	17	GAK	4.507366	0.643909	7
RCN1	6.095823	0.358578	17	C19orf25	4.332101	0.618872	7
HBG2	4.729845	0.278226	17	NAV1	3.751485	0.535926	7
EBF3	3.910934	0.244433	16	HOXD3	3.302864	0.471838	7
LRMDA	5.250944	0.350063	15	VPS13D	3.270809	0.467258	7
BAIAP2	4.496185	0.299746	15	PACRG	3.188281	0.455469	7
NFATC1	4.454533	0.296969	15	CRADD	4.283501	0.713917	6
KIRREL3	4.373066	0.291538	15	FBXL18	3.71622	0.61937	6
GLI2	4.301867	0.286791	15	FMNL2	3.462802	0.577134	6
ZBTB20	3.974717	0.264981	15	WFIKK2	3.183348	0.530558	6
DLX6-AS1	3.564548	0.237637	15	TSNAX-DISC1	4.991709	0.998342	5
PRKAG2	5.022579	0.358756	14	RUNDC3A	4.645029	0.929006	5
CUX1	4.798593	0.342757	14	ARHGEF7	3.825064	0.765013	5
MIR548F5	3.780039	0.270003	14	MPP7	3.296489	0.659298	5
C7orf50	3.778709	0.269908	14	FYN	4.38385	1.095962	4
MOB2	3.306584	0.236185	14	CHTF18	3.828653	1.914327	2
MSI2	8.759201	0.673785	13	SLC25A10	3.373693	1.686847	2
RFX4	4.748792	0.365292	13	ANKLE2	3.350613	1.675307	2
GSE1	3.671473	0.282421	13				
MYT1L	3.629239	0.279172	13	TABLE 131:	Cancer Type	NB_TMMneg	
CMIP	6.157676	0.51314	12	Gene site	imp_sum	imp_mean	n
ZC3H3	5.181392	0.431783	12	PTPRN2	18.55652	0.226299	82
FBRSL1	4.383222	0.365268	12	PRDM16	10.22762	0.144051	71
TBX4	4.04326	0.336938	12	PCDHGA1	7.152279	0.121225	59
CSMD1	3.909171	0.325764	12	PCDHGA2	6.835893	0.119928	57
MAML3	3.776111	0.314676	12	PCDHGA3	6.474104	0.119891	54
TNS3	3.647926	0.303994	12	PCDHGB1	6.474104	0.122153	53
RASA3	3.439803	0.28665	12	PCDHGA4	6.046453	0.118558	51
RAD51B	4.731405	0.430128	11	PCDHGB2	5.625262	0.114801	49
CTBP2	3.3705	0.306409	11	PCDHGA5	5.941648	0.126418	47
TSPAN4	5.159493	0.515949	10	PCDHGB3	5.5052	0.128028	43
AKAP13	4.027337	0.402734	10	PCDHGA6	5.5052	0.13763	40
SH3RF3	3.721306	0.372131	10	HDAC4	17.16275	0.463858	37
SND1	5.288539	0.587615	9	PCDHGA7	4.872428	0.131687	37
ADAMTS2	4.883445	0.542605	9	PAX6	11.01388	0.314682	35
ATP11A	4.40828	0.489809	9	RBFOX3	5.676042	0.162173	35
TSPAN9	4.22834	0.469816	9	PCDHGB4	4.556042	0.130173	35

PCDHGA8	4.556042	0.130173	35	ARHGEF10	4.243537	0.30311	14
DIP2C	11.64339	0.363856	32	C7orf50	4.068381	0.290599	14
PCDHGB5	4.239656	0.132489	32	MOB2	3.985323	0.284666	14
GALNT9	5.149882	0.190736	27	MSI2	8.580374	0.660029	13
SHANK2	6.159903	0.236919	26	GSE1	5.724454	0.440343	13
AGAP1	12.75037	0.510015	25	MYT1L	5.487224	0.422094	13
PDGFRA	7.113649	0.284546	25	RFX4	4.115234	0.316556	13
CAMTA1	6.491436	0.259657	25	ZC3H3	6.797012	0.566418	12
SATB2	5.74169	0.239237	24	FBRSL1	5.057732	0.421478	12
MEIS1	5.664513	0.236021	24	ADGRD1	4.916863	0.409739	12
NXN	11.92044	0.51828	23	RASA3	4.568026	0.380669	12
RPTOR	10.02959	0.436069	23	MIRLET7BHG	4.045357	0.337113	12
NCOR2	6.754804	0.293687	23	CTBP2	4.887996	0.444363	11
INPP5A	6.090449	0.264802	23	RAD51B	4.828445	0.43895	11
PRKCZ	7.080414	0.321837	22	TSPAN4	5.385332	0.538533	10
SKI	10.28144	0.489592	21	ADAMTS2	5.853042	0.650338	9
HOXA-AS3	5.049535	0.240454	21	ATP11A	5.785182	0.642798	9
ZIC4	4.250293	0.202395	21	SND1	5.762779	0.640309	9
FRMD4A	7.176558	0.358828	20	TSPAN9	4.99043	0.554492	9
ABR	6.081806	0.30409	20	AXIN2	4.640668	0.51563	9
SDK1	5.981355	0.299068	20	TRAPPC12	4.439527	0.493281	9
MAD1L1	12.41341	0.653337	19	CACNA2D4	4.422186	0.491354	9
ZNF423	6.238529	0.328344	19	KCNH2	4.06122	0.451247	9
KCNQ1	5.876033	0.309265	19	MSRA	4.849491	0.606186	8
SMG1P2	5.859726	0.308407	19	TRAPPC9	4.147563	0.518445	8
BOLA2	5.859726	0.308407	19	SYNJ2	4.056103	0.507013	8
LOC613038	5.859726	0.308407	19	RXRA	4.522346	0.646049	7
CASZ1	4.319617	0.227348	19	NAV1	4.433724	0.633389	7
TBC1D16	8.686104	0.482561	18	VPS13D	4.250029	0.607147	7
FOKK1	7.477284	0.415405	18	C19orf25	4.135319	0.59076	7
MCF2L	4.662193	0.259011	18	GAK	4.046351	0.57805	7
ANKRD11	4.195478	0.233082	18	FBXL18	4.988075	0.831346	6
SEPTIN9	4.031914	0.223995	18	CRADD	4.433395	0.738899	6
PAX6-AS1	7.150191	0.420599	17	RUNDC3A	5.152499	1.0305	5
RCN1	7.150191	0.420599	17	TSNAX-DISC1	5.141396	1.028279	5
SIM1	4.51478	0.265575	17	ARHGEF7	4.761732	0.952346	5
FOXP1	6.436364	0.402273	16	DNAAF5	4.360708	0.872142	5
NAV2	4.623006	0.288938	16				
GLI2	6.19981	0.413321	15	TABLE 132:	Cancer Type NB_TMMpos		
NFIX	4.786288	0.319086	15	Gene site	imp_sum	imp_mean	n
BAIAP2	4.435057	0.29567	15	PTPRN2	16.11115	0.196477	82
SLX1B-				PRDM16	6.965467	0.098105	71
SULT1A4	4.290474	0.286032	15	HDAC4	13.48037	0.364334	37
SLX1A	4.290474	0.286032	15	PAX6	10.13358	0.289531	35
LOC606724	4.290474	0.286032	15	RBFOX3	4.920339	0.140581	35
KIRREL3	4.274786	0.284986	15	DIP2C	9.275777	0.289868	32
RPS6KA2	6.530167	0.466441	14	SHANK2	6.227641	0.239525	26
PRKAG2	4.493534	0.320967	14	AGAP1	9.214808	0.368592	25

CAMTA1	7.199671	0.287987	25	ADGRD1	3.856339	0.321362	12
SATB2	3.007551	0.125315	24	CTBP2	4.804597	0.436782	11
NXN	10.45491	0.454561	23	RAD51B	3.351723	0.304702	11
RPTOR	10.04757	0.436851	23	TBCD	3.264218	0.296747	11
NCOR2	4.712774	0.204903	23	TSPAN4	4.852241	0.485224	10
INPP5A	4.166842	0.181167	23	CHST11	4.233357	0.423336	10
PRKCZ	4.993783	0.22699	22	RGS12	4.115475	0.411548	10
SKI	8.623933	0.410663	21	ACOT7	3.890732	0.389073	10
HOXA-AS3	3.366629	0.160316	21	CBFA2T3	3.433004	0.3433	10
ZIC4	3.156767	0.150322	21	AKAP13	3.410488	0.341049	10
FRMD4A	4.815185	0.240759	20	ADAMTS2	5.109962	0.567774	9
SDK1	4.46552	0.223276	20	TSPAN9	4.490392	0.498932	9
MAD1L1	11.1922	0.589063	19	CACNA2D4	3.80421	0.42269	9
SMG1P2	4.049626	0.213138	19	AXIN2	3.526607	0.391845	9
BOLA2	4.049626	0.213138	19	MGMT	3.378644	0.375405	9
LOC613038	4.049626	0.213138	19	SMAD3	5.640512	0.705064	8
ZNF423	3.8885	0.204658	19	MSRA	4.373575	0.546697	8
CASZ1	3.476123	0.182954	19	VRK2	3.327552	0.415944	8
FO XK1	6.894914	0.383051	18	LINC00311	3.275629	0.409454	8
TBC1D16	6.826437	0.379246	18	PPP2R2B	3.03431	0.379289	8
SEPTIN9	3.450705	0.191706	18	MCIDAS	2.978913	0.372364	8
ANKRD11	3.271443	0.181747	18	NAV1	3.844465	0.549209	7
PAX6-AS1	6.216273	0.365663	17	C19orf25	3.733425	0.533346	7
RCN1	6.216273	0.365663	17	VPS13D	3.641552	0.520222	7
HBG2	3.132325	0.184254	17	GAK	3.314179	0.473454	7
FOXP1	4.6681	0.291756	16	RXRA	3.115199	0.445028	7
NAV2	4.575986	0.285999	16	HOXD3	3.091484	0.441641	7
KIRREL3	4.406834	0.293789	15	MIR548H4	3.088767	0.441252	7
BAIAP2	4.20718	0.280479	15	FBXL18	4.014514	0.669086	6
SLX1B-				CRADD	3.515875	0.585979	6
SULT1A4	3.998125	0.266542	15	WFIKN2	3.429234	0.571539	6
SLX1A	3.998125	0.266542	15	COQ8A	3.36352	0.560587	6
LOC606724	3.998125	0.266542	15	MYO16	3.136848	0.522808	6
NFATC1	3.722419	0.248161	15	RUNDC3A	4.982688	0.996538	5
GLI2	3.137561	0.209171	15	ARHGEF7	3.83097	0.766194	5
RPS6KA2	5.499889	0.392849	14	TSNAX-DISC1	3.685278	0.737056	5
ARHGEF10	4.319529	0.308538	14	BCAR1	3.486815	0.697363	5
PRKAG2	3.795162	0.271083	14	DNAAF5	3.473447	0.694689	5
C7orf50	3.035132	0.216795	14	BACH2	3.340635	0.668127	5
MSI2	8.215674	0.631975	13	NPHP4	3.112474	0.622495	5
MYT1L	5.287032	0.406695	13	DTNA	3.232674	0.808169	4
RFX4	3.737829	0.287525	13	GSG1	3.128085	0.782021	4
GSE1	3.008545	0.231427	13	DAGLB	3.09399	1.03133	3
ZC3H3	6.773834	0.564486	12	DICER1	2.99365	0.997883	3
CMIP	4.753958	0.396163	12	SLC25A10	3.024731	1.512366	2
GNA12	4.582202	0.38185	12				
MIRLET7BHG	4.044978	0.337082	12				
FBRSL1	3.964516	0.330376	12				

TABLE 133: Cancer Type NFIB_PLEX

Gene site imp_sum imp_mean n

PTPRN2	13.6038	0.1659	82	FO XK1	4.820062	0.267781	18
PRDM16	12.74187	0.179463	71	SEPTIN9	4.378197	0.243233	18
PCDHGA1	7.609956	0.128982	59	ANKRD11	4.17047	0.231693	18
PCDHGA2	7.609956	0.133508	57	PAX6-AS1	4.700585	0.276505	17
PCDHGA3	7.29357	0.135066	54	RCN1	4.700585	0.276505	17
PCDHGB1	7.29357	0.137615	53	FOXP1	4.200912	0.262557	16
PCDHGA4	6.977184	0.136808	51	SORBS2	4.032652	0.252041	16
PCDHGB2	6.977184	0.142392	49	SLX1B-			
PCDHGA5	6.532484	0.138989	47	SULT1A4	5.361231	0.357415	15
PCDHGB3	5.899712	0.137203	43	SLX1A	5.361231	0.357415	15
PCDHGA6	5.583326	0.139583	40	LOC606724	5.361231	0.357415	15
HDAC4	12.87329	0.347927	37	GLI2	5.193071	0.346205	15
PCDHGA7	5.26694	0.14235	37	ZBTB20	3.750908	0.250061	15
PAX6	10.60945	0.303127	35	KIRREL3	3.40391	0.226927	15
RBFOX3	4.967367	0.141925	35	CUX1	5.001913	0.357279	14
PCDHGB4	4.950554	0.141444	35	IQSEC1	4.782704	0.341622	14
PCDHGA8	4.950554	0.141444	35	RPS6KA2	4.680709	0.334336	14
DIP2C	7.630068	0.23844	32	ARHGEF10	3.493473	0.249534	14
PCDHGB5	5.26694	0.164592	32	PRKAG2	3.428263	0.244876	14
PCDHGA9	5.26694	0.169901	31	C7orf50	3.396421	0.242602	14
SOX2-OT	5.19331	0.17908	29	MSI2	6.004289	0.461868	13
PCDHGB6	4.950554	0.170709	29	GSE1	5.190069	0.399236	13
PCDHGA10	4.950554	0.176805	28	MYT1L	3.452289	0.265561	13
GALNT9	3.903223	0.144564	27	RFX4	3.397458	0.261343	13
SHANK2	3.595971	0.138307	26	FBRSL1	5.176679	0.43139	12
AGAP1	11.34453	0.453781	25	CMIP	5.04849	0.420708	12
PDGFRA	4.704498	0.18818	25	ADGRD1	4.376901	0.364742	12
CAMTA1	4.597499	0.1839	25	GNA12	4.328821	0.360735	12
PCDHGB7	4.317782	0.179908	24	ZC3H3	3.725687	0.310474	12
MEIS1	3.490617	0.145442	24	SPON2	6.316248	0.574204	11
RPTOR	8.659899	0.376517	23	CTBP2	4.24005	0.385459	11
NCOR2	7.426108	0.322874	23	ANAPC16	4.089777	0.371798	11
NXN	6.34216	0.275746	23	TBCD	4.036366	0.366942	11
INPP5A	5.801975	0.25226	23	RAD51B	3.70189	0.336535	11
PCDHGA11	4.317782	0.18773	23	ACOT7	5.140454	0.514045	10
RIMBP2	3.42345	0.148846	23	AKAP13	4.18378	0.418378	10
PRKCZ	4.501056	0.204593	22	TSPAN4	3.740082	0.374008	10
SKI	9.150488	0.435738	21	KLHL29	3.563838	0.356384	10
FRMD4A	5.618711	0.280936	20	SND1	4.427409	0.491934	9
SDK1	4.48406	0.224203	20	AXIN2	3.728727	0.414303	9
ABR	3.444359	0.172218	20	ASAP1	3.678608	0.408734	9
MAD1L1	8.973465	0.472288	19	CACNA2D4	3.512472	0.390275	9
SMG1P2	6.52842	0.343601	19	LINC00311	4.314256	0.539282	8
BOLA2	6.52842	0.343601	19	SMAD3	4.240593	0.530074	8
LOC613038	6.52842	0.343601	19	MSRA	3.942701	0.492838	8
KCNQ1	4.698431	0.247286	19	C19orf25	3.692036	0.527434	7
ZNF423	3.51037	0.184756	19	FBXL18	4.951015	0.825169	6
TBC1D16	5.027192	0.279288	18	CCDC177	4.125511	0.687585	6

RUNDC3A	4.905148	0.98103	5	GLI2	8.548733	0.569916	15
LOC100130872	4.289063	0.857813	5	KIRREL3	3.966147	0.26441	15
TSNAX-DISC1	3.660081	0.732016	5	BAIAP2	3.944493	0.262966	15
BCAR1	3.402498	0.6805	5	ZBTB20	3.690344	0.246023	15
GSG1	3.580673	0.895168	4	LRMDA	3.364631	0.224309	15
TABLE 134: Cancer Type O_IDH				RPS6KA2	6.139807	0.438558	14
				IQSEC1	4.328154	0.309154	14
				CUX1	3.333429	0.238102	14
Gene site	imp_sum	imp_mean	n	MSI2	6.180821	0.475448	13
PTPRN2	17.77707	0.216793	82	TNS3	5.496717	0.45806	12
PRDM16	10.35636	0.145864	71	ADGRD1	4.486901	0.373908	12
HDAC4	11.77959	0.318367	37	MIRLET7BHG	4.423029	0.368586	12
PAX6	9.742512	0.278357	35	CMIP	4.400102	0.366675	12
RBFOX3	9.319109	0.26626	35	FBRSL1	4.210507	0.350876	12
DIP2C	5.326051	0.166439	32	MEGF6	3.597623	0.299802	12
SOX2-OT	7.391918	0.254894	29	RASA3	3.442699	0.286892	12
GALNT9	3.939244	0.145898	27	ZC3H3	3.320047	0.276671	12
SHANK2	3.989276	0.153434	26	RAD51B	4.015803	0.365073	11
AGAP1	5.848567	0.233943	25	FGFR2	3.234357	0.294032	11
CAMTA1	5.732686	0.229307	25	TSPAN4	4.43102	0.443102	10
PDGFRA	4.617729	0.184709	25	ACOT7	4.035124	0.403512	10
SATB2	4.763835	0.198493	24	NR2F1-AS1	3.742456	0.374246	10
MEIS1	4.006012	0.166917	24	SND1	6.183886	0.687098	9
RPTOR	8.845044	0.384567	23	ATP11A	6.073319	0.674813	9
NXN	4.586101	0.199396	23	ADAMTS2	5.297555	0.588617	9
NCOR2	3.685137	0.160223	23	TSPAN9	4.699971	0.522219	9
INPP5A	3.656301	0.15897	23	AXIN2	4.010917	0.445657	9
RIMBP2	3.332114	0.144875	23	NEAT1	3.679876	0.408875	9
PRKCZ	4.32746	0.196703	22	ASAP1	3.604679	0.40052	9
SKI	9.339571	0.444741	21	RUNX1	3.36976	0.374418	9
FRMD4A	6.884633	0.344232	20	MSRA	4.663132	0.582891	8
ABR	5.443179	0.272159	20	DNMT3A	4.382435	0.547804	8
SDK1	4.502169	0.225108	20	LINC00311	4.286512	0.535814	8
MAD1L1	12.02304	0.632791	19	PPP2R2B	4.000987	0.500123	8
ZNF423	6.304621	0.331822	19	ESRRG	3.56145	0.445181	8
SMG1P2	5.86104	0.308476	19	NAV1	4.088238	0.584034	7
BOLA2	5.86104	0.308476	19	DUSP6	4.062795	0.580399	7
LOC613038	5.86104	0.308476	19	VPS13D	3.777117	0.539588	7
CASZ1	5.032192	0.264852	19	LINC00461	3.447133	0.492448	7
KCNQ1	3.876356	0.204019	19	C19orf25	3.425021	0.489289	7
CFAP46	3.865955	0.203471	19	FBXL18	4.856634	0.809439	6
FO XK1	5.340903	0.296717	18	SLC22A18AS	3.61879	0.603132	6
ANKRD11	5.290515	0.293918	18	FAM181A	3.292217	0.548703	6
TBC1D16	4.520863	0.251159	18	CRADD	3.249844	0.541641	6
SEPTIN9	4.430265	0.246126	18	RUNDC3A	4.771459	0.954292	5
MCF2L	3.959938	0.219997	18	PRR5L	4.24277	0.848554	5
OPCML	4.990801	0.293577	17	MRC2	4.151333	0.830267	5
NAV2	5.052861	0.315804	16	ARHGEF7	3.679727	0.735945	5
FOXP1	4.679177	0.292449	16				

TSNAX-DISC1	3.665763	0.733153	5	ABR	4.684248	0.234212	20
AP2A2	3.421652	0.68433	5	FRMD4A	4.50663	0.225332	20
TK1	3.408928	0.681786	5	SDK1	4.455217	0.222761	20
STAP2	5.527156	1.381789	4	MAD1L1	11.15551	0.587132	19
RBMS3	4.067302	1.016826	4	CASZ1	5.790791	0.304778	19
DTNA	3.836485	0.959121	4	KCNQ1	3.722935	0.195944	19
DAGLB	3.993437	1.331146	3	ZNF423	3.597687	0.189352	19
SRRM3	3.919526	1.306509	3	SMG1P2	3.572242	0.188013	19
ANKLE2	4.01036	2.00518	2	BOLA2	3.572242	0.188013	19
SLC25A10	3.973706	1.986853	2	LOC613038	3.572242	0.188013	19
SOX10	3.856613	1.928306	2	TBC1D16	6.813484	0.378527	18
CHTF18	3.272229	1.636114	2	ANKRD11	6.188601	0.343811	18
TABLE 135:	Cancer Type		n	FOXK1	5.396017	0.299779	18
				SEPTIN9	4.022652	0.223481	18
Gene site	imp_sum	imp_mean		MCF2L	3.929171	0.218287	18
PTPRN2	21.63143	0.263798	82	TBX15	5.634993	0.33147	17
PRDM16	14.17415	0.199636	71	OPCML	5.175403	0.304435	17
PCDHGA1	6.739654	0.114231	59	PAX6-AS1	4.060002	0.238824	17
PCDHGA2	6.423268	0.112689	57	RCN1	4.060002	0.238824	17
PCDHGA3	6.106882	0.11309	54	FOXP1	5.074186	0.317137	16
PCDHGB1	6.106882	0.115224	53	SORBS2	4.261092	0.266318	16
PCDHGA4	6.106882	0.119743	51	NAV2	4.257525	0.266095	16
PCDHGB2	6.106882	0.12463	49	GLI2	7.121	0.474733	15
PCDHGA5	5.790496	0.123202	47	SLX1B-			
PCDHGB3	4.710492	0.109546	43	SULT1A4	4.871386	0.324759	15
HDAC4	12.47842	0.337255	37	SLX1A	4.871386	0.324759	15
PCDHGA7	3.868612	0.104557	37	LOC606724	4.871386	0.324759	15
PAX6	10.51905	0.300544	35	NFIX	4.779389	0.318626	15
RBFOX3	8.446715	0.241335	35	BAIAP2	4.73258	0.315505	15
PCDHGB4	3.868612	0.110532	35	ZBTB20	4.376098	0.29174	15
PCDHGA8	3.868612	0.110532	35	IQSEC1	4.898046	0.34986	14
DIP2C	8.32832	0.26026	32	RPS6KA2	4.826184	0.344727	14
SOX2-OT	5.793454	0.199774	29	PRKAG2	4.522356	0.323025	14
GALNT9	4.635391	0.171681	27	C7orf50	4.165446	0.297532	14
PDGFRA	6.113805	0.244552	25	MIR548F5	3.918394	0.279885	14
AGAP1	5.365893	0.214636	25	ARHGEF10	3.677818	0.262701	14
CAMTA1	4.25973	0.170389	25	MSI2	4.478717	0.344517	13
SATB2	5.00547	0.208561	24	SPTBN4	4.149056	0.319158	13
MEIS1	4.846214	0.201926	24	MYT1L	3.576019	0.275078	13
PCDHGB7	3.885005	0.161875	24	ISLR2	5.440996	0.453416	12
RPTOR	10.2269	0.444648	23	FBRSL1	4.808985	0.400749	12
INPP5A	6.950543	0.302198	23	MIRLET7BHG	4.647168	0.387264	12
NCOR2	6.548584	0.284721	23	TNS3	3.685582	0.307132	12
PRKCZ	6.525097	0.296595	22	GNA12	3.615064	0.301255	12
SKI	7.803382	0.37159	21	CMIP	3.567877	0.297323	12
SIM2	4.1068	0.195562	21	CTBP2	4.14712	0.377011	11
ZIC4	3.965825	0.188849	21	SPON2	3.576957	0.325178	11
				SKOR1	4.506284	0.450628	10

MAML2	3.792377	0.379238	10	ADARB2	5.29415	0.203621	26
TSPAN4	3.691292	0.369129	10	AGAP1	11.35434	0.454173	25
ADGRB1	4.933429	0.548159	9	CAMTA1	10.98461	0.439384	25
AXIN2	4.733289	0.525921	9	PDGFRA	6.909238	0.27637	25
ASAP1	4.082458	0.453606	9	SATB2	8.571627	0.357151	24
KCNH2	3.947404	0.4386	9	MEIS1	7.849198	0.32705	24
KAZN	3.921414	0.435713	9	PCDHGB7	5.309981	0.221249	24
ADAMTS2	3.82162	0.424624	9	RPTOR	13.02038	0.566103	23
APBA2	3.721262	0.413474	9	INPP5A	9.175249	0.398924	23
VRK2	4.851925	0.606491	8	NCOR2	8.533146	0.371006	23
LINC00311	4.619994	0.577499	8	NXN	6.064108	0.263657	23
DLEU1	4.410582	0.551323	8	HOXB3	5.491228	0.238749	23
MCC	4.231691	0.528961	8	PCDHGA11	5.309981	0.230869	23
DNMT3A	3.769963	0.471245	8	PRKCZ	6.851413	0.311428	22
C19orf25	4.000033	0.571433	7	SKI	12.70136	0.604827	21
SLC22A18AS	3.7963	0.632717	6	SIM2	6.757476	0.321785	21
CRADD	3.744372	0.624062	6	FRMD4A	10.16063	0.508031	20
TSNAX-DISC1	4.748255	0.949651	5	SDK1	6.123697	0.306185	20
RUNDC3A	4.609288	0.921858	5	ABR	5.984562	0.299228	20
STAP2	5.128221	1.282055	4	MAD1L1	12.05065	0.634245	19
RBMS3	3.735742	0.933936	4	ZNF423	12.0421	0.633795	19
TABLE 136: Cancer Type PA_CORT				SMG1P2	6.543669	0.344404	19
				BOLA2	6.543669	0.344404	19
Gene site	imp_sum	imp_mean	n	LOC613038	6.543669	0.344404	19
PTPRN2	26.60108	0.324403	82	CASZ1	5.71895	0.300997	19
PRDM16	21.33245	0.300457	71	FOXK1	9.183113	0.510173	18
PCDHGA1	9.343276	0.158361	59	MCF2L	7.131597	0.3962	18
PCDHGA2	9.659662	0.169468	57	RBFOX1	5.787189	0.321511	18
PCDHGA3	9.184591	0.170085	54	ANKRD11	5.647336	0.313741	18
PCDHGB1	8.868205	0.167325	53	TBC1D16	5.201895	0.288994	18
PCDHGA4	8.868205	0.173886	51	OPCML	9.879184	0.581128	17
PCDHGB2	8.726713	0.178096	49	FOXP1	7.81498	0.488436	16
PCDHGA5	8.040168	0.171067	47	SORBS2	6.551892	0.409493	16
PCDHGB3	7.407396	0.172265	43	NAV2	6.508386	0.406774	16
PCDHGA6	6.682433	0.167061	40	GLI2	11.30732	0.753821	15
HDAC4	14.9952	0.405276	37	ZBTB20	7.170015	0.478001	15
PCDHGA7	6.366047	0.172055	37	KIRREL3	5.782804	0.38552	15
PAX6	14.82851	0.423672	35	LRMDA	5.330559	0.355371	15
RBFOX3	10.41433	0.297552	35	BAIAP2	5.257505	0.3505	15
PCDHGB4	6.321425	0.180612	35	RPS6KA2	6.803775	0.485984	14
PCDHGA8	6.321425	0.180612	35	IQSEC1	6.731631	0.480831	14
DIP2C	11.97159	0.374112	32	PRKAG2	6.726839	0.480489	14
PCDHGB5	6.005039	0.187657	32	CUX1	6.109245	0.436375	14
PCDHGA9	6.005039	0.193711	31	ARHGEF10	5.664014	0.404572	14
SOX2-OT	12.47069	0.430024	29	C7orf50	5.596942	0.399782	14
PCDHGB6	5.441033	0.187622	29	MSI2	6.596031	0.507387	13
GALNT9	5.83543	0.216127	27	MIR9-3HG	5.784035	0.444926	13
SHANK2	9.288615	0.357254	26	MYT1L	5.43139	0.417799	13

KIF26B	5.38755	0.414427	13	DIP2C	12.43841	0.3887	32
RFX4	5.191773	0.399367	13	PCDHGB5	5.188257	0.162133	32
CMIP	6.630744	0.552562	12	PCDHGA9	5.188257	0.167363	31
MIRLET7BHG	6.544033	0.545336	12	SOX2-OT	13.43776	0.463371	29
MEIS2	5.905022	0.492085	12	SHANK2	5.102298	0.196242	26
ADGRD1	5.134363	0.427864	12	CAMTA1	10.52437	0.420975	25
RAD51B	6.287653	0.571605	11	AGAP1	10.44052	0.417621	25
FGFR2	6.131599	0.557418	11	PDGFRA	7.810578	0.312423	25
VGLL4	6.041934	0.549267	11	MEIS1	8.770815	0.365451	24
CCDC140	5.647124	0.513375	11	SATB2	6.73535	0.28064	24
SPON2	5.191216	0.471929	11	RPTOR	13.2166	0.574635	23
LBX1-AS1	6.618751	0.661875	10	INPP5A	7.865212	0.341966	23
AKAP13	5.601161	0.560116	10	HOXB3	6.650084	0.289134	23
CHST11	5.46443	0.546443	10	NXN	5.752376	0.250103	23
NTM	5.110489	0.511049	10	NCOR2	5.49232	0.238797	23
SND1	6.666831	0.740759	9	PRKCZ	6.759222	0.307237	22
ADGRB1	6.605145	0.733905	9	SKI	12.17179	0.579609	21
TSPAN9	6.101004	0.677889	9	SIM2	5.437087	0.258909	21
ATP11A	5.788809	0.643201	9	FRMD4A	8.140409	0.40702	20
NOTCH1	5.409682	0.601076	9	ABR	6.71436	0.335718	20
AXIN2	5.36063	0.595626	9	SDK1	5.668025	0.283401	20
TRAPPC12	5.300167	0.588907	9	MAD1L1	13.69774	0.720933	19
LINC00311	5.447325	0.680916	8	ZNF423	10.42024	0.548433	19
MSRA	5.326954	0.665869	8	SMG1P2	8.785156	0.462377	19
DLEU1	5.270307	0.658788	8	BOLA2	8.785156	0.462377	19
DUSP6	7.401435	1.057348	7	LOC613038	8.785156	0.462377	19
LINC00461	6.722238	0.96032	7	CASZ1	5.862427	0.308549	19
RUNDC3A	5.392471	1.078494	5	FO XK1	9.295546	0.516419	18
TABLE 137: Cancer Type PA_INF				MCF2L	7.672036	0.426224	18
				SEPTIN9	6.396588	0.355366	18
Gene site	imp_sum	imp_mean	n	TBC1D16	5.890404	0.327245	18
PTPRN2	26.36911	0.321575	82	ANKRD11	5.202671	0.289037	18
PRDM16	21.97585	0.309519	71	OPCML	10.85961	0.6388	17
PCDHGA1	8.267047	0.140119	59	TBX15	5.389743	0.317044	17
PCDHGA2	7.950661	0.139485	57	NAV2	7.235721	0.452233	16
PCDHGA3	7.950661	0.147234	54	FOXP1	6.534835	0.408427	16
PCDHGB1	7.950661	0.150012	53	SORBS2	5.818589	0.363662	16
PCDHGA4	7.950661	0.155895	51	GLI2	11.79622	0.786415	15
PCDHGB2	7.634275	0.155802	49	ZBTB20	7.39887	0.493258	15
PCDHGA5	7.108589	0.151247	47	EMX2OS	5.889967	0.392664	15
PCDHGB3	7.108589	0.165316	43	KIRREL3	5.272782	0.351519	15
PCDHGA6	6.708268	0.167707	40	BAIAP2	5.193254	0.346217	15
HDAC4	13.94982	0.377022	37	IQSEC1	6.665892	0.476135	14
PCDHGA7	5.947182	0.160735	37	RPS6KA2	6.482534	0.463038	14
PAX6	14.94418	0.426977	35	CUX1	6.332662	0.452333	14
RBFOX3	8.664253	0.24755	35	TBX5	5.998658	0.428476	14
PCDHGB4	5.947182	0.169919	35	PRKAG2	5.424972	0.387498	14
PCDHGA8	5.947182	0.169919	35	MSI2	8.809547	0.677657	13

MIR9-3HG	7.266107	0.558931	13	PCDHGB3	3.113131	0.072398	43
MYT1L	6.182617	0.475586	13	PCDHGA6	2.796745	0.069919	40
TNS3	6.483199	0.540267	12	HDAC4	7.246665	0.195856	37
CMIP	6.235741	0.519645	12	RBFOX3	4.115757	0.117593	35
ADGRD1	6.01181	0.500984	12	PAX6	2.950393	0.084297	35
ZC3H3	5.848371	0.487364	12	DIP2C	3.94419	0.123256	32
MIRLET7BHG	5.809331	0.484111	12	SOX2-OT	6.305877	0.217444	29
TBX4	5.309311	0.442443	12	AGAP1	5.710979	0.228439	25
RAD51B	6.756107	0.614192	11	CAMTA1	4.469934	0.178797	25
FGFR2	5.887634	0.535239	11	PDGFRA	4.121216	0.164849	25
VGLL4	5.848507	0.531682	11	MEIS1	4.003889	0.166829	24
CCDC140	5.387338	0.489758	11	SATB2	2.608137	0.108672	24
LBX1-AS1	6.170454	0.617045	10	RPTOR	5.723025	0.248827	23
SH3RF3	5.498813	0.549881	10	INPP5A	3.546366	0.15419	23
ACOT7	5.262586	0.526259	10	NCOR2	2.912079	0.126612	23
AKAP13	5.213203	0.52132	10	PRKCZ	4.349281	0.197695	22
CHST11	5.049935	0.504993	10	SKI	6.671857	0.317707	21
SND1	6.644614	0.73829	9	FRMD4A	5.899552	0.294978	20
ATP11A	6.482206	0.720245	9	ABR	2.703796	0.13519	20
AXIN2	5.892237	0.654693	9	SDK1	2.608231	0.130412	20
ADGRB1	5.660024	0.628892	9	ZNF423	7.885591	0.415031	19
NOTCH1	5.494313	0.610479	9	MAD1L1	7.709643	0.405771	19
TSPAN9	5.424342	0.602705	9	SMG1P2	4.091947	0.215366	19
LINC00311	5.644053	0.705507	8	BOLA2	4.091947	0.215366	19
DLEU1	5.378806	0.672351	8	LOC613038	4.091947	0.215366	19
GRIK2	5.373596	0.671699	8	FOXK1	5.212468	0.289582	18
DUSP6	7.573024	1.081861	7	MCF2L	5.179781	0.287766	18
LINC00461	5.998306	0.856901	7	OPCML	5.864633	0.344978	17
ITPKB	5.242199	0.748886	7	TBX15	2.668844	0.156991	17
SOX6	5.231915	0.747416	7	NAV2	5.230587	0.326912	16
FBXL18	5.169746	0.861624	6	FOXP1	4.08692	0.255432	16
CRADD	5.025567	0.837595	6	GLI2	7.167995	0.477866	15
RUNDC3A	5.624716	1.124943	5	LRMDA	4.316013	0.287734	15
TSNAX-DISC1	5.453342	1.090668	5	EMX2OS	3.598047	0.23987	15
SOX10	5.45089	2.725445	2	ZBTB20	2.822678	0.188179	15
TABLE 138:	Cancer Type			CUX1	3.947981	0.281999	14
	PA_INF_FGFR			TBX5	3.517706	0.251265	14
	Gene site	imp_sum	imp_mean	PRKAG2	2.751418	0.19653	14
	PTPRN2	11.26445	0.137371	RPS6KA2	2.59765	0.185546	14
	PRDM16	8.496392	0.119667	IQSEC1	2.530759	0.180769	14
	PCDHGA1	3.049854	0.051692	MSI2	4.465475	0.343498	13
	PCDHGA2	2.733468	0.047956	RFX4	2.444632	0.188049	13
	PCDHGA3	3.049854	0.056479	CMIP	4.639566	0.38663	12
	PCDHGB1	3.049854	0.057544	MIRLET7BHG	2.910187	0.242516	12
	PCDHGA4	3.049854	0.059801	RAD51B	3.984986	0.362271	11
	PCDHGB2	3.049854	0.062242	VGLL4	3.739061	0.339915	11
	PCDHGA5	3.049854	0.064891	SLC38A10	2.577776	0.234343	11
			47	BCL11B	3.701392	0.370139	10

LBX1-AS1	3.091577	0.309158	10	PCDHGA1	9.007676	0.152672	59
NTM	2.980801	0.29808	10	PCDHGA2	9.007676	0.158029	57
GAS7	2.846296	0.28463	10	PCDHGA3	8.374904	0.155091	54
SH3RF3	2.667166	0.266717	10	PCDHGB1	8.374904	0.158017	53
SPPL2B	2.645354	0.264535	10	PCDHGA4	8.374904	0.164214	51
ACOT7	2.448463	0.244846	10	PCDHGB2	7.995381	0.163171	49
CHST11	2.421619	0.242162	10	PCDHGA5	7.177763	0.152718	47
NOTCH1	4.133478	0.459275	9	PCDHGB3	6.848598	0.15927	43
SND1	3.736434	0.415159	9	PCDHGA6	6.891039	0.172276	40
ATP11A	3.493815	0.388202	9	HDAC4	13.57788	0.36697	37
AXIN2	3.352521	0.372502	9	PCDHGA7	6.574653	0.177693	37
RUNX1	3.281493	0.36461	9	PAX6	11.37816	0.32509	35
ASAP1	3.213416	0.357046	9	RBFOX3	7.228479	0.206528	35
TSPAN9	3.02109	0.335677	9	PCDHGB4	5.610741	0.160307	35
TRAPPC12	2.816738	0.312971	9	PCDHGA8	5.610741	0.160307	35
PACS2	2.584394	0.287155	9	DIP2C	12.45531	0.389228	32
SLC22A18	2.443995	0.271555	9	PCDHGB5	5.335334	0.166729	32
MSRA	3.595183	0.449398	8	PCDHGA9	5.65172	0.182314	31
SMAD3	2.708286	0.338536	8	SOX2-OT	11.54569	0.398127	29
LINC00311	2.682674	0.335334	8	PCDHGB6	5.428568	0.187192	29
DNMT3A	2.550167	0.318771	8	PCDHGA10	5.744954	0.205177	28
MCC	2.440322	0.30504	8	GALNT9	4.869047	0.180335	27
DUSP6	4.996075	0.713725	7	SHANK2	7.031771	0.270453	26
SOX6	3.850643	0.550092	7	AGAP1	10.51541	0.420616	25
LINC00461	3.688793	0.52697	7	CAMTA1	10.12603	0.405041	25
NAV1	3.635722	0.519389	7	PDGFRA	8.291798	0.331672	25
LOC145845	3.302787	0.550464	6	SATB2	7.24036	0.301682	24
FBXL18	3.030425	0.505071	6	MEIS1	6.286198	0.261925	24
LRRFIP1	2.755256	0.459209	6	PCDHGB7	5.112182	0.213008	24
COQ8A	2.530892	0.421815	6	RPTOR	12.23551	0.531979	23
RUNDC3A	4.458772	0.891754	5	INPP5A	8.05987	0.350429	23
TEAD1	3.100721	0.620144	5	NCOR2	6.856589	0.298113	23
TSNAX-DISC1	2.784059	0.556812	5	NXN	5.412195	0.235313	23
STARD13	2.516872	0.503374	5	HOXB3	5.195531	0.225893	23
RBMS3	2.565293	0.641323	4	PRKCZ	6.410068	0.291367	22
DTNA	2.55449	0.638623	4	SKI	11.88106	0.565765	21
MYT1	2.492204	0.623051	4	ZIC4	5.131981	0.24438	21
LINC00856	2.470881	0.61772	4	SIM2	5.037634	0.239887	21
VOPPI	2.447651	0.611913	4	FRMD4A	8.255047	0.412752	20
GRIN2B	3.976503	1.325501	3	ABR	7.36424	0.368212	20
BFSP2	2.8358	0.945267	3	SDK1	4.85756	0.242878	20
SOX10	4.418234	2.209117	2	MAD1L1	10.80834	0.56886	19
SLC25A10	2.584089	1.292045	2	SMG1P2	8.670162	0.456324	19
				BOLA2	8.670162	0.456324	19
TABLE 139:	Cancer Type	PA_MID		LOC613038	8.670162	0.456324	19
Gene site	imp_sum	imp_mean	n	ZNF423	6.865541	0.361344	19
PTPRN2	24.92907	0.304013	82	FOXK1	9.060215	0.503345	18
PRDM16	22.38057	0.315219	71	TBC1D16	8.611254	0.478403	18

MCF2L	6.904808	0.3836	18	ARHGEF7	4.927637	0.985527	5
RBFOX1	6.215358	0.345298	18	SOX10	5.52976	2.76488	2
ANKRD11	6.088915	0.338273	18				
SEPTIN9	4.9001	0.272228	18	TABLE 140:	Cancer Type	PB_FOXR2	
OPCML	9.261312	0.544783	17	Gene site	imp_sum	imp_mean	n
PAX6-AS1	5.151432	0.303025	17	PTPRN2	7.990592	0.097446	82
RCN1	5.151432	0.303025	17	PRDM16	5.878697	0.082799	71
NAV2	6.342771	0.396423	16	HDAC4	9.817625	0.265341	37
FOXP1	5.687228	0.355452	16	PAX6	4.582936	0.130941	35
SORBS2	5.485831	0.342864	16	RBFOX3	4.257452	0.121641	35
GLI2	10.1483	0.676553	15	DIP2C	4.849074	0.151534	32
ZBTB20	6.74146	0.449431	15	GALNT9	4.664578	0.172762	27
EMX2OS	6.561478	0.437432	15	ADARB2	2.531088	0.09735	26
KIRREL3	5.503255	0.366884	15	CAMTA1	7.388806	0.295552	25
BAIAP2	4.921008	0.328067	15	AGAP1	5.664287	0.226571	25
RPS6KA2	7.793022	0.556644	14	PDGFRA	2.983932	0.119357	25
CUX1	6.182666	0.441619	14	MEIS1	2.457591	0.1024	24
IQSEC1	6.070246	0.433589	14	RPTOR	6.022756	0.261859	23
TBX5	5.372219	0.38373	14	NXN	4.43426	0.192794	23
PRKAG2	5.282265	0.377305	14	NCOR2	4.165875	0.181125	23
MSI2	6.939435	0.533803	13	RIMBP2	3.892405	0.169235	23
RFX4	5.583069	0.429467	13	INPP5A	3.431163	0.149181	23
MYT1L	5.004928	0.384994	13	SKI	4.913274	0.233965	21
SPTBN4	4.915305	0.3781	13	SDK1	2.733652	0.136683	20
CMIP	5.591839	0.465987	12	MAD1L1	10.74638	0.565599	19
FBRSL1	5.362243	0.446854	12	CASZ1	3.359893	0.176836	19
MEIS2	5.221624	0.435135	12	ZNF423	3.082744	0.16225	19
TNS3	4.892318	0.407693	12	SMG1P2	2.643986	0.139157	19
FGFR2	6.145005	0.558637	11	BOLA2	2.643986	0.139157	19
VGLL4	6.111036	0.555549	11	LOC613038	2.643986	0.139157	19
RAD51B	5.814694	0.528609	11	FO XK1	3.833278	0.21296	18
CCDC140	5.413668	0.492152	11	TBC1D16	2.536714	0.140929	18
LBX1-AS1	6.627648	0.662765	10	ANKRD11	2.507306	0.139295	18
SH3RF3	6.510324	0.651032	10	HBG2	5.796202	0.340953	17
NTM	4.970905	0.497091	10	TBX15	5.622326	0.330725	17
ATP11A	6.420082	0.713342	9	FOXP1	3.682609	0.230163	16
SND1	6.282092	0.69801	9	NAV2	3.015244	0.188453	16
NOTCH1	5.579218	0.619913	9	KNDC1	3.337509	0.222501	15
ADGRB1	5.235298	0.5817	9	SLX1B-			
TSPAN9	4.850493	0.538944	9	SULT1A4	2.538607	0.16924	15
LINC00311	6.110924	0.763866	8	SLX1A	2.538607	0.16924	15
GRIK2	5.325754	0.665719	8	LOC606724	2.538607	0.16924	15
MSRA	5.235986	0.654498	8	NFATC1	2.416337	0.161089	15
DLEU1	5.195263	0.649408	8	CUX1	2.668292	0.190592	14
DUSP6	7.486675	1.069525	7	C7orf50	2.4789	0.177064	14
LINC00461	5.641189	0.805884	7	TBX5	2.46133	0.175809	14
NAV1	5.002949	0.714707	7	MOB2	2.370305	0.169307	14
RUNDC3A	5.714321	1.142864	5	MSI2	4.002983	0.307922	13

MYT1L	3.035138	0.233472	13	CHTF18	4.125188	2.062594	2
GSE1	2.260512	0.173886	13	UTRN	2.665067	1.332534	2
TNS3	4.970195	0.414183	12	KIF21B	2.591026	1.295513	2
FBRSL1	3.684879	0.307073	12	UHRF1	2.588786	1.294393	2
ZC3H3	3.247704	0.270642	12	TRIM65	2.373132	1.186566	2
GNA12	2.330387	0.194199	12	DDX31	2.254488	1.127244	2
CTBP2	2.994621	0.272238	11	ARL6IP6	2.833138	2.833138	1
RAD51B	2.761373	0.251034	11	KCNV2	2.68683	2.68683	1
ETS1	2.687183	0.268718	10	DDT	2.658782	2.658782	1
AKAP13	2.401156	0.240116	10	DNAJC27	2.281123	2.281123	1
AUTS2	2.378175	0.237818	10				
SND1	4.92843	0.547603	9				
CACNA2D4	4.16434	0.462704	9	TABLE 141: Cancer Type PB_Grp1A			
ATP11A	3.792183	0.421354	9	Gene site	imp_sum	imp_mean	n
ADAMTS2	3.289882	0.365542	9	PTPRN2	13.14354	0.160287	82
TSPAN9	3.275225	0.363914	9	PRDM16	12.4281	0.175044	71
GPC6	2.691387	0.299043	9	PCDHGA1	4.717988	0.079966	59
PDE6B	2.400909	0.266768	9	PCDHGA2	4.717988	0.082772	57
RUNX1	2.349199	0.261022	9	PCDHGA3	4.290336	0.079451	54
MGMT	2.259619	0.251069	9	PCDHGB1	4.290336	0.08095	53
SSBP3	2.23661	0.248512	9	PCDHGA4	4.606722	0.090328	51
VRK2	5.188252	0.648532	8	PCDHGB2	4.606722	0.094015	49
PPP2R2B	3.874229	0.484279	8	PCDHGA5	4.606722	0.098015	47
DNMT3A	3.389235	0.423654	8	PCDHGB3	4.290336	0.099775	43
DLEU1	2.512305	0.314038	8	PCDHGA6	4.290336	0.107258	40
TRAPPC9	2.408322	0.30104	8	HDAC4	15.02807	0.406164	37
MIR124-2HG	2.862366	0.408909	7	PCDHGA7	3.97395	0.107404	37
F11R	2.743506	0.391929	7	RBFOX3	8.054898	0.23014	35
TRIM6-TRIM34	2.397273	0.342468	7	PAX6	6.607636	0.18879	35
PITPNC1	2.387203	0.341029	7	PCDHGB4	3.97395	0.113541	35
MIR548H4	2.325792	0.332256	7	PCDHGA8	3.97395	0.113541	35
HOTAIR	2.259323	0.32276	7	DIP2C	7.234737	0.226086	32
LDLRAD4	2.259092	0.322727	7	PCDHGB5	3.97395	0.124186	32
TRAK1	2.697156	0.449526	6	PCDHGA9	3.657564	0.117986	31
DNAJB6	2.595136	0.432523	6	GALNT9	5.728502	0.212167	27
MYO16	2.504651	0.417442	6	SHANK2	4.017317	0.154512	26
TRIM34	2.397273	0.399546	6	CAMTA1	9.204105	0.368164	25
TSNAX-DISC1	4.231114	0.846223	5	AGAP1	7.880278	0.315211	25
ARHGEF7	2.573357	0.514671	5	PDGFRA	3.962118	0.158485	25
TSTD1	2.266536	0.453307	5	PCDHGB7	4.265517	0.17773	24
GSG1	2.662472	0.665618	4	MEIS1	4.019856	0.167494	24
EXT1	2.49718	0.624295	4	RPTOR	10.82454	0.470632	23
RASGRP3	3.037567	1.012522	3	NCOR2	8.674575	0.377155	23
SLC25A22	2.963633	0.987878	3	NXN	8.626693	0.375074	23
SLC12A9	2.824573	0.941524	3	INPP5A	7.050943	0.306563	23
ANKRD33B	2.399937	0.799979	3	RIMBP2	6.203164	0.269703	23
CCDC167	2.397717	0.799239	3	PCDHGA11	4.265517	0.185457	23
DAGLB	2.310307	0.770102	3	PRKCZ	4.345374	0.197517	22

SKI	7.982678	0.380128	21	AXIN2	5.396535	0.599615	9
MAD1L1	14.00072	0.73688	19	TSPAN9	4.939725	0.548858	9
SMG1P2	6.150135	0.323691	19	ADAMTS2	4.653586	0.517065	9
BOLA2	6.150135	0.323691	19	ATP11A	4.587726	0.509747	9
LOC613038	6.150135	0.323691	19	CACNA2D4	4.375753	0.486195	9
CASZ1	6.003889	0.315994	19	PDE6B	3.91789	0.435321	9
KCNQ1	5.093913	0.268101	19	VRK2	8.419695	1.052462	8
CFAP46	3.876613	0.204032	19	PPP2R2B	4.94812	0.618515	8
ZNF423	3.739536	0.196818	19	TRAPPC9	3.803547	0.475443	8
FOXK1	5.324759	0.29582	18	ASPSCR1	3.785069	0.473134	8
SEPTIN9	3.795298	0.21085	18	DLEU1	3.769648	0.471206	8
ANKRD11	3.789854	0.210547	18	MIR548H4	4.051045	0.578721	7
HBG2	5.257775	0.309281	17	MIR124-2HG	3.881805	0.554544	7
TBX15	4.572216	0.268954	17	CALD1	4.047304	0.674551	6
OPCML	3.915604	0.23033	17	TRAK1	3.896317	0.649386	6
NAV2	5.577801	0.348613	16	TSNAX-DISC1	4.975083	0.995017	5
FOXP1	3.802156	0.237635	16	ARHGEF7	3.716847	0.743369	5
BAIAP2	4.821444	0.32143	15	CHTF18	4.686664	2.343332	2
KNDC1	4.609228	0.307282	15				
ZBTB20	4.515262	0.301017	15	TABLE 142:	Cancer Type PB_Grp1B		
CUX1	6.211835	0.443703	14	Gene site	imp_sum	imp_mean	n
C7orf50	5.385842	0.384703	14	PTPRN2	4.33509	0.052867	82
IQSEC1	5.384054	0.384575	14	PRDM16	3.020796	0.042546	71
MIR548F5	4.897931	0.349852	14	PCDHGA1	2.763024	0.046831	59
GNG7	3.984604	0.284615	14	PCDHGA2	2.763024	0.048474	57
MOB2	3.924169	0.280298	14	PCDHGA3	2.763024	0.051167	54
ARHGEF10	3.835325	0.273952	14	PCDHGB1	2.763024	0.052133	53
PCDHGA12	3.632745	0.259482	14	PCDHGA4	2.763024	0.054177	51
MSI2	8.145857	0.626604	13	PCDHGB2	2.763024	0.056388	49
MYT1L	5.718421	0.439879	13	PCDHGA5	2.763024	0.058788	47
GSE1	4.969846	0.382296	13	PCDHGB3	2.763024	0.064256	43
RFX4	4.509334	0.346872	13	HDAC4	8.343297	0.225495	37
FBRSL1	5.839394	0.486616	12	RBFOX3	4.992446	0.142641	35
MIRLET7BHG	5.794207	0.482851	12	AGAP1	2.587405	0.103496	25
ZC3H3	5.362076	0.44684	12	RPTOR	5.172582	0.224895	23
CMIP	4.219709	0.351642	12	INPP5A	4.131043	0.179611	23
MAML3	3.660775	0.305065	12	NXN	3.094062	0.134524	23
CTBP2	4.396751	0.399705	11	HOXB3	2.730562	0.11872	23
SLC38A10	4.038955	0.367178	11	SKI	3.986412	0.189829	21
RAD51B	3.924346	0.356759	11	FRMD4A	2.158766	0.107938	20
LBX1-AS1	5.08053	0.508053	10	MAD1L1	9.902993	0.52121	19
AKAP13	4.666204	0.46662	10	CASZ1	4.723625	0.248612	19
FMN1	4.42103	0.442103	10	SMG1P2	2.819412	0.14839	19
AUTS2	4.372976	0.437298	10	BOLA2	2.819412	0.14839	19
ETS1	4.309239	0.430924	10	LOC613038	2.819412	0.14839	19
NR5A2	4.294828	0.429483	10	FOXK1	3.799291	0.211072	18
NBEA	3.794825	0.379483	10	TBX15	4.455878	0.26211	17
SND1	6.776733	0.75297	9	FOXP1	4.913795	0.307112	16

NAV2	3.62173	0.226358	16	TSNAX-DISC1	3.917575	0.783515	5
DLX6-AS1	2.999526	0.199968	15	LOC100132215	2.575006	0.515001	5
GLI2	2.899444	0.193296	15	CACNA2D2	2.279359	0.455872	5
KIRREL3	2.675446	0.178363	15	CASP8	2.221321	0.444264	5
BAIAP2	2.320908	0.154727	15	OTP	2.208145	0.441629	5
CUX1	2.991178	0.213656	14	ARHGEF7	2.133698	0.42674	5
MIR548F5	2.280434	0.162888	14	ITGA5	2.638831	0.659708	4
PPP2R2A	2.269914	0.162137	14	EXT1	2.523982	0.630995	4
MSI2	4.460783	0.343137	13	GSG1	2.312788	0.578197	4
MYT1L	3.527057	0.271312	13	MSC-AS1	2.179854	0.544963	4
ZC3H3	3.987479	0.33229	12	SLC12A9	2.456232	0.818744	3
MIRLET7BHG	3.400021	0.283335	12	SLC1A7	2.330836	0.776945	3
CMIP	3.032205	0.252684	12	EPAS1	2.278496	0.759499	3
RAD51B	2.502474	0.227498	11	ANKRD33B	2.113427	0.704476	3
WNT5A	2.212228	0.201112	11	DAGLB	2.10671	0.702237	3
LBX1-AS1	4.354166	0.435417	10	CHTF18	3.997221	1.99861	2
AUTS2	3.360625	0.336062	10	TRIM65	2.555016	1.277508	2
ETS1	2.697473	0.269747	10	KIF21B	2.54759	1.273795	2
ANKS1B	2.618779	0.261878	10	UHRF1	2.546712	1.273356	2
RGS12	2.286667	0.228667	10	DDX31	2.195924	1.097962	2
SKOR1	2.18314	0.218314	10	ERI3	2.141521	1.07076	2
NR5A2	2.165993	0.216599	10	KCNV2	2.80926	2.80926	1
NBEA	2.145445	0.214545	10	DDT	2.680828	2.680828	1
BCL11B	2.102114	0.210211	10	ARL6IP6	2.602609	2.602609	1
SND1	4.161108	0.462345	9	DNAJC27	2.364602	2.364602	1
CACNA2D4	3.857369	0.428597	9				
ATP11A	3.444519	0.382724	9	TABLE 143:	Cancer Type PB_Grp2		
TSPAN9	3.284664	0.364963	9	Gene site	imp_sum	imp_mean	n
AXIN2	3.194411	0.354935	9	PTPRN2	5.879729	0.071704	82
MGMT	2.792104	0.310234	9	PRDM16	6.245735	0.087968	71
GPC6	2.725476	0.302831	9	PCDHGA1	2.531088	0.0429	59
RUNX1	2.635013	0.292779	9	PCDHGA2	2.531088	0.044405	57
VRK2	4.104786	0.513098	8	PCDHGA3	2.531088	0.046872	54
VEPH1	3.963503	0.495438	8	PCDHGB1	2.531088	0.047756	53
PPP2R2B	3.139021	0.392378	8	PCDHGA4	2.214702	0.043426	51
MACROD1	2.846503	0.355813	8	PCDHGB2	2.214702	0.045198	49
MSRA	2.51368	0.31421	8	PCDHGA5	2.214702	0.047121	47
TRAPPC9	2.181993	0.272749	8	HDAC4	6.957028	0.188028	37
DLEU1	2.165119	0.27064	8	PAX6	3.41803	0.097658	35
GDNF	3.616465	0.516638	7	DIP2C	3.646075	0.11394	32
MIR124-2HG	3.448424	0.492632	7	AGAP1	6.205598	0.248224	25
MIR548H4	3.005505	0.429358	7	CAMTA1	5.497657	0.219906	25
DUSP6	2.645882	0.377983	7	MEIS1	6.099519	0.254147	24
PITPNC1	2.205611	0.315087	7	INPP5A	4.568314	0.198622	23
NAV1	2.160334	0.308619	7	RPTOR	4.296497	0.186804	23
TRAK1	2.474917	0.412486	6	RIMBP2	3.736288	0.162447	23
COLEC11	2.403608	0.400601	6	NCOR2	3.441629	0.149636	23
ARHGAP18	2.123442	0.353907	6	HOXB3	2.803838	0.121906	23

NXN	2.478876	0.107777	23	TRAPPC9	3.05946	0.382433	8
PRKCZ	3.156096	0.143459	22	POU6F2	2.759699	0.344962	8
SKI	4.063587	0.193504	21	TENM2	2.439959	0.304995	8
FRMD4A	2.151691	0.107585	20	MIR124-2HG	2.84696	0.406709	7
MAD1L1	10.73492	0.564996	19	MIR548H4	2.247968	0.321138	7
CASZ1	4.948578	0.260451	19	PBX1	2.68946	0.448243	6
SMG1P2	4.05105	0.213213	19	ARHGAP18	2.545821	0.424303	6
BOLA2	4.05105	0.213213	19	TRAK1	2.507813	0.417969	6
LOC613038	4.05105	0.213213	19	COLEC11	2.262199	0.377033	6
ZNF423	2.440375	0.128441	19	DNAJB6	2.220931	0.370155	6
ANKRD11	3.160691	0.175594	18	FBXL18	2.177682	0.362947	6
FOXK1	2.457772	0.136543	18	TSNAX-DISC1	4.397586	0.879517	5
TBX15	4.553703	0.267865	17	OTP	3.698275	0.739655	5
FOXP1	6.345018	0.396564	16	ARHGEF7	2.679132	0.535826	5
NAV2	3.64718	0.227949	16	IL17D	2.157772	0.431554	5
EBF3	2.315293	0.144706	16	SDK2	2.15301	0.430602	5
KNDC1	2.920987	0.194732	15	GSG1	2.673792	0.668448	4
BAIAP2	2.468116	0.164541	15	EXT1	2.545343	0.636336	4
SLX1B-				PCSK9	2.268441	0.56711	4
SULT1A4	2.427079	0.161805	15	SLC25A22	2.812923	0.937641	3
SLX1A	2.427079	0.161805	15	LOC339874	2.524663	0.841554	3
LOC606724	2.427079	0.161805	15	DAGLB	2.358333	0.786111	3
NFIX	2.350296	0.156686	15	ARMC2	2.267345	0.755782	3
NFATC1	2.289517	0.152634	15	RASGRP3	2.162284	0.720761	3
GLI2	2.25982	0.150655	15	CHTF18	4.034748	2.017374	2
ARHGEF10	3.657226	0.26123	14	KIF21B	2.700938	1.350469	2
GNG7	2.38778	0.170556	14	UHRF1	2.699644	1.349822	2
PRKAG2	2.314672	0.165334	14	TRIM65	2.5883	1.29415	2
MYT1L	5.2682	0.405246	13	UTRN	2.432967	1.216483	2
MSI2	2.388799	0.183754	13	KCNV2	2.747887	2.747887	1
MIRLET7BHG	5.382895	0.448575	12	ARL6IP6	2.674833	2.674833	1
ZC3H3	3.236118	0.269677	12	DDT	2.616198	2.616198	1
FBRSL1	2.620636	0.218386	12	DNAJC27	2.40222	2.40222	1
CMIP	2.242281	0.186857	12				
AKAP13	2.754346	0.275435	10	TABLE 144: Cancer Type PGG			
LBX1-AS1	2.32726	0.232726	10	Gene site	imp_sum	imp_mean	n
NR5A2	2.32255	0.232255	10	PTPRN2	16.42773	0.200338	82
NBEA	2.279871	0.227987	10	PRDM16	14.89853	0.209838	71
KCNIP4	2.153457	0.215346	10	PCDHGA1	5.194941	0.08805	59
SND1	4.69454	0.521616	9	PCDHGA2	4.647119	0.081528	57
ADAMTS2	4.195005	0.466112	9	PCDHGA3	4.647119	0.086058	54
TSPAN9	4.119054	0.457673	9	PCDHGB1	4.647119	0.087681	53
CACNA2D4	3.496569	0.388508	9	PCDHGA4	4.647119	0.09112	51
MGMT	3.047656	0.338628	9	PCDHGB2	4.330733	0.088382	49
ATP11A	2.55549	0.283943	9	PCDHGA5	4.330733	0.092143	47
VRK2	4.823612	0.602952	8	PCDHGB3	4.014347	0.093357	43
DNMT3A	3.277359	0.40967	8	PCDHGA6	3.697961	0.092449	40
PPP2R2B	3.154545	0.394318	8	HDAC4	14.70154	0.397339	37

PCDHGA7	3.697961	0.099945	37	ARHGEF10	4.04954	0.289253	14
PAX6	9.396488	0.268471	35	PRKAG2	3.917642	0.279832	14
RBFOX3	6.943902	0.198397	35	MIR548F5	3.862537	0.275896	14
DIP2C	12.19685	0.381152	32	MSI2	6.451313	0.496255	13
PCDHGB5	3.697961	0.115561	32	MYT1L	5.457573	0.419813	13
PCDHGA9	3.697961	0.119289	31	GSE1	4.099706	0.315362	13
GALNT9	4.477861	0.165847	27	KIF26B	3.745511	0.288116	13
SHANK2	6.641535	0.255444	26	MIRLET7BHG	5.921882	0.49349	12
ADARB2	4.992732	0.192028	26	ZC3H3	4.467121	0.37226	12
AGAP1	7.522315	0.300893	25	ADGRD1	4.429613	0.369134	12
CAMTA1	6.748919	0.269957	25	MAML3	4.106386	0.342199	12
PDGFRA	6.040879	0.241635	25	FBRSL1	3.995056	0.332921	12
MEIS1	4.902005	0.20425	24	RAD51B	4.875002	0.443182	11
SATB2	4.458027	0.185751	24	CACNA1C	4.625387	0.42049	11
RPTOR	10.34906	0.449959	23	CTBP2	4.50338	0.409398	11
NCOR2	6.429091	0.279526	23	TBCD	4.406564	0.400597	11
NXN	4.656189	0.202443	23	ZC3H12D	3.972821	0.361166	11
INPP5A	4.200631	0.182636	23	TSPAN4	4.339881	0.433988	10
RIMBP2	4.182212	0.181835	23	ACOT7	4.068272	0.406827	10
PRKCZ	6.843107	0.31105	22	GAS7	3.926778	0.392678	10
SKI	6.831861	0.325327	21	SND1	7.366746	0.818527	9
SIM2	4.967137	0.23653	21	ADAMTS2	6.07964	0.675516	9
ZIC4	4.39678	0.20937	21	ATP11A	4.000599	0.444511	9
HOXA-AS3	4.352134	0.207244	21	TSPAN9	3.858385	0.428709	9
ABR	5.548789	0.277439	20	CACNA2D4	3.789858	0.421095	9
SDK1	5.017472	0.250874	20	SYNJ2	5.070239	0.63378	8
FRMD4A	4.471013	0.223551	20	MSRA	4.537357	0.56717	8
MAD1L1	13.69728	0.720909	19	CELF4	4.18234	0.522792	8
SMG1P2	6.309543	0.332081	19	DNMT3A	4.131511	0.516439	8
BOLA2	6.309543	0.332081	19	C19orf25	5.169302	0.738472	7
LOC613038	6.309543	0.332081	19	NAV1	4.871626	0.695947	7
CASZ1	5.556523	0.292449	19	RXRA	4.485045	0.640721	7
KCNQ1	5.062779	0.266462	19	GAK	4.428979	0.632711	7
ZNF423	4.958846	0.260992	19	FBXL18	5.28216	0.88036	6
FO XK1	8.033926	0.446329	18	COQ8A	3.727351	0.621225	6
ANKRD11	6.119522	0.339973	18	TSNAX-DISC1	5.16109	1.032218	5
HOXA3	4.581533	0.25453	18	ARHGEF7	3.877893	0.775579	5
SEPTIN9	3.734312	0.207462	18	DAGLB	3.770107	1.256702	3
OPCML	7.091087	0.417123	17	SLC25A10	3.948105	1.974052	2
FOXP1	8.141302	0.508831	16	GRTP1	3.86273	3.86273	1
EBF3	4.276513	0.267282	16				
SORBS2	3.805694	0.237856	16	TABLE 145:	Cancer Type PGNT		
GLI2	5.218606	0.347907	15	Gene site	imp_sum	imp_mean	n
BAIAP2	4.62765	0.30851	15	PTPRN2	9.670636	0.117935	82
ZBTB20	3.998661	0.266577	15	PRDM16	8.537715	0.12025	71
RPS6KA2	6.719789	0.479985	14	PCDHGA1	2.847474	0.048262	59
CUX1	5.035008	0.359643	14	PCDHGA2	2.847474	0.049956	57
C7orf50	4.943359	0.353097	14	PCDHGA3	2.847474	0.052731	54

PCDHGB1	2.847474	0.053726	53	BCL11B	2.919731	0.291973	10
PCDHGA4	2.847474	0.055833	51	CHST11	2.693586	0.269359	10
PCDHGB2	2.531088	0.051655	49	ACOT7	2.588561	0.258856	10
PCDHGA5	2.214702	0.047121	47	KLHL29	2.406422	0.240642	10
HDAC4	7.100621	0.191909	37	TSPAN4	2.280454	0.228045	10
PAX6	4.879341	0.13941	35	ATP11A	3.527614	0.391957	9
RBFOX3	2.850514	0.081443	35	KCNMA1	3.421058	0.380118	9
DIP2C	5.382506	0.168203	32	NOTCH1	3.228355	0.358706	9
SOX2-OT	2.240588	0.077262	29	SND1	2.915387	0.323932	9
SHANK2	3.518303	0.135319	26	AXIN2	2.791748	0.310194	9
AGAP1	5.469833	0.218793	25	TSPAN9	2.749423	0.305491	9
CAMTA1	4.959348	0.198374	25	ASAP1	2.576769	0.286308	9
MEIS1	2.463832	0.10266	24	ADGRB1	2.478578	0.275398	9
RPTOR	6.32875	0.275163	23	KCNH2	2.303838	0.255982	9
PRKCZ	3.144122	0.142915	22	BAHCC1	3.218199	0.402275	8
SKI	5.674442	0.270212	21	MSRA	3.205927	0.400741	8
SIM2	2.861346	0.136255	21	GRIK2	2.896612	0.362077	8
FRMD4A	5.798668	0.289933	20	RORA	2.826827	0.353353	8
MAD1L1	6.815063	0.358688	19	SYNJ2	2.665264	0.333158	8
ZNF423	5.541159	0.29164	19	RGS20	2.654073	0.331759	8
SMG1P2	3.766805	0.198253	19	DNMT3A	2.543642	0.317955	8
BOLA2	3.766805	0.198253	19	LINC00311	2.510965	0.313871	8
LOC613038	3.766805	0.198253	19	DPP6	2.350778	0.293847	8
SEPTIN9	3.855717	0.214207	18	ARHGAP22	2.221081	0.277635	8
FOXK1	3.789053	0.210503	18	DUSP6	3.995818	0.570831	7
MCF2L	2.451037	0.136169	18	NAV1	3.539936	0.505705	7
TBC1D16	2.251131	0.125063	18	LINC00461	2.956634	0.422376	7
OPCML	6.251591	0.367741	17	FBXL18	2.998454	0.499742	6
TBX15	2.563061	0.150768	17	COQ8A	2.471408	0.411901	6
SORBS2	4.230863	0.264429	16	FAM181A	2.180075	0.363346	6
FOXP1	3.326476	0.207905	16	CACNA2D3	2.170913	0.361819	6
NAV2	2.86515	0.179072	16	RUNDC3A	4.022233	0.804447	5
GLI2	8.035971	0.535731	15	TSNAX-DISC1	3.170826	0.634165	5
ZBTB20	2.977912	0.198527	15	ARHGEF7	2.536285	0.507257	5
KIRREL3	2.341256	0.156084	15	RBMS3	2.939999	0.735	4
IQSEC1	3.602837	0.257345	14	LINC00856	2.41614	0.604035	4
CUX1	2.624781	0.187484	14	DTNA	2.32145	0.580363	4
MYT1L	3.361744	0.258596	13	CORO2B	2.251054	0.562763	4
MSI2	3.038353	0.233719	13	DAGLB	2.701334	0.900445	3
RFX4	2.731063	0.210082	13	RGL1	2.50912	0.836373	3
MIR9-3HG	2.453844	0.188757	13	LOXL3	2.453125	0.817708	3
CMIP	2.524447	0.210371	12	GRIN2B	2.211003	0.737001	3
ADGRD1	2.355411	0.196284	12	SOX10	4.516727	2.258363	2
MEIS2	2.345753	0.195479	12	CORO1C	2.939766	1.469883	2
MIRLET7BHG	2.28207	0.190173	12	SLC25A10	2.621386	1.310693	2
RAD51B	3.396644	0.308786	11	SMURF1	2.53297	1.266485	2
LBX1-AS1	3.297492	0.329749	10	DUSP7	3.308439	3.308439	1
SH3RF3	3.275721	0.327572	10				

TABLE 146:	Cancer Type PIN_CYT			GPC6	2.079566	0.231063	9
Gene site	imp_sum	imp_mean	n	CACNA2D4	1.944875	0.216097	9
PTPRN2	1.741058	0.021232	82	AXIN2	1.744232	0.193804	9
PRDM16	3.334924	0.046971	71	ATP11A	1.715972	0.190664	9
HDAC4	5.936564	0.160448	37	SSBP3	1.468395	0.163155	9
RBFOX3	1.518927	0.043398	35	VRK2	2.977551	0.372194	8
GALNT9	2.24148	0.083018	27	PPP2R2B	2.61938	0.327422	8
CAMTA1	3.032036	0.121281	25	DNMT3A	2.384503	0.298063	8
AGAP1	2.468052	0.098722	25	NR2E1	1.935458	0.241932	8
PDGFRA	1.916142	0.076646	25	DLEU1	1.926288	0.240786	8
INPP5A	3.35832	0.146014	23	MCIDAS	1.619196	0.202399	8
RIMBP2	2.847474	0.123803	23	AFF3	1.575851	0.196981	8
RPTOR	2.690902	0.116996	23	NAV1	2.3868	0.340971	7
NXN	1.606425	0.069845	23	MIR548H4	1.755887	0.250841	7
PRKCZ	2.295075	0.104322	22	LDLRAD4	1.680758	0.240108	7
SKI	2.26782	0.107991	21	NRG1	1.569307	0.224187	7
SIM2	1.479891	0.070471	21	PACRG	1.542894	0.220413	7
ABR	2.010051	0.100503	20	TRAK1	2.55303	0.425505	6
MAD1L1	7.546451	0.397182	19	CRADD	2.177719	0.362953	6
SMG1P2	2.546606	0.134032	19	CCDC85C	1.924137	0.32069	6
BOLA2	2.546606	0.134032	19	PRKCE	1.78586	0.297643	6
LOC613038	2.546606	0.134032	19	HIVEP3	1.765887	0.294315	6
CASZ1	1.756619	0.092454	19	FBXL18	1.574633	0.262439	6
ANKRD11	1.688539	0.093808	18	STK24	1.44151	0.240252	6
BAIAP2	3.160719	0.210715	15	TSNAX-DISC1	3.510266	0.702053	5
GLI2	1.781405	0.11876	15	VAV2	2.269564	0.453913	5
KNDC1	1.753354	0.11689	15	SNX29	1.787393	0.357479	5
KIRREL3	1.430049	0.095337	15	SCOC	1.782484	0.356497	5
CUX1	2.227876	0.159134	14	ARHGEF7	1.750087	0.350017	5
MIR548F5	1.83105	0.130789	14	SDK2	1.669768	0.333954	5
IQSEC1	1.792469	0.128034	14	BCAR1	1.634295	0.326859	5
ARHGEF10	1.58193	0.112995	14	PARD3	1.515853	0.303171	5
MYT1L	2.873446	0.221034	13	EXT1	2.145258	0.536314	4
MSI2	2.667305	0.205177	13	EML1	1.453677	0.363419	4
RFX4	2.219412	0.170724	13	DAGLB	2.341444	0.780481	3
GSE1	1.898316	0.146024	13	SLC25A22	1.992387	0.664129	3
ZC3H3	2.480448	0.206704	12	LOC339874	1.933398	0.644466	3
CMIP	2.010323	0.167527	12	BFSP2	1.802792	0.600931	3
TBCD	1.497155	0.136105	11	CHTF18	3.607335	1.803668	2
ACOT7	1.987582	0.198758	10	TRIM65	2.240251	1.120126	2
LBX1-AS1	1.898316	0.189832	10	UHRF1	1.879138	0.939569	2
AUTS2	1.756206	0.175621	10	DISC1	1.837896	0.918948	2
CHST11	1.58193	0.158193	10	ERI3	1.784265	0.892132	2
ETS1	1.459477	0.145948	10	KIF21B	1.741481	0.87074	2
SND1	4.04963	0.449959	9	SLC25A10	1.56997	0.784985	2
ADAMTS2	2.74312	0.304791	9	KCNV2	2.351678	2.351678	1
MGMT	2.635724	0.292858	9	ARL6IP6	2.349183	2.349183	1
TSPAN9	2.101132	0.233459	9	DNAJC27	2.020613	2.020613	1

DDT	1.965552	1.965552	1	HBG2	3.055271	0.179722	17
GTF2E2	1.722938	1.722938	1	FOXP1	5.64517	0.352823	16
DLG4	1.600331	1.600331	1	GLI2	3.31874	0.221249	15
SMAGP	1.589762	1.589762	1	ZBTB20	2.717999	0.1812	15
CAMK4	1.487366	1.487366	1	MOB2	3.821702	0.272979	14
CPEB4	1.450927	1.450927	1	C7orf50	3.812754	0.27234	14
				CUX1	3.309291	0.236378	14
TABLE 147: Cancer Type PIN_RB				MYT1L	5.914172	0.454936	13
Gene site	imp_sum	imp_mean	n	MSI2	5.606145	0.431242	13
PTPRN2	6.807633	0.08302	82	GSE1	3.507548	0.269811	13
PRDM16	8.820872	0.124238	71	RFX4	3.292323	0.253256	13
PCDHGA1	3.070622	0.052044	59	HOXC4	3.167416	0.243647	13
PCDHGA2	3.070622	0.053871	57	FBRSL1	3.437212	0.286434	12
PCDHGA3	3.070622	0.056863	54	ZC3H3	2.976908	0.248076	12
PCDHGB1	2.754236	0.051967	53	ADGRD1	2.819879	0.23499	12
PCDHGA4	2.754236	0.054005	51	VGLL4	3.617583	0.328871	11
PCDHGB2	2.754236	0.056209	49	CTBP2	3.607351	0.327941	11
HDAC4	10.06115	0.271923	37	RAD51B	3.084489	0.280408	11
PCDHGA7	2.754236	0.074439	37	AUTS2	3.876295	0.38763	10
RBFOX3	7.194733	0.205564	35	AKAP13	3.807734	0.380773	10
PAX6	4.643137	0.132661	35	LBX1-AS1	3.365908	0.336591	10
PCDHGB4	2.754236	0.078692	35	ANKS1B	3.045053	0.304505	10
PCDHGA8	2.754236	0.078692	35	ETS1	2.974553	0.297455	10
DIP2C	5.631461	0.175983	32	KLHL29	2.870455	0.287046	10
PCDHGB5	2.754236	0.08607	32	ACOT7	2.7672	0.27672	10
PCDHGA9	2.754236	0.088846	31	SH3RF3	2.758512	0.275851	10
GALNT9	4.351717	0.161175	27	SND1	6.161496	0.684611	9
SHANK2	2.77855	0.106867	26	ADAMTS2	5.206113	0.578457	9
AGAP1	7.896254	0.31585	25	ATP11A	4.405099	0.489455	9
CAMTA1	5.377977	0.215119	25	TSPAN9	4.084057	0.453784	9
RPTOR	7.070887	0.30743	23	CACNA2D4	3.871799	0.4302	9
NXN	6.481997	0.281826	23	AXIN2	3.679095	0.408788	9
INPP5A	6.462468	0.280977	23	GPC6	2.841096	0.315677	9
NCOR2	4.823809	0.209731	23	TRAPPC12	2.810486	0.312276	9
HOXB3	3.182751	0.13838	23	PACS2	2.7717	0.307967	9
PRKCZ	4.531267	0.205967	22	VRK2	5.571942	0.696493	8
SKI	5.140933	0.244806	21	PPP2R2B	4.519998	0.565	8
MAD1L1	11.37283	0.59857	19	MSRA	3.153244	0.394156	8
KCNQ1	4.609785	0.24262	19	LHX4	3.040615	0.380077	8
CASZ1	4.242069	0.223267	19	DNMT3A	2.998912	0.374864	8
CFAP46	3.058498	0.160974	19	ASPSCR1	2.759335	0.344917	8
SEPTIN9	4.156349	0.230908	18	PITPNC1	3.392984	0.484712	7
TBC1D16	4.078198	0.226567	18	VPS13D	3.215465	0.459352	7
FO XK1	3.599246	0.199958	18	MIR548H4	2.873085	0.410441	7
RBFOX1	2.905804	0.161434	18	NAV1	2.784796	0.397828	7
TBX15	3.849284	0.226428	17	TRAK1	2.702981	0.450497	6
PAX6-AS1	3.403635	0.200214	17	TSNAX-DISC1	4.436183	0.887237	5
RCN1	3.403635	0.200214	17	ARHGEF7	3.758143	0.751629	5

	SDK2	3.042551	0.60851	5	HOXB3	3.719388	0.161713	23
	CPEB1-AS1	2.902565	0.580513	5	PRKCZ	5.345998	0.243	22
	GSG1	3.067506	0.766877	4	SKI	7.127028	0.339382	21
	EXT1	2.905124	0.726281	4	SDK1	6.179441	0.308972	20
	CCDC167	2.885096	0.961699	3	MAD1L1	12.31632	0.648227	19
	DAGLB	2.788926	0.929642	3	CASZ1	5.175372	0.272388	19
	CHTF18	4.526632	2.263316	2	SMG1P2	4.984239	0.262328	19
	UHRF1	2.829708	1.414854	2	BOLA2	4.984239	0.262328	19
	TRIM65	2.721111	1.360556	2	LOC613038	4.984239	0.262328	19
	ANKLE2	2.696564	1.348282	2	KCNQ1	4.91896	0.258893	19
	KCNV2	3.041097	3.041097	1	ZNF423	3.344899	0.176047	19
	DDT	2.931778	2.931778	1	FOXK1	7.797997	0.433222	18
	ARL6IP6	2.85111	2.85111	1	MCF2L	5.436094	0.302005	18
TABLE 148:	Cancer Type PITAD_ACTH				TBC1D16	5.1288	0.284933	18
					ANKRD11	4.182539	0.232363	18
					OPCML	6.113981	0.359646	17
Gene site	imp_sum	imp_mean	n		PAX6-AS1	4.225622	0.248566	17
	PTPRN2	19.17421	0.233832	82	RCN1	4.225622	0.248566	17
	PRDM16	9.122084	0.12848	71	HBG2	4.047264	0.238074	17
	PCDHGA1	5.542064	0.093933	59	FOXP1	7.553211	0.472076	16
	PCDHGA2	5.138416	0.090148	57	GLI2	3.75433	0.250289	15
	PCDHGA3	4.82203	0.089297	54	BAIAP2	3.658439	0.243896	15
	PCDHGB1	4.505644	0.085012	53	CUX1	6.189493	0.442107	14
	PCDHGA4	3.741984	0.073372	51	IQSEC1	5.463401	0.390243	14
	PCDHGB2	3.741984	0.076367	49	PRKAG2	5.378718	0.384194	14
	PCDHGA5	3.425598	0.072885	47	RPS6KA2	4.50413	0.321724	14
	PCDHGB3	3.425598	0.079665	43	C7orf50	3.729526	0.266395	14
	PCDHGA6	3.741984	0.09355	40	MIR548F5	3.263675	0.23312	14
	HDAC4	12.09289	0.326835	37	GSE1	5.168568	0.397582	13
	PCDHGA7	3.425598	0.092584	37	MSI2	4.73444	0.364188	13
	PAX6	10.45792	0.298798	35	MYT1L	3.517965	0.270613	13
	RBFOX3	7.596219	0.217035	35	CMIP	6.7903	0.565858	12
	PCDHGB4	3.425598	0.097874	35	FBRSL1	5.656115	0.471343	12
	PCDHGA8	3.425598	0.097874	35	GNA12	4.95367	0.412806	12
	DIP2C	6.007771	0.187743	32	ZC3H3	4.462214	0.371851	12
	PCDHGB5	3.425598	0.10705	32	TNS3	4.14463	0.345386	12
	GALNT9	3.861279	0.14301	27	ADGRD1	3.764111	0.313676	12
	SHANK2	6.779732	0.260759	26	CTNNA2	3.461448	0.288454	12
	ADARB2	3.476029	0.133693	26	CACNA1C	4.810843	0.437349	11
	AGAP1	11.98423	0.479369	25	AKAP13	4.99846	0.499846	10
	CAMTA1	7.135416	0.285417	25	ACOT7	4.708338	0.470834	10
	PDGFRA	4.281752	0.17127	25	TP73	3.68141	0.368141	10
	MEIS1	3.580472	0.149186	24	MAML2	3.65158	0.365158	10
	RPTOR	12.00629	0.522013	23	CHST11	3.513526	0.351353	10
	NCOR2	5.886835	0.255949	23	RGS12	3.455723	0.345572	10
	RIMBP2	5.040982	0.219173	23	TSPAN4	3.341946	0.334195	10
	INPP5A	4.731128	0.205701	23	STK32C	3.235654	0.323565	10
	NXN	4.077344	0.177276	23	SND1	7.617901	0.846433	9

ATP11A	7.281694	0.809077	9	PRKCZ	6.175028	0.280683	22
ADAMTS2	4.790399	0.532267	9	SKI	9.224385	0.439256	21
SSBP3	3.831948	0.425772	9	SDK1	5.625445	0.281272	20
TSPAN9	3.532304	0.392478	9	ABR	4.106215	0.205311	20
CPNE4	3.276085	0.364009	9	FRMD4A	3.90104	0.195052	20
SYNJ2	3.941616	0.492702	8	MAD1L1	12.00363	0.63177	19
VRK2	3.743569	0.467946	8	CASZ1	6.659107	0.350479	19
DNMT3A	3.547929	0.443491	8	SMG1P2	4.54033	0.238965	19
TRAPPC9	3.488493	0.436062	8	BOLA2	4.54033	0.238965	19
MSRA	3.329945	0.416243	8	LOC613038	4.54033	0.238965	19
NAV1	4.903574	0.700511	7	KCNQ1	4.009293	0.211015	19
C19orf25	4.106974	0.586711	7	ZNF423	3.732505	0.196448	19
ITPK1	3.776112	0.539445	7	FOXK1	7.302009	0.405667	18
GAK	3.584731	0.512104	7	ANKRD11	5.736872	0.318715	18
SLC22A18AS	3.579437	0.596573	6	SEPTIN9	4.774176	0.265232	18
COQ8A	3.330149	0.555025	6	TBC1D16	3.603049	0.200169	18
FBXL18	3.249672	0.541612	6	MCF2L	3.522413	0.19569	18
ARHGEF7	3.920434	0.784087	5	FOXP1	6.732947	0.420809	16
AP2A2	3.275345	0.655069	5	NAV2	5.31472	0.33217	16
DAGLB	3.283237	1.094412	3	KIRREL3	5.025011	0.335001	15
CHTF18	3.458887	1.729444	2	GLI2	4.239524	0.282635	15
TABLE 149:	Cancer Type PITAD_GON			NFIX	3.86524	0.257683	15
				ZBTB20	3.610608	0.240707	15
Gene site	imp_sum	imp_mean	n	RPS6KA2	6.927184	0.494799	14
PTPRN2	15.85732	0.193382	82	PRKAG2	5.894677	0.421048	14
PRDM16	12.4923	0.175948	71	CUX1	4.79929	0.342806	14
PCDHGA1	3.525377	0.059752	59	C7orf50	4.465788	0.318985	14
PCDHGA2	3.525377	0.061849	57	MSI2	6.420891	0.493915	13
PCDHGA3	3.841763	0.071144	54	GSE1	4.474357	0.344181	13
PCDHGB1	3.525377	0.066517	53	MYT1L	3.477324	0.267486	13
PCDHGA4	3.525377	0.069125	51	CMIP	6.222363	0.51853	12
PCDHGA5	3.525377	0.075008	47	ZC3H3	4.932071	0.411006	12
PCDHGB3	3.525377	0.081986	43	FBRSL1	4.480177	0.373348	12
PCDHGA6	3.525377	0.088134	40	GNA12	4.310212	0.359184	12
HDAC4	13.45165	0.363558	37	ADGRD1	4.306251	0.358854	12
PAX6	7.585868	0.216739	35	MIRLET7BHG	3.922727	0.326894	12
RBFOX3	6.519025	0.186258	35	TNS3	3.742759	0.311897	12
DIP2C	9.028569	0.282143	32	MAML3	3.663325	0.305277	12
GALNT9	6.832147	0.253042	27	CTBP2	4.493697	0.408518	11
SHANK2	5.430148	0.208852	26	RAD51B	3.947974	0.358907	11
ADARB2	3.809447	0.146517	26	AKAP13	5.092606	0.509261	10
AGAP1	11.92867	0.477147	25	TSPAN4	4.565719	0.456572	10
CAMTA1	6.389659	0.255586	25	ACOT7	4.106723	0.410672	10
RPTOR	12.3548	0.537165	23	CHST11	3.920325	0.392032	10
NCOR2	7.588369	0.329929	23	SND1	6.453557	0.717062	9
NXN	7.13107	0.310047	23	ATP11A	6.421095	0.713455	9
INPP5A	5.005737	0.217641	23	ADAMTS2	5.474662	0.608296	9
RIMBP2	4.987523	0.216849	23	CACNA2D4	4.585301	0.509478	9

TRAPPC12	4.327882	0.480876	9	SHANK2	3.848093	0.148004	26
KCNH2	3.714634	0.412737	9	AGAP1	6.120262	0.24481	25
AXIN2	3.553005	0.394778	9	CAMTA1	5.518994	0.22076	25
ASAP1	3.381626	0.375736	9	RPTOR	8.079101	0.351265	23
VRK2	5.230801	0.65385	8	NCOR2	5.196516	0.225935	23
SYNJ2	4.191457	0.523932	8	NXN	4.64885	0.202124	23
MSRA	4.182854	0.522857	8	INPP5A	3.51989	0.153039	23
PPP2R2B	4.044417	0.505552	8	RIMBP2	3.375559	0.146763	23
LINC00311	3.788514	0.473564	8	PCDHGA11	2.531088	0.110047	23
AFF3	3.6804	0.46005	8	PRKCZ	6.614886	0.300677	22
MACROD1	3.556003	0.4445	8	SKI	7.920704	0.377176	21
DNMT3A	3.45295	0.431619	8	SDK1	6.738556	0.336928	20
VPS13D	4.166295	0.595185	7	FRMD4A	4.832466	0.241623	20
MIR548H4	3.94891	0.56413	7	ABR	3.304098	0.165205	20
GAK	3.462955	0.494708	7	MAD1L1	9.049154	0.476271	19
NAV1	3.447503	0.4925	7	CFAP46	3.751009	0.197422	19
RXRA	3.371265	0.481609	7	KCNQ1	3.581092	0.188479	19
CRADD	5.277152	0.879525	6	SMG1P2	2.951013	0.155316	19
FBXL18	4.201993	0.700332	6	BOLA2	2.951013	0.155316	19
SLC22A18AS	3.40043	0.566738	6	LOC613038	2.951013	0.155316	19
TSNAX-DISC1	5.18505	1.03701	5	FOXK1	6.068214	0.337123	18
ARHGEF7	4.85859	0.971718	5	ANKRD11	3.188781	0.177154	18
AP2A2	4.302334	0.860467	5	OPCML	4.582781	0.269575	17
RUNDC3A	4.192518	0.838504	5	FOXP1	5.549672	0.346855	16
FAM53B	3.451051	0.69021	5	EBF3	3.280538	0.205034	16
DENND2B	3.757544	0.939386	4	NAV2	3.09908	0.193693	16
CHTF18	3.908401	1.954201	2	GLI2	4.199646	0.279976	15
ANKLE2	3.602716	1.801358	2	ZBTB20	3.087348	0.205823	15
TABLE 150:	Cancer Type PITAD_PRL			KIRREL3	3.044419	0.202961	15
				ARHGEF10	4.468218	0.319158	14
Gene site	imp_sum	imp_mean	n	CUX1	3.573829	0.255273	14
PTPRN2	10.92341	0.133212	82	PRKAG2	2.858734	0.204195	14
PRDM16	17.84186	0.251294	71	RPS6KA2	2.641252	0.188661	14
PCDHGA1	2.870937	0.04866	59	RFX4	3.881895	0.298607	13
PCDHGA2	3.480246	0.061057	57	GSE1	2.848839	0.219141	13
PCDHGA3	3.16386	0.05859	54	TNS3	4.855949	0.404662	12
PCDHGB1	3.16386	0.059695	53	CMIP	4.550525	0.37921	12
PCDHGA4	3.16386	0.062036	51	FBRSL1	3.956517	0.32971	12
PCDHGB2	3.16386	0.064569	49	ZC3H3	3.604721	0.300393	12
PCDHGA5	3.16386	0.067316	47	ADGRD1	2.568643	0.214054	12
PCDHGB3	2.531088	0.058863	43	SLC38A10	3.41188	0.310171	11
HDAC4	9.680024	0.261622	37	RAD51B	3.317418	0.301583	11
PCDHGA7	2.531088	0.068408	37	CACNA1C	3.123701	0.283973	11
RBFOX3	9.268066	0.264802	35	TBCD	2.849245	0.259022	11
PAX6	4.731554	0.135187	35	AKAP13	3.419932	0.341993	10
DIP2C	4.837681	0.151178	32	CHST11	3.350029	0.335003	10
GALNT9	3.34937	0.124051	27	KLHL29	3.337935	0.333793	10
ADARB2	4.48861	0.172639	26	ACOT7	2.874701	0.28747	10

TSPAN4	2.770126	0.277013	10	ADARB2	2.548463	0.098018	26
NBEA	2.651581	0.265158	10	AGAP1	6.683091	0.267324	25
KCNH2	5.639847	0.62665	9	CAMTA1	4.304365	0.172175	25
ATP11A	4.264072	0.473786	9	PDGFRA	2.864174	0.114567	25
KAZN	3.524144	0.391572	9	SATB2	2.826366	0.117765	24
SND1	3.523703	0.391523	9	RPTOR	6.468808	0.281253	23
AXIN2	3.172624	0.352514	9	NXN	4.209588	0.183026	23
TSPAN9	2.975484	0.330609	9	NCOR2	4.094608	0.178026	23
CACNA2D4	2.82727	0.314141	9	INPP5A	2.309147	0.100398	23
PRDM8	5.089011	0.636126	8	PRKCZ	3.7406	0.170027	22
TRAPPC9	3.2271	0.403387	8	SKI	5.727075	0.272718	21
SYNJ2	3.139206	0.392401	8	SDK1	5.562399	0.27812	20
AFF3	2.851203	0.3564	8	ABR	5.144643	0.257232	20
TENM2	2.744674	0.343084	8	FRMD4A	2.272281	0.113614	20
VRK2	2.73707	0.342134	8	MAD1L1	7.497513	0.394606	19
CDH4	2.54359	0.317949	8	CFAP46	2.668222	0.140433	19
GAK	3.126348	0.446621	7	CASZ1	2.446375	0.128757	19
RXRA	3.028493	0.432642	7	TBC1D16	2.486189	0.138122	18
BTBD11	2.810303	0.401472	7	MCF2L	2.353362	0.130742	18
NAV1	2.770524	0.395789	7	HBG2	2.993198	0.17607	17
MYO16	3.435703	0.572617	6	OPCML	2.840465	0.167086	17
FBXL18	3.395152	0.565859	6	FOXP1	2.89223	0.180764	16
CRADD	2.952569	0.492095	6	NAV2	2.421048	0.151316	16
C10orf90	2.779358	0.463226	6	BAIAP2	4.257113	0.283808	15
ANKS1A	2.620006	0.436668	6	GLI2	3.74488	0.249659	15
TSNAX-DISC1	3.402578	0.680516	5	LRMDA	3.245548	0.21637	15
ARHGEF7	3.189843	0.637969	5	KNDC1	2.746169	0.183078	15
AP2A2	2.800656	0.560131	5	ARHGEF10	3.637593	0.259828	14
NPHP4	2.718223	0.543645	5	CUX1	3.39947	0.242819	14
BCAR1	2.691854	0.538371	5	IQSEC1	2.79111	0.199365	14
STON1-				MIR548F5	2.63285	0.188061	14
GTF2A1L	2.564437	0.512887	5	CACNA1H	2.559313	0.182808	14
GSG1	2.88867	0.722167	4	GNG7	2.308896	0.164921	14
DICER1	2.718233	0.906078	3	RPS6KA2	2.262334	0.161595	14
ERI3	2.857462	1.428731	2	MSI2	4.443542	0.341811	13
SLC25A10	2.623878	1.311939	2	RFX4	3.866979	0.29746	13
Cancer Type				GSE1	3.189499	0.245346	13
TABLE 151:	imp_sum	imp_mean	n	CMIP	4.92255	0.410213	12
Gene site				FBRSL1	3.633172	0.302764	12
PTPRN2	10.27842	0.125347	82	TNS3	3.298056	0.274838	12
PRDM16	11.33441	0.15964	71	ZC3H3	2.913897	0.242825	12
HDAC4	12.51061	0.338124	37	MEGF6	2.726935	0.227245	12
RBFOX3	10.33693	0.295341	35	ADGRD1	2.691479	0.22429	12
PAX6	7.931791	0.226623	35	CTNNA2	2.554934	0.212911	12
DIP2C	4.742445	0.148201	32	GNA12	2.465474	0.205456	12
SOX2-OT	3.740453	0.128981	29	CTBP2	3.160477	0.287316	11
GALNT9	2.654267	0.098306	27	TSPAN4	3.575588	0.357559	10
SHANK2	6.240972	0.240037	26	TP73	2.661734	0.266173	10

LMF1	2.552461	0.255246	10	PRDM16	18.99297	0.267507	71
RGS12	2.538724	0.253872	10	PCDHGA1	7.882026	0.133594	59
BCL11B	2.524088	0.252409	10	PCDHGA2	7.437325	0.130479	57
ACOT7	2.448677	0.244868	10	PCDHGA3	6.804553	0.12601	54
TRAPPC12	4.772877	0.53032	9	PCDHGB1	6.804553	0.128388	53
ATP11A	4.469811	0.496646	9	PCDHGA4	6.804553	0.133423	51
CACNA2D4	4.395031	0.488337	9	PCDHGB2	6.488167	0.132412	49
KCNH2	4.206333	0.46737	9	PCDHGA5	6.171781	0.131314	47
KAZN	3.652715	0.405857	9	PCDHGB3	5.539009	0.128814	43
ADAMTS2	3.514329	0.390481	9	PCDHGA6	4.458758	0.111469	40
SND1	3.276925	0.364103	9	HDAC4	14.43817	0.390221	37
PRDM8	5.748341	0.718543	8	PCDHGA7	4.458758	0.120507	37
MSRA	3.95826	0.494783	8	RBFOX3	9.902052	0.282916	35
AFF3	3.37929	0.422411	8	PAX6	7.951795	0.227194	35
TRAPPC9	3.052095	0.381512	8	PCDHGB4	4.142372	0.118353	35
DNMT3A	2.812413	0.351552	8	PCDHGA8	4.142372	0.118353	35
MACROD1	2.75926	0.344908	8	DIP2C	5.458819	0.170588	32
PPP2R2B	2.59441	0.324301	8	PCDHGB5	4.775144	0.149223	32
VRK2	2.574109	0.321764	8	PCDHGA9	4.277945	0.137998	31
CELF4	2.360714	0.295089	8	PCDHGB6	4.594331	0.158425	29
RXRA	2.621084	0.374441	7	SOX2-OT	4.381182	0.151075	29
LHPP	2.36559	0.337941	7	PCDHGA10	4.277945	0.152784	28
ITPKB	2.339152	0.334165	7	GALNT9	3.40227	0.12601	27
CRADD	3.538289	0.589715	6	ADARB2	8.255536	0.317521	26
FBXL18	3.002949	0.500492	6	SHANK2	6.470832	0.248878	26
C10orf90	2.578042	0.429674	6	AGAP1	6.24246	0.249698	25
GRK5	2.534788	0.422465	6	CAMTA1	4.805518	0.192221	25
TRAK1	2.488331	0.414722	6	PDGFRA	4.758412	0.190336	25
TSNAX-DISC1	3.761812	0.752362	5	PCDHGB7	3.961559	0.165065	24
TEAD1	2.984378	0.596876	5	RPTOR	9.501283	0.413099	23
AP2A2	2.937556	0.587511	5	NCOR2	8.322187	0.361834	23
VAV2	2.282187	0.456437	5	NXN	6.27367	0.272768	23
GSG1	2.90875	0.727187	4	HOXB3	6.035781	0.262425	23
SCG5	2.765914	0.691479	4	RIMBP2	4.314302	0.187578	23
LINC00856	2.394591	0.598648	4	PCDHGA11	3.645173	0.158486	23
DAGLB	3.118583	1.039528	3	PRKCZ	6.665697	0.302986	22
GNAS	2.364452	0.788151	3	SKI	6.064214	0.288772	21
TRIM65	2.832082	1.416041	2	ZIC4	3.876225	0.184582	21
ERI3	2.578356	1.289178	2	ABR	4.708382	0.235419	20
GALK2	2.572375	1.286187	2	FRMD4A	4.646882	0.232344	20
SLC25A10	2.480457	1.240229	2	SDK1	4.557783	0.227889	20
CACNA1D	2.393238	1.196619	2	SMG1P2	6.376076	0.335583	19
DISC1	2.322679	1.16134	2	BOLA2	6.376076	0.335583	19
				LOC613038	6.376076	0.335583	19
				MAD1L1	6.313695	0.3323	19
				ZNF423	5.971828	0.314307	19
				KCNQ1	4.104771	0.216041	19
				CASZ1	3.518041	0.18516	19
TABLE 152: Cancer Type							
PITAD_STH_DENSE2							
Gene site	imp_sum	imp_mean	n				
PTPRN2	15.26347	0.18614	82				

FO XK1	5.737213	0.318734	18	TRAPPC9	3.415412	0.426927	8
ANKRD11	5.407599	0.300422	18	AP2A2	3.729851	0.74597	5
SEPTIN9	4.293449	0.238525	18	TSNAX-DISC1	3.398771	0.679754	5
HOXA3	3.872172	0.215121	18	DAGLB	3.850281	1.283427	3
RBFOX1	3.745567	0.208087	18				
OPCML	6.021126	0.354184	17	TABLE 153:	Cancer Type		
PAX6-AS1	3.880785	0.228281	17		PITAD_STH_SPARSE		
RCN1	3.880785	0.228281	17	Gene site	imp_sum	imp_mean	n
FOXP1	6.844759	0.427797	16	PTPRN2	13.40369	0.16346	82
NAV2	5.02674	0.314171	16	PRDM16	12.82439	0.180625	71
EBF3	3.502228	0.218889	16	PCDHGB1	3.352538	0.063255	53
SORBS2	3.432584	0.214536	16	PCDHGB2	3.352538	0.068419	49
GLI2	6.503929	0.433595	15	PCDHGB3	3.352538	0.077966	43
ZBTB20	4.605473	0.307032	15	PCDHGA6	3.352538	0.083813	40
SLX1B-				HDAC4	16.85468	0.455532	37
SULT1A4	3.622028	0.241469	15	RBFOX3	14.15142	0.404326	35
SLX1A	3.622028	0.241469	15	PAX6	9.704796	0.27728	35
LOC606724	3.622028	0.241469	15	DIP2C	8.826223	0.275819	32
BAIAP2	3.511134	0.234076	15	GALNT9	4.266274	0.15801	27
CACNA1H	4.422444	0.315889	14	SHANK2	7.465451	0.287133	26
CUX1	4.074849	0.291061	14	ADARB2	4.498758	0.173029	26
ARHGEF10	3.826456	0.273318	14	AGAP1	7.299004	0.29196	25
PRKAG2	3.716511	0.265465	14	CAMTA1	5.061254	0.20245	25
GSE1	5.515004	0.424231	13	PDGFRA	3.664179	0.146567	25
MSI2	5.261013	0.404693	13	SATB2	4.242972	0.176791	24
RFX4	5.115566	0.393505	13	RPTOR	11.09559	0.482417	23
SPTBN4	4.003012	0.307924	13	NCOR2	6.299198	0.273878	23
ZC3H3	4.158095	0.346508	12	INPP5A	6.283045	0.273176	23
CMIP	3.573186	0.297766	12	RIMBP2	5.67775	0.246859	23
CSMD1	3.466178	0.288848	12	NXN	5.0646	0.2202	23
CTBP2	4.442545	0.403868	11	HOXB3	3.682036	0.160089	23
RAD51B	3.346196	0.3042	11	PRKCZ	5.625055	0.255684	22
AKAP13	4.173414	0.417341	10	SKI	8.432147	0.401531	21
ACOT7	3.680344	0.368034	10	FRMD4A	5.518485	0.275924	20
IGF1R	3.578494	0.357849	10	SDK1	4.798074	0.239904	20
AUTS2	3.505236	0.350524	10	ABR	3.574142	0.178707	20
ATP11A	6.090584	0.676732	9	MAD1L1	9.960365	0.52423	19
CACNA2D4	5.851531	0.65017	9	ZNF423	5.497898	0.289363	19
TRAPPC12	4.298298	0.477589	9	SMG1P2	4.80028	0.252646	19
TSPAN9	4.152279	0.461364	9	BOLA2	4.80028	0.252646	19
KCNH2	4.010049	0.445561	9	LOC613038	4.80028	0.252646	19
ASAP1	3.541546	0.393505	9	KCNQ1	4.395199	0.231326	19
VRK2	5.539611	0.692451	8	CASZ1	3.608576	0.189925	19
PRDM8	5.353148	0.669143	8	FO XK1	8.166915	0.453717	18
PPP2R2B	4.450425	0.556303	8	ANKRD11	6.129595	0.340533	18
AFF3	4.31238	0.539048	8	TBC1D16	3.452645	0.191814	18
LINC00311	3.475399	0.434425	8	OPCML	5.462946	0.32135	17
MSRA	3.461528	0.432691	8	PAX6-AS1	4.304029	0.253178	17

RCN1	4.304029	0.253178	17	TRAPPC9	3.46805	0.433506	8
TBX15	3.435127	0.202066	17	RXRA	3.794134	0.542019	7
FOXP1	5.410888	0.338181	16	MIR548H4	3.691354	0.527336	7
NAV2	4.808997	0.300562	16	GAK	3.459276	0.494182	7
EBF3	4.764121	0.297758	16	TACC2	3.360077	0.480011	7
GLI2	6.997879	0.466525	15	CRADD	3.897166	0.649528	6
BAIAP2	5.692046	0.37947	15	FBXL18	3.662146	0.610358	6
KNDC1	4.077211	0.271814	15	TSNAX-DISC1	4.760379	0.952076	5
EMX2OS	3.885562	0.259037	15	AP2A2	4.038805	0.807761	5
SLX1B-				GSG1	3.372484	0.843121	4
SULT1A4	3.659946	0.243996	15	DAGLB	3.99515	1.331717	3
SLX1A	3.659946	0.243996	15	CHTF18	3.713627	1.856814	2
LOC606724	3.659946	0.243996	15	ANKLE2	3.494424	1.747212	2
RPS6KA2	6.638682	0.474192	14				
PRKAG2	6.132531	0.438038	14				
ARHGEF10	4.643365	0.331669	14	TABLE 154:	Cancer Type	PITAD_TSH	
C7orf50	4.411775	0.315127	14	Gene site	imp_sum	imp_mean	n
IQSEC1	3.399586	0.242828	14	PTPRN2	9.40886	0.114742	82
MIR548F5	3.376316	0.241165	14	PRDM16	8.15208	0.114818	71
MSI2	6.528839	0.502218	13	PCDHGA1	3.588337	0.060819	59
RFX4	5.217316	0.401332	13	PCDHGA2	3.588337	0.062953	57
MYT1L	4.046081	0.311237	13	PCDHGA3	3.588337	0.066451	54
GSE1	4.011884	0.308606	13	PCDHGB1	3.588337	0.067704	53
SPTBN4	3.601558	0.277043	13	PCDHGA4	3.271951	0.064156	51
CMIP	6.117375	0.509781	12	PCDHGB2	2.955565	0.060318	49
ZC3H3	5.444204	0.453684	12	PCDHGA5	2.639179	0.056153	47
TNS3	5.354996	0.44625	12	PCDHGB3	2.758601	0.064154	43
ADGRD1	5.26842	0.439035	12	PCDHGA6	2.758601	0.068965	40
FBRSL1	4.25555	0.354629	12	HDAC4	10.52559	0.284475	37
GNA12	3.503295	0.291941	12	PCDHGA7	2.442215	0.066006	37
ZC3H12D	4.218637	0.383512	11	PAX6	6.486982	0.185342	35
SORCS2	3.698609	0.336237	11	RBFOX3	3.830891	0.109454	35
AKAP13	4.70569	0.470569	10	PCDHGB4	2.442215	0.069778	35
ACOT7	3.971765	0.397176	10	PCDHGA8	2.442215	0.069778	35
TSPAN4	3.701377	0.370138	10	DIP2C	7.394914	0.231091	32
GAS7	3.366629	0.336663	10	SHANK2	3.225038	0.12404	26
ATP11A	5.825838	0.647315	9	ADARB2	2.658934	0.102267	26
SND1	5.535797	0.615089	9	AGAP1	7.263333	0.290533	25
ADAMTS2	5.045606	0.560623	9	CAMTA1	2.501118	0.100045	25
TSPAN9	4.213473	0.468164	9	SATB2	2.786999	0.116125	24
KCNH2	3.969071	0.441008	9	NXN	5.136839	0.223341	23
AXIN2	3.460817	0.384535	9	NCOR2	5.129748	0.223033	23
ASAP1	3.383619	0.375958	9	RPTOR	4.39311	0.191005	23
SLC22A18	3.362796	0.373644	9	HOXB3	2.82018	0.122617	23
PRDM8	8.49027	1.061284	8	PRKCZ	3.016776	0.137126	22
VRK2	4.955177	0.619397	8	SKI	6.751464	0.321498	21
MSRA	4.39264	0.54908	8	SDK1	4.373052	0.218653	20
AFF3	4.035116	0.50439	8	FRMD4A	3.314172	0.165709	20
				ABR	2.657323	0.132866	20

MAD1L1	6.086807	0.320358	19	DLEU1	2.465536	0.308192	8
CASZ1	3.663955	0.19284	19	RGS20	2.391527	0.298941	8
CFAP46	2.797395	0.147231	19	MIR548H4	3.555513	0.50793	7
MCF2L	4.413719	0.245207	18	GAK	3.04005	0.434293	7
ANKRD11	2.864419	0.159134	18	NAV1	2.746391	0.392342	7
FO XK1	2.683913	0.149106	18	WVOX	2.399897	0.342842	7
TBC1D16	2.389987	0.132777	18	CRADD	3.84197	0.640328	6
OPCML	4.165582	0.245034	17	MYO16	3.041736	0.506956	6
HBG2	2.690066	0.158239	17	C10orf90	2.747828	0.457971	6
FOXP1	4.589209	0.286826	16	CCDC177	2.686978	0.44783	6
NAV2	2.811994	0.17575	16	FBXL18	2.558178	0.426363	6
EBF3	2.623072	0.163942	16	SLC22A18AS	2.501483	0.416914	6
GLI2	3.237879	0.215859	15	FMNL2	2.451875	0.408646	6
KIRREL3	2.622052	0.174803	15	TSNAX-DISC1	3.926508	0.785302	5
ARHGEF10	4.635274	0.331091	14	RUNDC3A	2.731088	0.546218	5
C7orf50	2.702027	0.193002	14	VAV2	2.390701	0.47814	5
TBX5	2.650681	0.189334	14	TRIM65	2.9884	1.4942	2
PRKAG2	2.608078	0.186291	14	ERI3	2.800313	1.400157	2
MOB2	2.462272	0.175877	14	DISC1	2.716734	1.358367	2
MIR548F5	2.406059	0.171861	14	SLC25A10	2.528998	1.264499	2
MSI2	3.551726	0.27321	13				
GSE1	3.496661	0.268974	13	TABLE 155:	Cancer Type PITUI		
RFX4	3.356876	0.258221	13	Gene site	imp_sum	imp_mean	n
CMIP	4.937844	0.411487	12	PTPRN2	16.35368	0.199435	82
FBRSL1	4.458035	0.371503	12	PRDM16	17.93226	0.252567	71
ZC3H3	3.146758	0.26223	12	PCDHGA1	5.085676	0.086198	59
ANAPC16	2.795207	0.25411	11	PCDHGA2	4.76929	0.083672	57
CTBP2	2.687582	0.244326	11	PCDHGA3	4.452904	0.082461	54
TSPAN4	3.957528	0.395753	10	PCDHGB1	4.452904	0.084017	53
ACOT7	2.81231	0.281231	10	PCDHGA4	4.452904	0.087312	51
RGS12	2.686067	0.268607	10	HDAC4	14.25155	0.385177	37
CHST11	2.678145	0.267815	10	PAX6	9.270981	0.264885	35
LMF1	2.640024	0.264002	10	RBFOX3	7.115698	0.203306	35
GAS7	2.375665	0.237566	10	DIP2C	13.48333	0.421354	32
ATP11A	3.874103	0.430456	9	SOX2-OT	8.123976	0.280137	29
CACNA2D4	3.353338	0.372593	9	GALNT9	4.640102	0.171856	27
AXIN2	3.323844	0.369316	9	SHANK2	4.865952	0.187152	26
SND1	3.224096	0.358233	9	AGAP1	11.49114	0.459645	25
TRAPPC12	3.075952	0.341772	9	CAMTA1	7.897637	0.315905	25
SLC22A18	2.797384	0.31082	9	PDGFRA	7.691037	0.307641	25
TSPAN9	2.676189	0.297354	9	MEIS1	4.320301	0.180013	24
PRDM8	6.328073	0.791009	8	RPTOR	12.62394	0.548867	23
AFF3	3.212441	0.401555	8	INPP5A	5.879629	0.255636	23
SYNJ2	3.208876	0.40111	8	NXN	5.407584	0.235112	23
VRK2	2.968834	0.371104	8	NCOR2	4.989473	0.216934	23
TMEM132D	2.829233	0.353654	8	HOXB3	4.541869	0.197473	23
MSRA	2.729491	0.341186	8	PRKCZ	6.302859	0.286494	22
DNMT3A	2.627419	0.328427	8	SKI	11.24166	0.535317	21

SDK1	6.244901	0.312245	20	SPON2	4.76136	0.432851	11
FRMD4A	5.904146	0.295207	20	CTBP2	4.157937	0.377994	11
ABR	5.17257	0.258628	20	ANAPC16	4.073549	0.370323	11
MAD1L1	11.27934	0.593649	19	TSPAN4	4.648571	0.464857	10
ZNF423	7.31106	0.384793	19	SND1	7.283474	0.809275	9
CASZ1	7.082702	0.372774	19	TSPAN9	6.014893	0.668321	9
SMG1P2	4.913495	0.258605	19	ATP11A	5.609787	0.62331	9
BOLA2	4.913495	0.258605	19	ADAMTS2	5.269587	0.58551	9
LOC613038	4.913495	0.258605	19	AXIN2	5.174351	0.574928	9
CFAP46	4.129305	0.217332	19	TRAPPC12	5.121161	0.569018	9
TBC1D16	6.475237	0.359735	18	NOTCH1	4.106032	0.456226	9
FO XK1	6.437992	0.357666	18	APBA2	4.026487	0.447387	9
ANKRD11	6.218053	0.345447	18	MSRA	4.601965	0.575246	8
SEPTIN9	5.672606	0.315145	18	DLEU1	4.408934	0.551117	8
MCF2L	5.129604	0.284978	18	LINC00311	4.229846	0.528731	8
HOUA3	4.503527	0.250196	18	NAV1	4.588824	0.655546	7
OPCML	4.540251	0.267074	17	LHPP	4.53367	0.647667	7
FOXP1	7.982608	0.498913	16	ITPK1	4.415617	0.630802	7
EBF3	4.580607	0.286288	16	GAK	4.379344	0.625621	7
NAV2	4.297127	0.26857	16	MIR548H4	4.350271	0.621467	7
GLI2	7.704142	0.513609	15	CXXC5	4.263329	0.609047	7
KIRREL3	6.256932	0.417129	15	FBXL18	5.388879	0.898147	6
SLX1B-				KDM4B	4.607895	0.767983	6
SULT1A4	4.782061	0.318804	15	CRADD	4.43432	0.739053	6
SLX1A	4.782061	0.318804	15	SLC22A18AS	4.289809	0.714968	6
LOC606724	4.782061	0.318804	15	RUNDC3A	5.516918	1.103384	5
NFIX	4.600342	0.306689	15	TSNAX-DISC1	5.126587	1.025317	5
LRMDA	4.532995	0.3022	15	ARHGEF7	4.647192	0.929438	5
ZBTB20	4.05497	0.270331	15				
RPS6KA2	7.382522	0.527323	14				
CUX1	6.962169	0.497298	14	TABLE 156:	Cancer Type		
IQSEC1	6.392684	0.45662	14	Gene site	imp_sum	imp_mean	n
PRKAG2	5.315705	0.379693	14	PTPRN2	8.246297	0.100565	82
C7orf50	4.96574	0.354696	14	PRDM16	5.021667	0.070728	71
MIR548F5	4.911218	0.350801	14	PCDHGA1	2.531088	0.0429	59
MSI2	6.700335	0.51541	13	PCDHGA2	2.214702	0.038854	57
MYT1L	5.452084	0.419391	13	PCDHGA3	2.214702	0.041013	54
KIF26B	4.344524	0.334194	13	PCDHGB1	2.214702	0.041787	53
RASA3	5.80698	0.483915	12	PCDHGA4	2.214702	0.043426	51
ZC3H3	5.498845	0.458237	12	PCDHGB2	2.214702	0.045198	49
TNS3	5.471934	0.455995	12	PCDHGA5	2.214702	0.047121	47
MIRLET7BHG	5.35895	0.446579	12	PCDHGB3	1.898316	0.044147	43
ADGRD1	4.977938	0.414828	12	HDAC4	6.778115	0.183192	37
MEGF6	4.348627	0.362386	12	RBFOX3	2.794424	0.079841	35
FBRSL1	4.31256	0.35938	12	DIP2C	2.766692	0.086459	32
CMIP	4.105199	0.3421	12	ADARB2	2.563395	0.098592	26
GNA12	4.057769	0.338147	12	SHANK2	2.42321	0.0932	26
TBCD	5.109895	0.464536	11	AGAP1	3.322519	0.132901	25

CAMTA1	1.999995	0.08	25	VRK2	3.179022	0.397378	8
PDGFRA	1.744295	0.069772	25	PPP2R2B	2.486706	0.310838	8
NCOR2	5.251438	0.228323	23	AFF3	2.243318	0.280415	8
RPTOR	4.188742	0.182119	23	LMX1B	2.190566	0.273821	8
RIMBP2	2.680694	0.116552	23	TENM2	1.774757	0.221845	8
NXN	1.627722	0.070771	23	CXXC5	2.699262	0.385609	7
SKI	4.880693	0.232414	21	VPS13D	2.384939	0.340706	7
SDK1	3.198217	0.159911	20	GAK	2.216817	0.316688	7
FRMD4A	1.928019	0.096401	20	PTPN20	2.158241	0.30832	7
MAD1L1	6.103592	0.321242	19	SBNO2	1.747097	0.249585	7
ZNF423	2.655007	0.139737	19	C19orf25	1.722623	0.246089	7
CFAP46	2.078795	0.10941	19	NRG1	1.701523	0.243075	7
FOXK1	3.750882	0.208382	18	RXRA	1.669708	0.23853	7
RBFOX1	3.393021	0.188501	18	GALNT2	1.659583	0.237083	7
ANKRD11	2.943663	0.163537	18	RADIL	3.252262	0.542044	6
OPCML	3.435498	0.202088	17	SLC22A18AS	2.353238	0.392206	6
FOXP1	3.530632	0.220665	16	COQ8A	2.030139	0.338356	6
GLI2	4.521672	0.301445	15	C10orf90	1.902737	0.317123	6
KIRREL3	2.842758	0.189517	15	ANKS1A	1.82408	0.304013	6
COL23A1	1.801013	0.120068	15	LRRFIP1	1.753638	0.292273	6
RPS6KA2	4.061507	0.290108	14	GPR39	1.713	0.2855	6
IQSEC1	2.897213	0.206944	14	RERE	1.686278	0.281046	6
CUX1	2.586123	0.184723	14	GRK5	1.631163	0.27186	6
C7orf50	2.041189	0.145799	14	TSNAX-DISC1	3.625664	0.725133	5
PPP2R2A	1.710245	0.12216	14	RUNDC3A	3.259257	0.651851	5
MOB2	1.619517	0.11568	14	SDK2	2.180742	0.436148	5
GSE1	4.175492	0.321192	13	CADM1	1.836276	0.367255	5
MSI2	3.493614	0.26874	13	AGAP2	1.816382	0.363276	5
KIF26B	1.842195	0.141707	13	EXT1	1.638349	0.409587	4
MYT1L	1.787706	0.137516	13	DICER1	2.158844	0.719615	3
CMIP	3.406765	0.283897	12	TBC1D7	2.089024	0.696341	3
FBRSL1	2.78353	0.231961	12	SLC25A22	1.787343	0.595781	3
ZC3H3	2.696535	0.224711	12	SLC25A10	2.297623	1.148812	2
CTNNA2	1.966395	0.163866	12	SOX10	1.903551	0.951776	2
RASA3	1.810327	0.150861	12	ANKLE2	1.717654	0.858827	2
ZC3H12D	2.712185	0.246562	11	CHTF18	1.680153	0.840077	2
COL4A1	2.341256	0.212841	11				
WNT5A	2.017909	0.183446	11	TABLE 157:	Cancer Type PLNTY		
TSPAN4	2.697755	0.269776	10	Gene site	imp_sum	imp_mean	n
AKAP13	1.847862	0.184786	10	PTPRN2	4.592259	0.056003	82
ACOT7	1.832347	0.183235	10	PRDM16	10.5896	0.149149	71
SND1	4.433875	0.492653	9	PCDHGA1	2.614902	0.04432	59
TSPAN9	2.937856	0.326428	9	PCDHGA2	2.614902	0.045875	57
TRAPPC12	2.580023	0.286669	9	PCDHGA3	2.931288	0.054283	54
ATP11A	2.491575	0.276842	9	PCDHGB1	2.931288	0.055307	53
SLC22A18	2.371564	0.263507	9	PCDHGA4	2.931288	0.057476	51
CACNA2D4	1.97832	0.219813	9	PCDHGB2	2.931288	0.059822	49
NOTCH1	1.954531	0.21717	9	PCDHGA5	2.614902	0.055636	47

PCDHGB3	2.298516	0.053454	43	ADGRD1	3.000292	0.250024	12
PCDHGA6	2.298516	0.057463	40	TNS3	2.650311	0.220859	12
HDAC4	3.59828	0.097251	37	RAD51B	3.031553	0.275596	11
PCDHGA7	2.298516	0.062122	37	ZC3H12D	2.559618	0.232693	11
PAX6	6.015438	0.17187	35	VGLL4	2.433622	0.221238	11
RBFOX3	3.828772	0.109393	35	IGF1R	3.313095	0.33131	10
PCDHGB4	2.298516	0.065672	35	ACOT7	2.988113	0.298811	10
PCDHGA8	2.298516	0.065672	35	LBX1-AS1	2.149892	0.214989	10
DIP2C	4.939448	0.154358	32	GRID1	2.12101	0.212101	10
PCDHGB5	2.298516	0.071829	32	KCNH2	3.479583	0.38662	9
PCDHGA9	2.298516	0.074146	31	ATP11A	3.173518	0.352613	9
SOX2-OT	3.593428	0.123911	29	SND1	3.141462	0.349051	9
ADARB2	3.330645	0.128102	26	AXIN2	2.811114	0.312346	9
CAMTA1	4.272184	0.170887	25	ASAP1	2.576206	0.286245	9
AGAP1	3.630501	0.14522	25	ADAMTS2	2.44998	0.27222	9
SATB2	3.604525	0.150189	24	ADGRB1	2.384403	0.264934	9
RPTOR	5.262184	0.228791	23	TSPAN9	2.143241	0.238138	9
INPP5A	3.839962	0.166955	23	DLEU1	3.024339	0.378042	8
NXN	2.55193	0.110953	23	ASPSCR1	2.599788	0.324973	8
NCOR2	2.510179	0.109138	23	LHX4	2.444245	0.305531	8
SKI	4.587922	0.218472	21	RORA	2.327736	0.290967	8
FRMD4A	4.040872	0.202044	20	DNMT3A	2.232974	0.279122	8
ABR	3.338525	0.166926	20	LINC00311	2.168563	0.27107	8
SDK1	2.746142	0.137307	20	GDF6	2.15933	0.269916	8
MAD1L1	6.361444	0.334813	19	MSRA	2.123309	0.265414	8
ZNF423	4.483254	0.235961	19	ESRRG	2.106696	0.263337	8
SMG1P2	3.957845	0.208308	19	DUSP6	3.533096	0.504728	7
BOLA2	3.957845	0.208308	19	C19orf25	2.548903	0.364129	7
LOC613038	3.957845	0.208308	19	NAV1	2.374574	0.339225	7
CASZ1	2.704101	0.142321	19	LINC01140	2.203162	0.314737	7
FOKK1	4.424514	0.245806	18	GLI3	2.193183	0.313312	7
MCF2L	2.873774	0.159654	18	CXXC5	2.112419	0.301774	7
TBC1D16	2.564648	0.14248	18	FBXL18	3.23133	0.538555	6
SEPTIN9	2.303752	0.127986	18	KIFC3	2.434479	0.486896	5
OPCML	3.49484	0.205579	17	BACH2	2.375159	0.475032	5
NAV2	2.375735	0.148483	16	PRR5L	2.340852	0.46817	5
GLI2	3.829269	0.255285	15	ARHGEF7	2.295883	0.459177	5
BAIAP2	2.233153	0.148877	15	UNQ6494	2.974765	0.743691	4
ZBTB20	2.214702	0.147647	15	SASH1	2.875664	0.718916	4
IQSEC1	2.635744	0.188267	14	GRIN2B	2.509571	0.836524	3
RPS6KA2	2.547296	0.18195	14	SOX10	2.661932	1.330966	2
CUX1	2.349358	0.167811	14	SLC25A10	2.5237	1.26185	2
MSI2	4.667992	0.359076	13	MAP3K3	2.450964	1.225482	2
MYT1L	3.166894	0.243607	13				
GSE1	3.007342	0.231334	13	TABLE 158:	Cancer Type PPTID_A		
RFX4	2.54279	0.195599	13	Gene site	imp_sum	imp_mean	n
SPTBN4	2.137458	0.16442	13	PTPRN2	8.648116	0.105465	82
CMIP	3.542088	0.295174	12	PRDM16	7.928549	0.11167	71

PCDHGA1	3.106457	0.052652	59	GNG7	3.253313	0.23238	14
PCDHGA2	3.106457	0.054499	57	MYT1L	5.567428	0.428264	13
PCDHGA6	3.106457	0.077661	40	MSI2	4.478131	0.344472	13
HDAC4	11.75065	0.317585	37	ZC3H3	5.773265	0.481105	12
PAX6	5.665158	0.161862	35	CMIP	3.940051	0.328338	12
RBFOX3	4.977408	0.142212	35	FBRSL1	3.777821	0.314818	12
DIP2C	7.142101	0.223191	32	MEGF6	3.331258	0.277605	12
GALNT9	3.925303	0.145382	27	ADGRD1	3.207913	0.267326	12
SHANK2	5.177983	0.199153	26	TNS3	3.131242	0.260937	12
AGAP1	6.640154	0.265606	25	RASA3	3.062385	0.255199	12
CAMTA1	5.470891	0.218836	25	TBX4	3.004938	0.250412	12
MEIS1	3.424578	0.142691	24	WNT5A	4.500214	0.40911	11
PCDHGB7	3.106457	0.129436	24	ZC3H12D	3.281566	0.298324	11
RPTOR	9.444429	0.410627	23	VGLL4	3.164956	0.287723	11
NXN	6.62009	0.28783	23	RAD51B	2.972988	0.270272	11
NCOR2	6.27054	0.272632	23	GRID1	3.841244	0.384124	10
INPP5A	5.072765	0.220555	23	AKAP13	3.603546	0.360355	10
PCDHGA11	3.106457	0.135063	23	ACOT7	3.424298	0.34243	10
RIMBP2	3.094265	0.134533	23	SKOR1	3.26378	0.326378	10
PRKCZ	4.55387	0.206994	22	SPPL2B	2.959423	0.295942	10
SKI	8.101099	0.385767	21	ASIC2	2.928988	0.292899	10
ABR	2.948097	0.147405	20	SND1	6.042522	0.671391	9
MAD1L1	13.62232	0.716964	19	ATP11A	5.278739	0.586527	9
CASZ1	5.498024	0.28937	19	ADAMTS2	4.97865	0.553183	9
ZNF423	4.953023	0.260685	19	CACNA2D4	4.332074	0.481342	9
SMG1P2	4.178841	0.219939	19	PACS2	3.237413	0.359713	9
BOLA2	4.178841	0.219939	19	GPC6	3.168188	0.352021	9
LOC613038	4.178841	0.219939	19	TSPAN9	2.999866	0.333318	9
KCNQ1	4.015099	0.211321	19	SSBP3	2.969011	0.32989	9
FOKK1	5.225656	0.290314	18	VRK2	6.574839	0.821855	8
TBC1D16	4.093026	0.22739	18	TRAPPC9	3.850618	0.481327	8
SEPTIN9	3.318672	0.184371	18	DNMT3A	3.237578	0.404697	8
ANKRD11	3.091681	0.17176	18	PPP2R2B	3.190039	0.398755	8
PAX6-AS1	3.842142	0.226008	17	MIR548H4	3.731732	0.533105	7
RCN1	3.842142	0.226008	17	CXXC5	3.725549	0.532221	7
FOXP1	5.118198	0.319887	16	TENM3	3.387221	0.483889	7
NAV2	3.377477	0.211092	16	GAK	3.332254	0.476036	7
KNDC1	4.38695	0.292463	15	RXRA	2.978021	0.425432	7
ZBTB20	3.861839	0.257456	15	PITPNC1	2.95111	0.421587	7
GLI2	3.446048	0.229737	15	FBXL18	3.449678	0.574946	6
BAIAP2	3.396298	0.22642	15	TRAK1	3.390001	0.565	6
NFATC1	3.386909	0.225794	15	CCDC85C	3.026196	0.504366	6
KIRREL3	2.94463	0.196309	15	TSNAX-DISC1	4.501816	0.900363	5
ARHGEF10	5.205047	0.371789	14	ARHGEF7	3.06617	0.613234	5
MOB2	4.696577	0.33547	14	SDK2	2.942077	0.588415	5
CUX1	4.484666	0.320333	14	PWWP2B	3.23489	0.808722	4
IQSEC1	3.452896	0.246635	14	GSG1	3.157531	0.789383	4
C7orf50	3.327407	0.237672	14	SLC25A22	3.273268	1.091089	3

CHTF18	4.393304	2.196652	2	FBRSL1	3.045172	0.253764	12
KCNV2	3.002687	3.002687	1	ZC3H3	2.82838	0.235698	12
TABLE 159:	Cancer Type	PPTID_B		TNS3	2.557913	0.213159	12
			CMIP	2.288377	0.190698	12	
Gene site	imp_sum	imp_mean	n	CTBP2	2.788195	0.253472	11
PTPRN2	8.484208	0.103466	82	ZC3H12D	2.239715	0.20361	11
PRDM16	6.943077	0.09779	71	AKAP13	3.237211	0.323721	10
HDAC4	8.404246	0.227142	37	GRID1	3.106122	0.310612	10
RBFOX3	6.997953	0.199942	35	AUTS2	2.828559	0.282856	10
PAX6	3.67728	0.105065	35	CHST11	2.687753	0.268775	10
DIP2C	3.475297	0.108603	32	ACOT7	2.607843	0.260784	10
GALNT9	3.870262	0.143343	27	RGS12	2.553201	0.25532	10
ADARB2	3.612563	0.138945	26	SH3RF3	2.431616	0.243162	10
SHANK2	3.330041	0.128079	26	BCL11B	2.284903	0.22849	10
CAMTA1	6.690953	0.267638	25	SND1	5.532557	0.614729	9
AGAP1	5.593718	0.223749	25	CACNA2D4	4.192445	0.465827	9
RPTOR	5.735448	0.249367	23	ATP11A	4.069455	0.452162	9
NXN	4.622589	0.200982	23	ADAMTS2	4.05582	0.450647	9
NCOR2	4.485016	0.195001	23	SSBP3	3.069115	0.341013	9
RIMBP2	3.27382	0.14234	23	AXIN2	3.020683	0.335631	9
INPP5A	2.682003	0.116609	23	GPC6	2.724216	0.302691	9
PRKCZ	3.291448	0.149611	22	MGMT	2.711353	0.301261	9
SKI	4.675435	0.22264	21	TSPAN9	2.675168	0.297241	9
FRMD4A	2.973194	0.14866	20	VRK2	5.368419	0.671052	8
MAD1L1	12.50555	0.658187	19	PPP2R2B	4.094538	0.511817	8
CASZ1	5.302585	0.279083	19	DNMT3A	3.275917	0.40949	8
SMG1P2	4.394225	0.231275	19	TRAPPC9	2.865515	0.358189	8
BOLA2	4.394225	0.231275	19	ASPSCR1	2.363132	0.295392	8
LOC613038	4.394225	0.231275	19	RORA	2.300871	0.287609	8
CFAP46	2.656597	0.139821	19	PITPNC1	2.553579	0.364797	7
KCNQ1	2.480621	0.130559	19	MIR548H4	2.484623	0.354946	7
ZNF423	2.454238	0.12917	19	TRAK1	3.108244	0.518041	6
FO XK1	3.026596	0.168144	18	COLEC11	2.68768	0.447947	6
TBC1D16	2.546024	0.141446	18	CRADD	2.675599	0.445933	6
SEPTIN9	2.507428	0.139302	18	ARHGAP18	2.507719	0.417953	6
FOXP1	5.314247	0.33214	16	MYO16	2.22252	0.37042	6
EBF3	3.263849	0.203991	16	TSNAX-DISC1	4.85897	0.971794	5
KNDC1	3.293924	0.219595	15	ARHGEF7	2.83885	0.56777	5
BAIAP2	2.481642	0.165443	15	CPEB1-AS1	2.454983	0.490997	5
CUX1	4.417765	0.315555	14	SDK2	2.210224	0.442045	5
ARHGEF10	3.118517	0.222751	14	GSG1	2.669005	0.667251	4
IQSEC1	2.944971	0.210355	14	EXT1	2.617463	0.654366	4
MIR548F5	2.813738	0.200981	14	RGL3	2.907137	0.969046	3
MSI2	4.724375	0.363413	13	SLC25A22	2.866456	0.955485	3
RFX4	3.458651	0.26605	13	SLC1A7	2.483699	0.8279	3
GSE1	3.364669	0.258821	13	ANKRD33B	2.320262	0.773421	3
MYT1L	2.990422	0.230032	13	DICER1	2.311872	0.770624	3
TBX4	3.882401	0.323533	12	CHTF18	4.241545	2.120773	2

UHRF1	2.699139	1.34957	2	RPS6KA2	3.344509	0.238894	14
UTRN	2.618679	1.309339	2	CUX1	3.268432	0.233459	14
KIF21B	2.540768	1.270384	2	MYT1L	3.692749	0.284058	13
TRIM65	2.452721	1.226361	2	GSE1	2.119264	0.16302	13
DISC1	2.234015	1.117008	2	ZC3H3	2.388201	0.199017	12
KCNV2	2.919489	2.919489	1	MIRLET7BHG	2.292468	0.191039	12
ARL6IP6	2.893929	2.893929	1	FBRSL1	2.218248	0.184854	12
DDT	2.784336	2.784336	1	CMIP	1.53067	0.127556	12
DNAJC27	2.448671	2.448671	1	ZC3H12D	2.136626	0.194239	11
				CTBP2	1.69002	0.153638	11
TABLE 160:	Cancer Type PTPR_A			OTX1	1.953174	0.195317	10
Gene site	imp_sum	imp_mean	n	BCL11B	1.950789	0.195079	10
PTPRN2	6.431058	0.078428	82	NR2F1-AS1	1.892998	0.1893	10
PRDM16	6.406972	0.090239	71	CHST11	1.58193	0.158193	10
HDAC4	4.815664	0.130153	37	ATP11A	3.986085	0.442898	9
RBFOX3	4.732637	0.135218	35	SND1	2.730913	0.303435	9
PAX6	3.06234	0.087495	35	CACNA2D4	2.522718	0.280302	9
DIP2C	1.560496	0.048765	32	KAZN	2.258768	0.250974	9
AGAP1	3.830952	0.153238	25	ASAP1	1.875856	0.208428	9
PDGFRA	2.657855	0.106314	25	AXIN2	1.840427	0.204492	9
CAMTA1	2.622421	0.104897	25	RUNX1	1.767827	0.196425	9
SATB2	1.957909	0.08158	24	TRAPPC12	1.712675	0.190297	9
NXN	4.055782	0.176338	23	KCNH2	1.708484	0.189832	9
INPP5A	3.642302	0.158361	23	VRK2	2.221373	0.277672	8
RIMBP2	2.060349	0.08958	23	DLEU1	1.917547	0.239693	8
RPTOR	1.800764	0.078294	23	AFF3	1.715766	0.214471	8
PRKCZ	2.333896	0.106086	22	PPP2R2B	1.570035	0.196254	8
SKI	2.951222	0.140534	21	LHX2	2.101609	0.30023	7
ZIC4	1.708484	0.081356	21	NAV1	1.77072	0.25296	7
SDK1	2.579709	0.128985	20	PACRG	1.681042	0.240149	7
FRMD4A	2.401239	0.120062	20	PITPNC1	1.670551	0.23865	7
MAD1L1	3.63752	0.191448	19	RXRA	1.564443	0.223492	7
CASZ1	3.147355	0.16565	19	ANKS1A	2.930102	0.48835	6
ZNF423	1.860218	0.097906	19	COLEC11	2.887782	0.481297	6
SEPTIN9	2.497207	0.138734	18	MYO16	1.966721	0.327787	6
FOXK1	1.89308	0.105171	18	LRRFIP1	1.686953	0.281159	6
ANKRD11	1.55778	0.086543	18	FBXL18	1.684368	0.280728	6
OPCML	2.030878	0.119463	17	RUNDC3A	2.696328	0.539266	5
NAV2	1.69002	0.105626	16	VAV2	2.04255	0.40851	5
GLI2	3.175797	0.21172	15	TSNAX-DISC1	1.952279	0.390456	5
NFIX	2.470268	0.164685	15	PRR5L	1.570697	0.314139	5
DLX6-AS1	1.898316	0.126554	15	TK1	1.518714	0.303743	5
LRMDA	1.835344	0.122356	15	ZBTB16	1.493677	0.298735	5
COL23A1	1.58193	0.105462	15	RBMS3	2.001273	0.500318	4
SLX1B-				VOPPI	1.77671	0.444177	4
SULT1A4	1.58193	0.105462	15	PPM1H	1.669106	0.417277	4
SLX1A	1.58193	0.105462	15	MDM4	1.521963	0.380491	4
LOC606724	1.58193	0.105462	15	CRB2	1.50801	0.377002	4

RREB1	1.501624	0.375406	4	ZNF423	6.394277	0.336541	19
NUDT1	2.223731	0.741244	3	MAD1L1	5.88838	0.309915	19
BFSP2	2.189251	0.72975	3	SMG1P2	5.428921	0.285733	19
SLC6A9	1.727698	0.575899	3	BOLA2	5.428921	0.285733	19
KCNIP1	1.709047	0.569682	3	LOC613038	5.428921	0.285733	19
GRIN2B	1.553661	0.517887	3	KCNQ1	5.30451	0.279185	19
SLC25A22	1.487383	0.495794	3	CASZ1	4.145031	0.21816	19
TRIM65	2.703379	1.351689	2	FOXK1	7.353913	0.408551	18
SLC7A5	2.459291	1.229645	2	SEPTIN9	5.788672	0.321593	18
CYTH1	1.918087	0.959043	2	MCF2L	4.622146	0.256786	18
DENND11	1.903764	0.951882	2	ANKRD11	3.704187	0.205788	18
SLC25A10	1.708904	0.854452	2	TBC1D16	3.524561	0.195809	18
PDE4D	1.688655	0.844328	2	OPCML	6.572972	0.386645	17
EXT2	1.667987	0.833993	2	FOXP1	5.653943	0.353371	16
ANKLE2	1.623952	0.811976	2	NAV2	4.61417	0.288386	16
RNF216	1.498119	0.74906	2	GLI2	6.422342	0.428156	15
GTF2E2	1.912954	1.912954	1	KIRREL3	5.718362	0.381224	15
TABLE 161:	Cancer Type PTPR_B			LRMDA	4.481352	0.298757	15
				BAIAP2	4.371077	0.291405	15
Gene site	imp_sum	imp_mean	n	KNDC1	4.080509	0.272034	15
PTPRN2	18.55999	0.226341	82	ZBTB20	3.991421	0.266095	15
PRDM16	13.61668	0.191784	71	DLX6-AS1	3.544562	0.236304	15
PCDHGA1	4.135023	0.070085	59	RPS6KA2	7.537867	0.538419	14
PCDHGA2	3.688052	0.064703	57	CUX1	6.525536	0.46611	14
HDAC4	16.42095	0.443809	37	IQSEC1	4.926658	0.351904	14
RBFOX3	7.485864	0.213882	35	C7orf50	3.627468	0.259105	14
PAX6	5.608833	0.160252	35	CACNA1H	3.439488	0.245678	14
DIP2C	9.689409	0.302794	32	MYT1L	5.823839	0.447988	13
SOX2-OT	4.770368	0.164495	29	GSE1	5.04051	0.387732	13
GALNT9	5.415977	0.200592	27	MSI2	4.337492	0.333653	13
SHANK2	7.102857	0.273187	26	RFX4	3.999428	0.307648	13
ADARB2	4.593242	0.176663	26	HOXC4	3.809413	0.293032	13
AGAP1	11.12632	0.445053	25	MAML3	5.628857	0.469071	12
CAMTA1	7.763658	0.310546	25	ZC3H3	5.147971	0.428998	12
PDGFRA	5.687196	0.227488	25	CMIP	4.897106	0.408092	12
SATB2	5.259094	0.219129	24	FBRSL1	4.625681	0.385473	12
RPTOR	11.15487	0.484994	23	ADGRD1	3.982114	0.331843	12
NXN	7.122185	0.30966	23	ZC3H12D	4.02877	0.366252	11
NCOR2	5.254821	0.22847	23	SLC38A10	3.986959	0.362451	11
INPP5A	5.161147	0.224398	23	ANAPC16	3.5516	0.322873	11
RIMBP2	4.389689	0.190856	23	CTBP2	3.407661	0.309787	11
PRKCZ	5.665208	0.257509	22	TSPAN4	4.745661	0.474566	10
SKI	6.496584	0.309361	21	AKAP13	3.975967	0.397597	10
SIM2	4.620253	0.220012	21	LBX1-AS1	3.623374	0.362337	10
ZIC4	4.306227	0.205058	21	SND1	5.018913	0.557657	9
ABR	5.388896	0.269445	20	ATP11A	4.871857	0.541317	9
FRMD4A	4.694034	0.234702	20	SSBP3	4.321963	0.480218	9
SDK1	3.941165	0.197058	20	ADAMTS2	4.314706	0.479412	9

ASAP1	4.019661	0.446629	9	SDK1	6.399034	0.319952	20
CACNA2D4	3.893763	0.43264	9	ABR	5.681297	0.284065	20
KCNH2	3.800532	0.422281	9	MAD1L1	11.5667	0.608774	19
AXIN2	3.775791	0.419532	9	ZNF423	6.335363	0.33344	19
RUNX1	3.624731	0.402748	9	CASZ1	5.397979	0.284104	19
VRK2	6.313109	0.789139	8	SMG1P2	4.917543	0.258818	19
DLEU1	5.319829	0.664979	8	BOLA2	4.917543	0.258818	19
PPP2R2B	4.572386	0.571548	8	LOC613038	4.917543	0.258818	19
DNMT3A	3.907375	0.488422	8	FOXK1	7.718463	0.428803	18
SYNJ2	3.601273	0.450159	8	TBC1D16	5.120114	0.284451	18
CXXC5	4.054631	0.579233	7	ANKRD11	4.25437	0.236354	18
MIR548H4	3.684494	0.526356	7	HOXA3	3.97575	0.220875	18
RXRA	3.553296	0.507614	7	PAX6-AS1	5.228992	0.307588	17
PLEC	3.466331	0.49519	7	RCN1	5.228992	0.307588	17
VPS13D	3.431918	0.490274	7	TBX15	5.186025	0.30506	17
COLEC11	3.717555	0.619593	6	FOXP1	6.348768	0.396798	16
FBXL18	3.690005	0.615001	6	NAV2	5.44581	0.340363	16
SLC22A18AS	3.658081	0.60968	6	SORBS2	5.172554	0.323285	16
RUNDC3A	4.428237	0.885647	5	GLI2	8.08092	0.538728	15
VAV2	3.785684	0.757137	5	ZBTB20	6.828758	0.455251	15
TSNAX-DISC1	3.404829	0.680966	5	LRMDA	5.159864	0.343991	15
AP2A2	3.400921	0.680184	5	BAIAP2	4.856771	0.323785	15
ANKLE2	3.509638	1.754819	2	EMX2OS	4.686864	0.312458	15
TRIM65	3.451435	1.725717	2	NFIX	4.573463	0.304898	15
TABLE 162: Cancer Type PXA				KIRREL3	4.522711	0.301514	15
				KNDC1	3.907792	0.260519	15
Gene site	imp_sum	imp_mean	n	PRKAG2	5.613557	0.400968	14
PTPRN2	20.26125	0.247088	82	RPS6KA2	5.561453	0.397247	14
PRDM16	19.38353	0.273007	71	CUX1	5.005901	0.357564	14
PCDHGA1	4.002326	0.067836	59	C7orf50	4.775226	0.341088	14
HDAC4	14.11703	0.381541	37	CACNA1H	4.104379	0.29317	14
PAX6	9.525175	0.272148	35	IQSEC1	3.912602	0.279472	14
RBFOX3	6.963974	0.198971	35	ARHGEF10	3.803718	0.271694	14
DIP2C	11.88264	0.371333	32	MIR548F5	3.773457	0.269533	14
SOX2-OT	5.857559	0.201985	29	MSI2	6.204519	0.477271	13
GALNT9	4.077147	0.151005	27	SPTBN4	5.489224	0.422248	13
CAMTA1	8.413322	0.336533	25	MYT1L	4.504388	0.346491	13
PDGFRA	7.680209	0.307208	25	RFX4	4.274853	0.328835	13
AGAP1	5.894966	0.235799	25	ZC3H3	6.241606	0.520134	12
SATB2	7.42217	0.309257	24	MIRLET7BHG	6.222207	0.518517	12
MEIS1	4.695101	0.195629	24	CMIP	4.766455	0.397205	12
RPTOR	12.58887	0.547342	23	ISLR2	4.365895	0.363825	12
NXN	7.073047	0.307524	23	FBRSL1	4.273014	0.356084	12
INPP5A	6.55427	0.284968	23	ADGRD1	4.122763	0.343564	12
NCOR2	5.953292	0.258839	23	MAML3	4.109295	0.342441	12
PRKCZ	7.531474	0.34234	22	CTNNA2	3.944939	0.328745	12
SKI	7.788973	0.370903	21	RASA3	3.937396	0.328116	12
FRMD4A	6.41236	0.320618	20	RAD51B	4.84344	0.440313	11

ZC3H12D	4.806616	0.436965	11	INPP5A	4.454718	0.193683	23
CTBP2	4.244572	0.38587	11	RPTOR	3.447995	0.149913	23
TBCD	3.967836	0.360712	11	PRKCZ	4.444889	0.20204	22
VGLL4	3.936592	0.357872	11	SKI	5.546912	0.264139	21
AUTS2	4.110377	0.411038	10	ZIC4	2.592634	0.123459	21
KLHL29	4.033775	0.403377	10	SDK1	3.813111	0.190656	20
SH3RF3	3.825704	0.38257	10	ABR	3.572512	0.178626	20
SND1	5.693729	0.632637	9	MAD1L1	10.37545	0.546076	19
TRAPPC12	4.834168	0.53713	9	SMG1P2	4.341857	0.228519	19
ADAMTS2	4.623229	0.513692	9	BOLA2	4.341857	0.228519	19
RUNX1	4.543854	0.504873	9	LOC613038	4.341857	0.228519	19
SSBP3	4.42173	0.491303	9	CASZ1	3.823251	0.201224	19
CACNA2D4	4.382012	0.48689	9	ZNF423	3.358649	0.176771	19
KAZN	4.311313	0.479035	9	KCNQ1	2.699977	0.142104	19
KCNMA1	4.033786	0.448198	9	ANKRD11	3.737851	0.207658	18
NEAT1	3.908167	0.434241	9	TBC1D16	2.700736	0.150041	18
EGFR	3.820696	0.424522	9	FOXK1	2.346755	0.130375	18
TSPAN9	3.772676	0.419186	9	OPCML	5.968518	0.351089	17
SLC22A18	3.769861	0.418873	9	PAX6-AS1	3.503387	0.206082	17
MCC	4.523935	0.565492	8	RCN1	3.503387	0.206082	17
AFF3	4.40779	0.550974	8	FOXP1	5.755484	0.359718	16
LINC00311	4.102662	0.512833	8	EBF3	3.313564	0.207098	16
DLEU1	3.844641	0.48058	8	SLX1B-			
DUSP6	5.719013	0.817002	7	SULT1A4	3.1196	0.207973	15
CRADD	4.168197	0.694699	6	SLX1A	3.1196	0.207973	15
SLC22A18AS	4.007575	0.667929	6	LOC606724	3.1196	0.207973	15
FBXL18	3.850436	0.641739	6	LRMDA	3.00295	0.200197	15
TSNAX-DISC1	4.344618	0.868924	5	KNDC1	2.790788	0.186053	15
ARHGEF7	3.753659	0.750732	5	CUX1	3.751913	0.267994	14
STAP2	3.92153	0.980383	4	PRKAG2	3.03044	0.21646	14
SLC25A10	3.852625	1.926312	2	ARHGEF10	2.916299	0.208307	14
				MOB2	2.684732	0.191767	14
				IQSEC1	2.533911	0.180994	14
				MYT1L	4.702899	0.361761	13
				MSI2	4.178197	0.3214	13
				GSE1	2.787183	0.214399	13
				MIRLET7BHG	4.585815	0.382151	12
				FBRSL1	3.606563	0.300547	12
				ZC3H3	3.079863	0.256655	12
				CMIP	2.793971	0.232831	12
				RAD51B	2.416006	0.219637	11
				RGS12	3.158603	0.31586	10
				AKAP13	2.677057	0.267706	10
				FMN1	2.601988	0.260199	10
				ADGRA1	2.36914	0.236914	10
				SH3RF3	2.355094	0.235509	10
				ADAMTS2	4.911167	0.545685	9
				ATP11A	4.712607	0.523623	9

TABLE 163:		Cancer Type					
		RB					
Gene site	imp_sum	imp_mean	n				
PTPRN2	4.901971	0.05978	82				
PRDM16	8.704295	0.122596	71				
HDAC4	9.898104	0.267516	37				
RBFOX3	4.910006	0.140286	35				
PAX6	2.413042	0.068944	35				
DIP2C	5.273425	0.164795	32				
GALNT9	5.441205	0.201526	27				
SHANK2	5.317331	0.204513	26				
AGAP1	6.973388	0.278936	25				
CAMTA1	5.24227	0.209691	25				
NCOR2	5.797198	0.252052	23				
NXN	5.140158	0.223485	23				
RIMBP2	4.585475	0.199368	23				

SND1	4.524242	0.502694	9	DIP2C	5.428499	0.169641	32
TSPAN9	3.336084	0.370676	9	GALNT9	3.318927	0.122923	27
CACNA2D4	2.887287	0.32081	9	SHANK2	3.188553	0.122637	26
MGMT	2.880248	0.320028	9	CAMTA1	9.759744	0.39039	25
AXIN2	2.525171	0.280575	9	AGAP1	7.47166	0.298866	25
VRK2	4.160478	0.52006	8	PDGFRA	2.523211	0.100928	25
ABLIM2	3.597908	0.449739	8	RPTOR	5.980657	0.260029	23
PPP2R2B	3.516886	0.439611	8	NCOR2	5.458186	0.237312	23
AFF3	2.643811	0.330476	8	INPP5A	5.290319	0.230014	23
DNMT3A	2.571322	0.321415	8	RIMBP2	3.048244	0.132532	23
ASPSCR1	2.46467	0.308084	8	HOXB3	2.345977	0.101999	23
MSRA	2.456027	0.307003	8	NXN	2.30479	0.100208	23
DLEU1	2.425934	0.303242	8	PRKCZ	4.998182	0.22719	22
HOXB-AS3	2.749782	0.392826	7	SKI	5.721301	0.272443	21
SOX6	2.533076	0.361868	7	MAD1L1	11.286	0.594	19
NAV1	2.501446	0.357349	7	SMG1P2	4.790748	0.252145	19
MIR548H4	2.427279	0.346754	7	BOLA2	4.790748	0.252145	19
ARHGAP45	3.888732	0.648122	6	LOC613038	4.790748	0.252145	19
CRADD	3.279068	0.546511	6	CASZ1	2.627735	0.138302	19
MYO16	2.502379	0.417063	6	FOXK1	2.847926	0.158218	18
PRKN	2.450354	0.408392	6	TBC1D16	2.641408	0.146745	18
COLEC11	2.353995	0.392332	6	PAX6-AS1	5.304462	0.312027	17
TSNAX-DISC1	4.482762	0.896552	5	RCN1	5.304462	0.312027	17
ARHGEF7	3.244894	0.648979	5	HBG2	3.274533	0.19262	17
SDK2	2.972038	0.594408	5	TBX15	2.751941	0.161879	17
EXT1	2.383674	0.595919	4	FOXP1	5.574482	0.348405	16
CCND2	3.257018	1.085673	3	EBF3	3.503737	0.218984	16
SLC25A22	3.094645	1.031548	3	NAV2	3.411115	0.213195	16
CCDC167	2.502263	0.834088	3	LRMDA	3.450637	0.230042	15
DICER1	2.371142	0.790381	3	KNDC1	3.081972	0.205465	15
CHTF18	4.258503	2.129251	2	BAIAP2	2.981749	0.198783	15
ANKLE2	3.009641	1.504821	2	IQSEC1	3.484644	0.248903	14
TRIM65	2.683372	1.341686	2	ARHGEF10	3.254416	0.232458	14
KIF21B	2.646695	1.323348	2	MIR548F5	2.976081	0.212577	14
UHRF1	2.60598	1.30299	2	GNG7	2.94744	0.210531	14
GNB5	2.408241	1.204121	2	MOB2	2.765342	0.197524	14
KCNV2	2.913913	2.913913	1	C7orf50	2.647253	0.18909	14
DDT	2.827667	2.827667	1	PPP2R2A	2.380527	0.170038	14
ARL6IP6	2.792841	2.792841	1	MSI2	6.174824	0.474986	13
DNAJC27	2.353962	2.353962	1	MYT1L	4.461313	0.343178	13
				FBRSL1	4.266439	0.355537	12
TABLE 164:	Cancer Type RB_MYCN			MIRLET7BHG	3.926465	0.327205	12
Gene site	imp_sum	imp_mean	n	ZC3H3	3.870611	0.322551	12
PTPRN2	7.195324	0.087748	82	VGLL4	2.825087	0.256826	11
PRDM16	4.382494	0.061725	71	GLUD1P2	2.322585	0.211144	11
HDAC4	8.272875	0.223591	37	LBX1-AS1	3.264628	0.326463	10
PAX6	5.111473	0.146042	35	ETS1	2.722256	0.272226	10
RBFOX3	4.800351	0.137153	35	AKAP13	2.48025	0.248025	10

AUTS2	2.349618	0.234962	10	TABLE 165:	Cancer Type RGNT		
NBEA	2.335896	0.23359	10	Gene site	imp_sum	imp_mean	n
SND1	5.29855	0.588728	9	PTPRN2	28.35935	0.345846	82
TSPAN9	4.693493	0.521499	9	PRDM16	18.3351	0.258241	71
ATP11A	3.860071	0.428897	9	PCDHGA1	4.71592	0.079931	59
ADAMTS2	3.566091	0.396232	9	PCDHGA2	4.71592	0.082735	57
AXIN2	3.420051	0.380006	9	PCDHGA3	4.71592	0.087332	54
MGMT	3.342588	0.371399	9	PCDHGB1	4.71592	0.08898	53
CACNA2D4	3.219986	0.357776	9	PCDHGA4	4.71592	0.092469	51
GPC6	3.118737	0.346526	9	PCDHGB2	5.032306	0.1027	49
PPP2R2B	4.045886	0.505736	8	HDAC4	12.65834	0.342117	37
TRAPPC9	3.484088	0.435511	8	PAX6	11.53394	0.329541	35
VRK2	3.126736	0.390842	8	RBFOX3	9.405788	0.268737	35
DNMT3A	3.056051	0.382006	8	DIP2C	8.505616	0.265801	32
AFF3	2.644018	0.330502	8	SOX2-OT	11.7201	0.404141	29
TRIM6-TRIM34	3.253256	0.464751	7	GALNT9	4.717065	0.174706	27
VPS13D	2.927376	0.418197	7	SHANK2	7.435439	0.285978	26
MIR548H4	2.505199	0.357886	7	ADARB2	4.672043	0.179694	26
CCDC85C	4.449552	0.741592	6	AGAP1	11.2714	0.450856	25
TRAK1	3.16209	0.527015	6	CAMTA1	9.239245	0.36957	25
CRADD	2.834375	0.472396	6	PDGFRA	7.122884	0.284915	25
PBX1	2.718575	0.453096	6	SATB2	7.173512	0.298896	24
TRIM34	2.707714	0.451286	6	MEIS1	6.522382	0.271766	24
MYO16	2.67766	0.446277	6	RPTOR	10.93966	0.475637	23
TSNAX-DISC1	4.532751	0.90655	5	NCOR2	8.649125	0.376049	23
SDK2	3.207546	0.641509	5	INPP5A	6.930626	0.301332	23
ARHGEF7	2.946983	0.589397	5	HOXB3	6.642556	0.288807	23
SNX29	2.567895	0.513579	5	NXN	5.837885	0.253821	23
CACNA2D2	2.316446	0.463289	5	PRKCZ	7.999369	0.363608	22
GSG1	2.796905	0.699226	4	SKI	11.84054	0.563835	21
EXT1	2.782114	0.695529	4	SIM2	9.07104	0.431954	21
DGKD	2.413085	0.603271	4	FRMD4A	8.287969	0.414398	20
TULP4	3.428444	1.142815	3	ABR	6.945064	0.347253	20
SLC25A22	2.87053	0.956843	3	SDK1	5.84499	0.292249	20
EPAS1	2.488338	0.829446	3	MAD1L1	13.51159	0.711136	19
DAGLB	2.487952	0.829317	3	SMG1P2	9.561161	0.503219	19
CHID1	2.437806	0.812602	3	BOLA2	9.561161	0.503219	19
ANKRD33B	2.360123	0.786708	3	LOC613038	9.561161	0.503219	19
CHTF18	4.257121	2.128561	2	ZNF423	8.580089	0.451584	19
KIF21B	2.723222	1.361611	2	CASZ1	6.041944	0.317997	19
UHRF1	2.656527	1.328264	2	KCNQ1	4.706689	0.24772	19
TRIM65	2.587965	1.293982	2	MCF2L	9.160776	0.508932	18
ATG4B	2.378033	1.189016	2	FO XK1	7.883264	0.437959	18
KCNV2	2.844112	2.844112	1	ANKRD11	6.391641	0.355091	18
ARL6IP6	2.692015	2.692015	1	TBC1D16	5.996482	0.333138	18
DDT	2.610675	2.610675	1	SEPTIN9	5.99005	0.332781	18
DNAJC27	2.459424	2.459424	1	OPCML	9.744459	0.573203	17
				NAV2	6.679508	0.417469	16

FOXP1	5.694375	0.355898	16	RUNDC3A	5.492642	1.098528	5
SORBS2	4.846608	0.302913	16	VAV2	4.711378	0.942276	5
EBF3	4.526261	0.282891	16	TSNAX-DISC1	4.625445	0.925089	5
GLI2	12.80633	0.853756	15	STAP2	5.101563	1.275391	4
ZBTB20	6.33536	0.422357	15	RBMS3	4.78651	1.196628	4
EMX2OS	5.934061	0.395604	15	SOX10	5.438382	2.719191	2
LRMDA	4.801419	0.320095	15				
BAIAP2	4.424395	0.29496	15	TABLE 166: Cancer Type SCHW			
IQSEC1	6.656421	0.475459	14	Gene site	imp_sum	imp_mean	n
RPS6KA2	6.340967	0.452926	14	PTPRN2	18.12891	0.221084	82
CUX1	6.335945	0.452568	14	PRDM16	17.27083	0.243251	71
PRKAG2	5.634796	0.402485	14	PCDHGA1	4.622623	0.07835	59
C7orf50	4.816359	0.344026	14	PCDHGA2	4.622623	0.081099	57
ARHGEF10	4.794289	0.342449	14	PCDHGA3	3.922562	0.07264	54
MSI2	7.173944	0.551842	13	PCDHGB1	3.922562	0.074011	53
MYT1L	6.796579	0.522814	13	PCDHGA4	3.922562	0.076913	51
RFX4	5.610106	0.431547	13	PCDHGB2	4.238948	0.086509	49
MIR9-3HG	4.546077	0.349698	13	PCDHGA5	3.922562	0.083459	47
CMIP	6.03703	0.503086	12	HDAC4	14.71199	0.397621	37
MIRLET7BHG	5.241599	0.4368	12	PAX6	12.27248	0.350642	35
ZC3H3	4.856416	0.404701	12	RBFOX3	6.903027	0.197229	35
TNS3	4.479188	0.373266	12	DIP2C	11.14531	0.348291	32
VGLL4	5.726971	0.520634	11	SOX2-OT	9.275725	0.319853	29
RAD51B	5.633707	0.512155	11	SHANK2	5.840376	0.22463	26
CCDC140	5.44346	0.49486	11	ADARB2	4.148071	0.159541	26
ZC3H12D	5.207577	0.473416	11	AGAP1	9.096533	0.363861	25
FGFR2	4.749396	0.431763	11	CAMTA1	6.895361	0.275814	25
SH3RF3	5.116472	0.511647	10	PDGFRA	6.799302	0.271972	25
KLHL29	4.973237	0.497324	10	SATB2	4.169054	0.173711	24
NTM	4.777075	0.477708	10	RPTOR	11.85899	0.515608	23
MAML2	4.754856	0.475486	10	INPP5A	7.671982	0.333564	23
CHST11	4.634003	0.4634	10	NCOR2	6.603778	0.287121	23
AKAP13	4.481869	0.448187	10	PRKCZ	6.016055	0.273457	22
ATP11A	6.542237	0.726915	9	SKI	13.01664	0.61984	21
SND1	6.464573	0.718286	9	FRMD4A	7.580493	0.379025	20
ASAP1	6.008052	0.667561	9	SDK1	5.778566	0.288928	20
ADAMTS2	5.236207	0.581801	9	ABR	5.296441	0.264822	20
NOTCH1	5.15284	0.572538	9	MAD1L1	11.97168	0.630088	19
AXIN2	4.595346	0.510594	9	ZNF423	7.148908	0.376258	19
ADGRB1	4.587885	0.509765	9	SMG1P2	6.66403	0.350738	19
TRAPPC12	4.519644	0.502183	9	BOLA2	6.66403	0.350738	19
LINC00311	6.528932	0.816116	8	LOC613038	6.66403	0.350738	19
MSRA	4.541659	0.567707	8	CASZ1	5.936643	0.312455	19
BAHCC1	4.471947	0.558993	8	FO XK1	8.515619	0.47309	18
DUSP6	7.783034	1.111862	7	TBC1D16	7.090589	0.393922	18
NAV1	5.24062	0.74866	7	SEPTIN9	6.76469	0.375816	18
LINC00461	4.893859	0.699123	7	ANKRD11	4.752093	0.264005	18
FBXL18	4.979822	0.82997	6	MCF2L	4.090501	0.22725	18

PAX6-AS1	7.6399	0.449406	17	LINC00461	4.541013	0.648716	7
RCN1	7.6399	0.449406	17	DUSP6	3.932552	0.561793	7
FOXP1	6.437553	0.402347	16	C19orf25	3.930343	0.561478	7
NAV2	6.150183	0.384386	16	RXRA	3.880434	0.554348	7
GLI2	7.068317	0.471221	15	FBXL18	5.204025	0.867338	6
ZBTB20	4.663726	0.310915	15	CCDC177	4.889198	0.814866	6
BAIAP2	4.607747	0.307183	15	SLC22A18AS	3.930148	0.655025	6
KIRREL3	4.381034	0.292069	15	RUNDC3A	5.719208	1.143842	5
NFIX	3.930406	0.262027	15	TSNAX-DISC1	4.920333	0.984067	5
CUX1	6.776737	0.484053	14	ARHGEF7	4.223877	0.844775	5
RPS6KA2	5.766261	0.411876	14	TBC1D7	3.852973	1.284324	3
C7orf50	4.866972	0.347641	14	SOX10	4.443244	2.221622	2
CACNA1H	4.858249	0.347018	14	SLC25A10	3.978218	1.989109	2
IQSEC1	4.78237	0.341598	14				
ARHGEF10	4.535499	0.323964	14	TABLE 167:	Cancer Type SEGA		
MIR548F5	3.867145	0.276225	14	Gene site	imp_sum	imp_mean	n
MSI2	6.901005	0.530847	13	PTPRN2	29.02048	0.353908	82
MYT1L	4.843067	0.372544	13	PRDM16	26.6926	0.375952	71
CMIP	6.485181	0.540432	12	PCDHGA1	8.996433	0.152482	59
ZC3H3	5.697761	0.474813	12	PCDHGA2	8.680047	0.152282	57
TNS3	5.012632	0.417719	12	PCDHGA3	8.034496	0.148787	54
ADGRD1	4.211266	0.350939	12	PCDHGB1	7.71811	0.145625	53
FBRSL1	4.155268	0.346272	12	PCDHGA4	7.71811	0.151335	51
VGLL4	4.828727	0.438975	11	PCDHGB2	7.401724	0.151056	49
FGFR2	4.826384	0.438762	11	PCDHGA5	6.994791	0.148825	47
RAD51B	4.779676	0.434516	11	PCDHGB3	6.269448	0.145801	43
CTBP2	4.41779	0.401617	11	PCDHGA6	6.269448	0.156736	40
SPON2	4.072423	0.37022	11	HDAC4	19.58775	0.529399	37
ANAPC16	3.97173	0.361066	11	PCDHGA7	5.953062	0.160894	37
ZC3H12D	3.883146	0.353013	11	PAX6	14.09937	0.402839	35
TSPAN4	4.781925	0.478193	10	RBFOX3	9.517654	0.271933	35
ACOT7	4.757242	0.475724	10	PCDHGB4	5.636676	0.161048	35
AKAP13	4.524347	0.452435	10	PCDHGA8	5.636676	0.161048	35
SH3RF3	4.35329	0.435329	10	DIP2C	13.04091	0.407528	32
GAS7	4.327703	0.43277	10	PCDHGB5	5.636676	0.176146	32
NR2F1-AS1	3.88907	0.388907	10	SOX2-OT	10.00762	0.34509	29
SND1	6.696641	0.744071	9	GALNT9	8.426724	0.312101	27
ATP11A	6.204406	0.689378	9	SHANK2	8.662506	0.333173	26
TRAPPC12	5.123195	0.569244	9	ADARB2	7.09401	0.272847	26
ADAMTS2	4.999018	0.555446	9	AGAP1	13.3909	0.535636	25
SPECC1	3.979139	0.442127	9	CAMTA1	10.94498	0.437799	25
KCNH2	3.875947	0.430661	9	PDGFRA	7.666178	0.306647	25
LINC00311	5.825952	0.728244	8	SATB2	8.571828	0.357159	24
MSRA	5.302974	0.662872	8	MEIS1	6.573848	0.27391	24
GRIK2	4.49141	0.561426	8	RPTOR	16.42404	0.714089	23
DNMT3A	4.206901	0.525863	8	NCOR2	12.07995	0.525215	23
DLEU1	3.939931	0.492491	8	NXN	7.265405	0.315887	23
MIR548H4	4.554369	0.650624	7	HOXB3	5.758261	0.250359	23

INPP5A	5.558288	0.241665	23	TNS3	5.780302	0.481692	12
PRKCZ	8.292005	0.376909	22	CTNNA2	5.759007	0.479917	12
SKI	11.23111	0.534815	21	TBX4	5.550192	0.462516	12
ZIC4	6.017229	0.286535	21	ZC3H12D	6.890304	0.626391	11
FRMD4A	8.362341	0.418117	20	VGLL4	6.233194	0.566654	11
SDK1	7.144768	0.357238	20	SPON2	6.144651	0.558605	11
ABR	6.229435	0.311472	20	FGFR2	5.607308	0.509755	11
MAD1L1	14.39206	0.757477	19	RAD51B	5.571527	0.506502	11
ZNF423	11.2155	0.59029	19	ACOT7	5.817013	0.581701	10
CASZ1	7.8292	0.412063	19	NR2F1-AS1	5.500147	0.550015	10
SMG1P2	7.050443	0.371076	19	ATP11A	7.600119	0.844458	9
BOLA2	7.050443	0.371076	19	SND1	7.195881	0.799542	9
LOC613038	7.050443	0.371076	19	ADAMTS2	6.730098	0.747789	9
FO XK1	9.55413	0.530785	18	AXIN2	6.121065	0.680118	9
ANKRD11	7.699424	0.427746	18	TRAPPC12	5.98463	0.664959	9
MCF2L	7.344672	0.408037	18	MSRA	6.237314	0.779664	8
TBC1D16	6.84073	0.380041	18	LINC00311	5.4446	0.680575	8
SEPTIN9	6.522388	0.362355	18	NAV1	5.966218	0.852317	7
OPCML	7.410812	0.43593	17	VPS13D	5.545241	0.792177	7
TBX15	6.290804	0.370047	17	TSNAX-DISC1	5.601673	1.120335	5
PAX6-AS1	5.799636	0.341155	17	RUNDC3A	5.495706	1.099141	5
RCN1	5.799636	0.341155	17				
NAV2	6.981482	0.436343	16	TABLE 168: Cancer Type SFT_HMPC			
FOXP1	6.970221	0.435639	16	Gene site	imp_sum	imp_mean	n
SORBS2	6.046814	0.377926	16	PTPRN2	12.24457	0.149324	82
GLI2	9.618994	0.641266	15	PRDM16	8.735533	0.123036	71
ZBTB20	7.555842	0.503723	15	PCDHGA1	2.896052	0.049086	59
LRMDA	6.710239	0.447349	15	PCDHGA2	3.212438	0.056359	57
SLX1B-SULT1A4	6.386947	0.425796	15	HDAC4	15.42218	0.416816	37
SLX1A	6.386947	0.425796	15	RBFOX3	5.849642	0.167133	35
LOC606724	6.386947	0.425796	15	PAX6	4.371199	0.124891	35
KIRREL3	6.201228	0.413415	15	DIP2C	7.825877	0.244559	32
NFIX	6.051682	0.403445	15	SOX2-OT	3.668157	0.126488	29
KNDC1	5.465558	0.364371	15	GALNT9	3.100134	0.11482	27
RPS6KA2	8.600181	0.614299	14	SHANK2	4.732856	0.182033	26
MIR548F5	6.434363	0.459597	14	ADARB2	3.034991	0.11673	26
CUX1	6.083478	0.434534	14	AGAP1	9.403838	0.376154	25
ARHGEF10	6.002265	0.428733	14	PDGFRA	5.60567	0.224227	25
PRKAG2	5.718673	0.408477	14	CAMTA1	3.06187	0.122475	25
MSI2	10.13503	0.779618	13	RPTOR	8.730063	0.379568	23
MYT1L	6.429776	0.494598	13	NXN	4.785711	0.208074	23
SPTBN4	5.741059	0.44162	13	NCOR2	3.654354	0.158885	23
RFX4	5.600712	0.430824	13	INPP5A	2.705938	0.117649	23
ZC3H3	7.296484	0.60804	12	PRKCZ	5.284244	0.240193	22
CMIP	6.604265	0.550355	12	SKI	5.042624	0.240125	21
MIRLET7BHG	6.154127	0.512844	12	FRMD4A	4.644678	0.232234	20
FBRSL1	6.109633	0.509136	12	SDK1	4.376963	0.218848	20
				MAD1L1	8.270841	0.435307	19

ZNF423	4.948134	0.260428	19	AXIN2	3.578296	0.397588	9
KCNQ1	3.124892	0.164468	19	ADAMTS2	3.089809	0.343312	9
SMG1P2	2.74439	0.144442	19	SSBP3	2.952884	0.328098	9
BOLA2	2.74439	0.144442	19	MGMT	2.887198	0.3208	9
LOC613038	2.74439	0.144442	19	EGFR	2.665465	0.296163	9
FO XK1	5.302466	0.294581	18	DLEU1	3.117279	0.38966	8
TBC1D16	4.312583	0.239588	18	VEPH1	2.998216	0.374777	8
SEPTIN9	3.934468	0.218582	18	C19orf25	4.207244	0.601035	7
MCF2L	3.924385	0.218021	18	VPS13D	3.727292	0.53247	7
ANKRD11	3.412792	0.1896	18	MIR548H4	3.215443	0.459349	7
TBX15	3.145523	0.185031	17	PCCA	3.061603	0.437372	7
OPCML	2.788615	0.164036	17	LINC01140	2.728831	0.389833	7
FOXP1	6.145645	0.384103	16	LINC00461	2.705385	0.386484	7
NAV2	5.405925	0.33787	16	TACC2	2.680219	0.382888	7
EBF3	4.332831	0.270802	16	NAV1	2.666223	0.380889	7
NFIX	4.838829	0.322589	15	CRADD	3.201265	0.533544	6
ZBTB20	4.600342	0.306689	15	FBXL18	3.084465	0.514077	6
GLI2	4.120826	0.274722	15	STRA6	3.051614	0.508602	6
SLX1B-				SLC22A18AS	2.968643	0.494774	6
SULT1A4	3.41389	0.227593	15	FMNL2	2.839545	0.473257	6
SLX1A	3.41389	0.227593	15	TSNAX-DISC1	4.482228	0.896446	5
LOC606724	3.41389	0.227593	15	RUNDC3A	4.415637	0.883127	5
RPS6KA2	6.101722	0.435837	14	BCAR1	2.89008	0.578016	5
IQSEC1	5.106277	0.364734	14	ARHGEF7	2.633655	0.526731	5
C7orf50	4.751788	0.339413	14	DAGLB	3.082435	1.027478	3
PRKAG2	3.580027	0.255716	14	DICER1	2.741322	0.913774	3
CUX1	3.278226	0.234159	14	SLC25A10	3.081614	1.540807	2
MSI2	4.156053	0.319696	13	CHTF18	2.836534	1.418267	2
MYT1L	3.817407	0.293647	13	RALGAPA2	2.792279	1.39614	2
RFX4	3.072925	0.236379	13				
HOXC4	2.635727	0.202748	13				
CMIP	5.84176	0.486813	12	TABLE 169: Cancer Type SNUC_IDH2			
FBRSL1	4.394747	0.366229	12	Gene site	imp_sum	imp_mean	n
ADGRD1	4.266942	0.355578	12	PTPRN2	1.943547	0.023702	82
MIRLET7BHG	3.586183	0.298849	12	PCDHGA1	1.997666	0.033859	59
MAML3	2.631919	0.219327	12	PCDHGA2	1.997666	0.035047	57
COL4A1	3.672924	0.333902	11	PCDHGA3	1.997666	0.036994	54
PCDHGC3	2.896052	0.263277	11	PCDHGB1	1.997666	0.037692	53
SLC38A10	2.870792	0.260981	11	PCDHGA4	1.997666	0.03917	51
TSPAN4	4.515049	0.451505	10	PCDHGB2	1.997666	0.040769	49
GAS7	3.967262	0.396726	10	PCDHGA5	1.997666	0.042504	47
AKAP13	3.756983	0.375698	10	PCDHGB3	1.997666	0.046457	43
ACOT7	3.560002	0.356	10	HDAC4	6.857323	0.185333	37
KLHL29	3.262059	0.326206	10	PAX6	2.847474	0.081356	35
BCL11B	2.961893	0.296189	10	DIP2C	4.269002	0.133406	32
SH3RF3	2.812441	0.281244	10	SOX2-OT	2.93842	0.101325	29
CHST11	2.709323	0.270932	10	SHANK2	1.912098	0.073542	26
SND1	4.516105	0.501789	9	AGAP1	5.525905	0.221036	25
				PDGFRA	2.284215	0.091369	25

RPTOR	4.514173	0.196268	23	TRAPPC9	1.898316	0.237289	8
RIMBP2	2.847474	0.123803	23	MIR548H4	2.378158	0.339737	7
NCOR2	2.500333	0.10871	23	ITPK1	2.179421	0.311346	7
INPP5A	2.413317	0.104927	23	NAV1	2.020792	0.288685	7
PRKCZ	2.569685	0.116804	22	VPS13D	1.986051	0.283722	7
SKI	5.805435	0.276449	21	CXXC5	1.916586	0.273798	7
SIM2	1.898316	0.090396	21	FBXL18	3.390413	0.565069	6
FRMD4A	3.44193	0.172097	20	COQ8A	2.523787	0.420631	6
MAD1L1	4.732794	0.249094	19	CRADD	2.414877	0.40248	6
SMG1P2	3.661984	0.192736	19	ANKS1A	2.243284	0.373881	6
BOLA2	3.661984	0.192736	19	CASP8	3.74288	0.748576	5
LOC613038	3.661984	0.192736	19	RUNDC3A	2.976877	0.595375	5
KCNQ1	3.422943	0.180155	19	ARHGEF7	2.906795	0.581359	5
ZNF423	1.898316	0.099911	19	ATP2B4	2.576039	0.515208	5
FOXK1	6.056056	0.336448	18	TSNAX-DISC1	2.401902	0.48038	5
HOXA3	2.782692	0.154594	18	GAREM2	2.047481	0.409496	5
FOXP1	4.921271	0.307579	16	BCAR1	1.962986	0.392597	5
BAIAP2	2.430132	0.162009	15	GRIP1	1.962096	0.392419	5
ZBTB20	2.120404	0.14136	15	CADM1	1.882871	0.376574	5
RPS6KA2	3.714062	0.26529	14	TUBA1C	3.333471	0.833368	4
CUX1	3.528898	0.252064	14	NHSL1	2.851141	0.712785	4
SYCP2L	2.657751	0.189839	14	STAP2	2.843336	0.710834	4
IQSEC1	2.574887	0.18392	14	GSG1	2.639775	0.659944	4
PRKAG2	2.135232	0.152517	14	RAI1	2.44892	0.61223	4
HOXA10- HOXA9	2.543701	0.195669	13	LINC00856	2.153666	0.538417	4
MSI2	1.916386	0.147414	13	ZMIZ1	2.070196	0.517549	4
CMIP	3.489611	0.290801	12	DTNA	2.010819	0.502705	4
FBRSL1	2.473605	0.206134	12	DICER1	2.424191	0.808064	3
MAML3	2.226349	0.185529	12	SLC6A9	2.405465	0.801822	3
TNS3	2.066662	0.172222	12	TMBIM1	1.95763	0.652543	3
GLUD1P2	2.424013	0.220365	11	DAGLB	1.900425	0.633475	3
RAD51B	1.840497	0.167318	11	RALGAPA2	2.676986	1.338493	2
TSPAN4	3.382803	0.33828	10	SFXN5	2.155911	1.077956	2
ACOT7	3.110649	0.311065	10	CHTF18	2.137129	1.068564	2
SPPL2B	3.037791	0.303779	10	ERI3	1.891715	0.945857	2
AKAP13	2.417812	0.241781	10	TRIP6	1.846681	0.923341	2
BCL11B	2.215527	0.221553	10	TOM1L2	1.848306	1.848306	1
ATP11A	5.310308	0.590034	9	TABLE 170: Cancer Type ST_EPN_RELA_A			
SND1	3.85585	0.428428	9				
ADAMTS2	3.107474	0.345275	9	Gene site	imp_sum	imp_mean	n
AXIN2	2.218268	0.246474	9	PTPRN2	17.2971	0.21094	82
SLC22A18	2.2033	0.244811	9	PRDM16	19.37879	0.272941	71
TSPAN9	2.069869	0.229985	9	PCDHGA1	4.72789	0.080134	59
LHX4	4.005276	0.500659	8	PCDHGA2	4.739979	0.083158	57
LINC00311	3.115602	0.38945	8	PCDHGA3	5.056365	0.093636	54
DLEU1	2.856946	0.357118	8	PCDHGB1	5.056365	0.095403	53
MSRA	2.169484	0.271186	8	PCDHGA4	5.056365	0.099144	51
				PCDHGB2	4.739979	0.096734	49

PCDHGA5	4.423593	0.094119	47	CUX1	6.280038	0.448574	14
HDAC4	14.85662	0.40153	37	MIR548F5	6.087254	0.434804	14
RBFOX3	11.18775	0.31965	35	ARHGEF10	5.1838	0.370271	14
PAX6	10.94274	0.31265	35	PRKAG2	4.945042	0.353217	14
DIP2C	9.369048	0.292783	32	IQSEC1	4.481342	0.320096	14
SOX2-OT	7.508662	0.258919	29	C7orf50	4.389609	0.313543	14
SHANK2	6.785761	0.260991	26	MSI2	5.643963	0.434151	13
ADARB2	5.195607	0.199831	26	KIF26B	4.835693	0.371976	13
AGAP1	10.34313	0.413725	25	MYT1L	4.631923	0.356302	13
CAMTA1	8.581708	0.343268	25	CMIP	6.13285	0.511071	12
PDGFRA	4.889735	0.195589	25	TNS3	5.978262	0.498189	12
SATB2	6.065678	0.252737	24	MIRLET7BHG	5.291088	0.440924	12
MEIS1	4.400045	0.183335	24	ZC3H3	4.69617	0.391347	12
RPTOR	10.77007	0.468264	23	MEGF6	4.450577	0.370881	12
NCOR2	7.261868	0.315733	23	ADGRD1	4.430574	0.369215	12
HOXB3	6.289484	0.273456	23	SPON2	6.044808	0.549528	11
RIMBP2	6.108486	0.265586	23	ZC3H12D	5.88004	0.534549	11
INPP5A	5.45339	0.237104	23	RAD51B	4.696695	0.426972	11
NXN	4.543369	0.197538	23	VGLL4	4.221628	0.383784	11
SKI	13.41231	0.638682	21	ACOT7	4.993015	0.499302	10
FRMD4A	7.713994	0.3857	20	TSPAN4	4.86048	0.486048	10
ABR	6.297255	0.314863	20	AKAP13	4.647912	0.464791	10
SDK1	4.755602	0.23778	20	RGS12	4.436793	0.443679	10
MAD1L1	12.61895	0.664155	19	TP73	4.201124	0.420112	10
CASZ1	9.451384	0.497441	19	ATP11A	6.458921	0.717658	9
ZNF423	9.394324	0.494438	19	SND1	6.24855	0.694283	9
SMG1P2	6.725338	0.353965	19	TSPAN9	5.107321	0.56748	9
BOLA2	6.725338	0.353965	19	TRAPPC12	4.820956	0.535662	9
LOC613038	6.725338	0.353965	19	KCNH2	4.469588	0.496621	9
FOKK1	7.081048	0.393392	18	LHX4	6.248439	0.781055	8
ANKRD11	6.395685	0.355316	18	DLEU1	5.49409	0.686761	8
MCF2L	5.828254	0.323792	18	ESRRG	4.802341	0.600293	8
TBC1D16	5.509621	0.30609	18	MCC	4.536967	0.567121	8
SEPTIN9	4.832762	0.268487	18	MSRA	4.388299	0.548537	8
RBFOX1	4.165318	0.231407	18	NAV1	4.705733	0.672248	7
OPCML	8.123436	0.477849	17	FBXL18	4.375528	0.729255	6
TBX15	5.684761	0.334398	17	FAM181A	4.224451	0.704075	6
PAX6-AS1	5.461725	0.321278	17	RAPGEF4	5.454854	1.090971	5
RCN1	5.461725	0.321278	17	RUNDC3A	5.18667	1.037334	5
FOXP1	7.261761	0.45386	16	TSNAX-DISC1	4.485901	0.89718	5
EBF3	5.979732	0.373733	16	CACNA1I	4.452073	0.890415	5
NAV2	5.436301	0.339769	16	RBMS3	4.961287	1.240322	4
SORBS2	4.579467	0.286217	16	AIRE	5.495247	1.831749	3
GLI2	10.33434	0.688956	15	SOX10	4.277515	2.138757	2
BAIAP2	5.463403	0.364227	15				
NFIX	4.619551	0.30797	15	TABLE 171: Cancer Type ST_EPN_REL_A_B			
KIRREL3	4.424412	0.294961	15	Gene site	imp_sum	imp_mean	n
RPS6KA2	8.107066	0.579076	14	PTPRN2	6.970855	0.08501	82

PRDM16	11.41428	0.160765	71	MYT1L	2.379207	0.183016	13
HDAC4	7.48412	0.202274	37	ZC3H3	4.9008	0.4084	12
PAX6	5.459408	0.155983	35	CMIP	3.312897	0.276075	12
RBFOX3	3.248363	0.09281	35	MIRLET7BHG	3.241903	0.270159	12
DIP2C	5.933432	0.18542	32	MEGF6	2.898242	0.24152	12
SOX2-OT	2.742155	0.094557	29	VGLL4	5.431527	0.493775	11
GALNT9	2.788617	0.103282	27	ZC3H12D	3.427563	0.311597	11
SHANK2	5.004528	0.192482	26	CTBP2	2.874648	0.261332	11
ADARB2	2.645506	0.10175	26	FGFR2	2.788321	0.253484	11
AGAP1	5.146507	0.20586	25	BCL11B	2.935288	0.293529	10
CAMTA1	3.906327	0.156253	25	ACOT7	2.739333	0.273933	10
PDGFRA	2.738299	0.109532	25	TSPAN4	2.616147	0.261615	10
MEIS1	2.669315	0.111221	24	CBFA2T3	2.411994	0.241199	10
RPTOR	6.480226	0.281749	23	TP73	2.352828	0.235283	10
NXN	3.638481	0.158195	23	ASAP1	5.023262	0.55814	9
PRKCZ	3.711455	0.168703	22	ATP11A	4.541166	0.504574	9
SKI	7.203011	0.343001	21	SND1	3.976947	0.441883	9
FRMD4A	5.16313	0.258157	20	TSPAN9	3.27575	0.363972	9
MAD1L1	6.181267	0.32533	19	MGMT	2.518999	0.279889	9
ZNF423	4.906818	0.258254	19	KCNMA1	2.49215	0.276906	9
SMG1P2	3.801968	0.200104	19	GPC6	2.304978	0.256109	9
BOLA2	3.801968	0.200104	19	SSBP3	2.286095	0.254011	9
LOC613038	3.801968	0.200104	19	DLEU1	3.149543	0.393693	8
CFAP46	3.182928	0.167523	19	MSRA	2.999965	0.374996	8
CASZ1	2.943001	0.154895	19	RGS20	2.536688	0.317086	8
ANKRD11	3.682395	0.204577	18	PPP2R2B	2.440601	0.305075	8
TBC1D16	3.537223	0.196512	18	RORA	2.42611	0.303264	8
FO XK1	2.351994	0.130666	18	CXXC5	3.429377	0.489911	7
OPCML	3.719092	0.21877	17	NAV1	2.688131	0.384019	7
FOXP1	4.956949	0.309809	16	C19orf25	2.569401	0.367057	7
NAV2	2.942074	0.18388	16	RXRA	2.485559	0.35508	7
GLI2	8.384025	0.558935	15	LRRFIP1	2.88193	0.480322	6
EMX2OS	4.11018	0.274012	15	FBXL18	2.636018	0.439336	6
NFIX	3.229254	0.215284	15	PTPRG	2.557336	0.426223	6
SLX1B-				TSPEAR	2.483097	0.41385	6
SULT1A4	2.887604	0.192507	15	FMNL2	2.451128	0.408521	6
SLX1A	2.887604	0.192507	15	FAM181A	2.388272	0.398045	6
LOC606724	2.887604	0.192507	15	ROR1	2.295268	0.382545	6
LRMDA	2.745954	0.183064	15	RUNDC3A	4.666214	0.933243	5
BAIAP2	2.742197	0.182813	15	ARHGEF7	3.127367	0.625473	5
RPS6KA2	5.374521	0.383894	14	CACNA1I	2.879023	0.575805	5
PPP2R2A	3.042989	0.217356	14	BACH2	2.637348	0.52747	5
C7orf50	2.841244	0.202946	14	KLHL25	2.629848	0.52597	5
MSI2	3.957011	0.304385	13	VAV2	2.287829	0.457566	5
GSE1	3.15414	0.242626	13	CRB2	2.916757	0.729189	4
RFX4	2.746025	0.211233	13	RBMS3	2.754591	0.688648	4
MIR9-3HG	2.662139	0.20478	13	STAP2	2.431634	0.607909	4
KIF26B	2.395133	0.184241	13	VO PP1	2.371361	0.59284	4

NDST1	2.286881	0.57172	4	MCF2L	1.973949	0.109664	18
DAGLB	2.907537	0.969179	3	SORBS2	3.428588	0.214287	16
SOX10	2.807608	1.403804	2	NAV2	2.842011	0.177626	16
ANKLE2	2.601542	1.300771	2	GLI2	3.321443	0.22143	15
				ZBTB20	3.16892	0.211261	15
TABLE 172:	Cancer Type VGLL			KIRREL3	2.682165	0.178811	15
Gene site	imp_sum	imp_mean	n	RPS6KA2	2.333337	0.166667	14
PTPRN2	8.129568	0.099141	82	CUX1	1.883684	0.134549	14
PRDM16	5.586161	0.078678	71	ZC3H3	3.189378	0.265781	12
PCDHGA1	3.18076	0.053911	59	CMIP	2.961735	0.246811	12
PCDHGA2	2.864374	0.050252	57	GNA12	2.147446	0.178954	12
PCDHGA3	2.864374	0.053044	54	MIRLET7BHG	2.0589	0.171575	12
PCDHGB1	2.864374	0.054045	53	FBRSL1	2.046613	0.170551	12
PCDHGA4	3.18076	0.062368	51	RAD51B	2.403676	0.218516	11
PCDHGB2	3.497146	0.07137	49	CTBP2	2.309302	0.209937	11
PCDHGA5	3.497146	0.074407	47	ZC3H12D	2.282122	0.207466	11
PCDHGB3	2.864374	0.066613	43	AKAP13	3.166309	0.316631	10
PCDHGA6	2.547988	0.0637	40	NR2F1-AS1	2.231467	0.223147	10
HDAC4	5.164737	0.139587	37	TSPAN4	2.168185	0.216819	10
PCDHGA7	2.231602	0.060314	37	SH3RF3	2.088737	0.208874	10
PAX6	4.799113	0.137118	35	RGS12	2.080292	0.208029	10
PCDHGB4	2.547988	0.0728	35	ATP11A	3.240776	0.360086	9
PCDHGA8	2.547988	0.0728	35	NOTCH1	3.133691	0.348188	9
RBFOX3	1.94682	0.055623	35	RUNX1	3.124978	0.34722	9
DIP2C	4.353201	0.136038	32	KCNMA1	3.046948	0.33855	9
PCDHGB5	2.864374	0.089512	32	TRAPPC12	2.487117	0.276346	9
PCDHGA9	2.864374	0.092399	31	SND1	2.33234	0.259149	9
SOX2-OT	2.601665	0.089713	29	ASAP1	2.204126	0.244903	9
PCDHGB6	2.337064	0.080588	29	AXIN2	2.039296	0.226588	9
PCDHGA10	2.337064	0.083467	28	LINC00311	3.314817	0.414352	8
CAMTA1	2.968054	0.118722	25	MSRA	2.891438	0.36143	8
AGAP1	2.343429	0.093737	25	NRXN1	2.7291	0.341137	8
SATB2	3.133869	0.130578	24	RORA	2.435753	0.304469	8
PCDHGB7	2.337064	0.097378	24	MCC	2.30493	0.288116	8
RPTOR	6.717009	0.292044	23	BAHCC1	2.268006	0.283501	8
INPP5A	3.589923	0.156084	23	DLEU1	2.029465	0.253683	8
PCDHGA11	2.020678	0.087856	23	LINC00461	3.59814	0.51402	7
PRKCZ	1.896197	0.086191	22	DUSP6	3.172866	0.453267	7
SKI	6.018103	0.286576	21	NAV1	2.787893	0.39827	7
FRMD4A	3.907012	0.195351	20	CXXC5	2.268509	0.324073	7
MAD1L1	4.300474	0.226341	19	PRKCA	2.199418	0.314203	7
SMG1P2	3.091146	0.162692	19	ITPK1	2.124622	0.303517	7
BOLA2	3.091146	0.162692	19	GAK	1.916057	0.273722	7
LOC613038	3.091146	0.162692	19	SLC22A18AS	2.826172	0.471029	6
ZNF423	2.608954	0.137313	19	RADIL	1.977831	0.329638	6
CASZ1	2.143041	0.112792	19	ARHGEF7	2.019588	0.403918	5
SEPTIN9	3.568942	0.198275	18	TSNAX-DISC1	1.943715	0.388743	5
FO XK1	2.279568	0.126643	18	RBMS3	2.803228	0.700807	4

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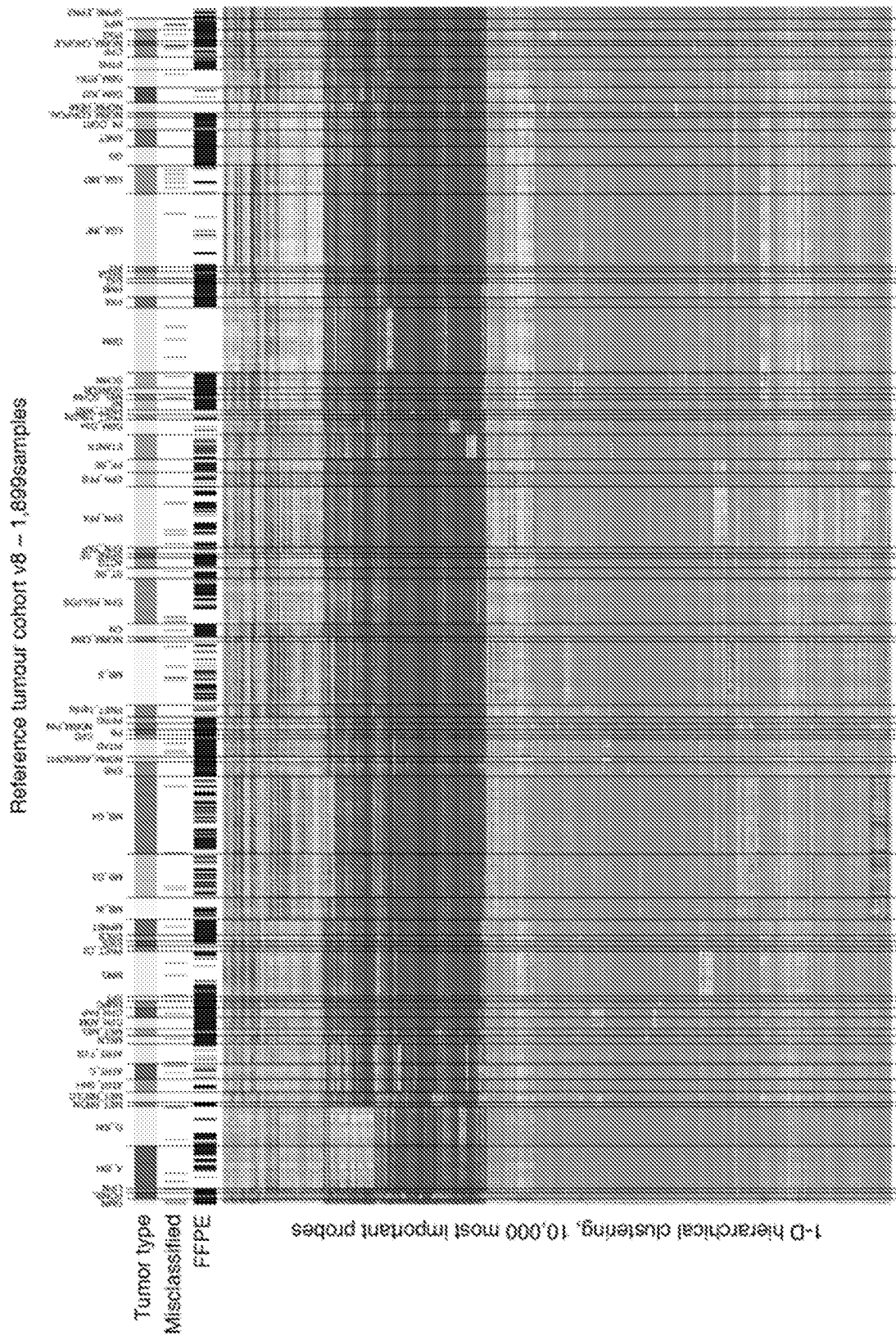
SASH1	1.943826	0.485956	4
PARD3B	1.914289	0.478572	4
GRIN2B	3.556806	1.185602	3
DAGLB	2.499239	0.83308	3
TBC1D7	2.400705	0.800235	3
ANKRD33B	2.062176	0.687392	3
SOX10	4.385587	2.192794	2
MTHFR	2.260277	1.130139	2
SLC25A10	2.107022	1.053511	2
PLEKHO2	2.755423	2.755423	1
ZNF280D	1.907871	1.907871	1

CLAIMS

1. A computer-implemented method for the diagnostic classification of cancer, the method comprising:
classifying a cancer using a classification algorithm trained using at least data pertaining to biological states of all gene sites in Table 1 (SEQ ID No. 1 to SEQ ID No. 688), wherein the biological states are derived from classified cancer types, wherein classifying the cancer comprises applying the classification algorithm to data pertaining to biological states of a set of gene sites of a cancer sample, wherein the set of gene sites comprises at least 3 gene sites of the cancer sample genome selected from the gene sites in Table 1 (SEQ ID No. 1 to SEQ ID No. 688).
2. The computer-implemented method of claim 1, wherein the classification algorithm is based on at least one of: discriminant analysis, discriminant functional analysis, a kernel method, multidimensional scaling, a nonparametric method, Partial Least Squares, a tree-based method, a generalized linear model, a principal components based method, a generalized additive model, a fuzzy logic based method, a neural network, and a genetic algorithm based method.
3. The computer-implemented method of claim 1 or 2, further comprising:
determining a biological state pertaining to each of the at least 3 gene sites of the cancer sample genome; and
determining a biological state pattern of the set of gene sites based on the determined biological states of the at least 3 gene sites.
4. The computer-implemented method of claims 1 to 3, wherein the biological state is selected from a group consisting of epigenetic state, mutation state, copy number and RNA expression, in particular wherein the epigenetic state is a methylation state.
5. The computer-implemented method of any one of claims 1 to 4, wherein the set of gene sites comprises at least 10, preferably at least 20 or at least 30 or at least 40 or at least 50 or at least 60 or at least 70 or at least 80 or at least 90 or at least 100 gene sites or all gene sites in Table 1 (SEQ ID No. 1 to SEQ ID No. 688).

6. The computer-implemented method of any one of claims 1 to 5, wherein the gene sites are the gene sites with the highest values of variable importance in Tables 3 to 172, respectively.
7. The computer-implemented method of any one of claims 1 to 6, wherein the biological states of the gene sites comprise the biological states of the gene sites as listed in Table 1 (SEQ ID No. 1 to SEQ ID No. 688) and up to 12 kb, preferably up to 10 kb or up to 8 kb or up to 6 kb or up to 4 kb or up to 2 kb, upstream and/or downstream of the genes.
8. The computer-implemented method of any one of claims 1 to 6, wherein the biological states of the gene sites comprise exclusively the biological states of the gene sites as listed in Table 1 (SEQ ID No. 1 to SEQ ID No. 688) without any bases upstream and/or downstream of the gene sites.
9. The computer-implemented method of any one of claims 1 to 8, wherein the biological state is a methylation state and/or the biological state pattern is a methylation state pattern.
10. The computer-implemented method of any one of claims 1 to 9, wherein the cancer is selected from the group consisting of carcinomas, sarcomas, myelomas, neural crest lineage tumors including melanoma, leukemia, lymphoma and mixed types.
11. The computer-implemented method of any one of claims 1 to 10, wherein the cancer is a cancer listed in Table 2.
12. The computer-implemented method of any one of claims 1 to 11, further comprising:
 - determining a further biological state different from the biological states and pertaining to at least one of the gene sites pertaining to the cancer sample genome, wherein the further biological state is selected from the group consisting of epigenetic state, mutation state, RNA expression and copy number; and
 - correlating the further biological state of the at least one gene site pertaining to the cancer sample genome with the classified cancer type.

13. The computer-implemented method of any one of claims 1 to 12, wherein the at least 3 gene sites include one or more of: PTPRN2 (SEQ ID No. 491), PRDM16 (SEQ ID No.477), HDAC4 (SEQ ID No.249), PAX6 (SEQ ID No. 431) and MAD1L1 (SEQ ID No. 349).
14. A computer-readable storage medium having computer-executable instructions stored, that, when executed, cause a computer to perform a method according to claim 1.
15. A system for diagnosing cancer, comprising:
 - one or more processors; and
 - a memory coupled to the one or more processors and comprising instructions executable by the one or more processors to implement the method according to claim 1.



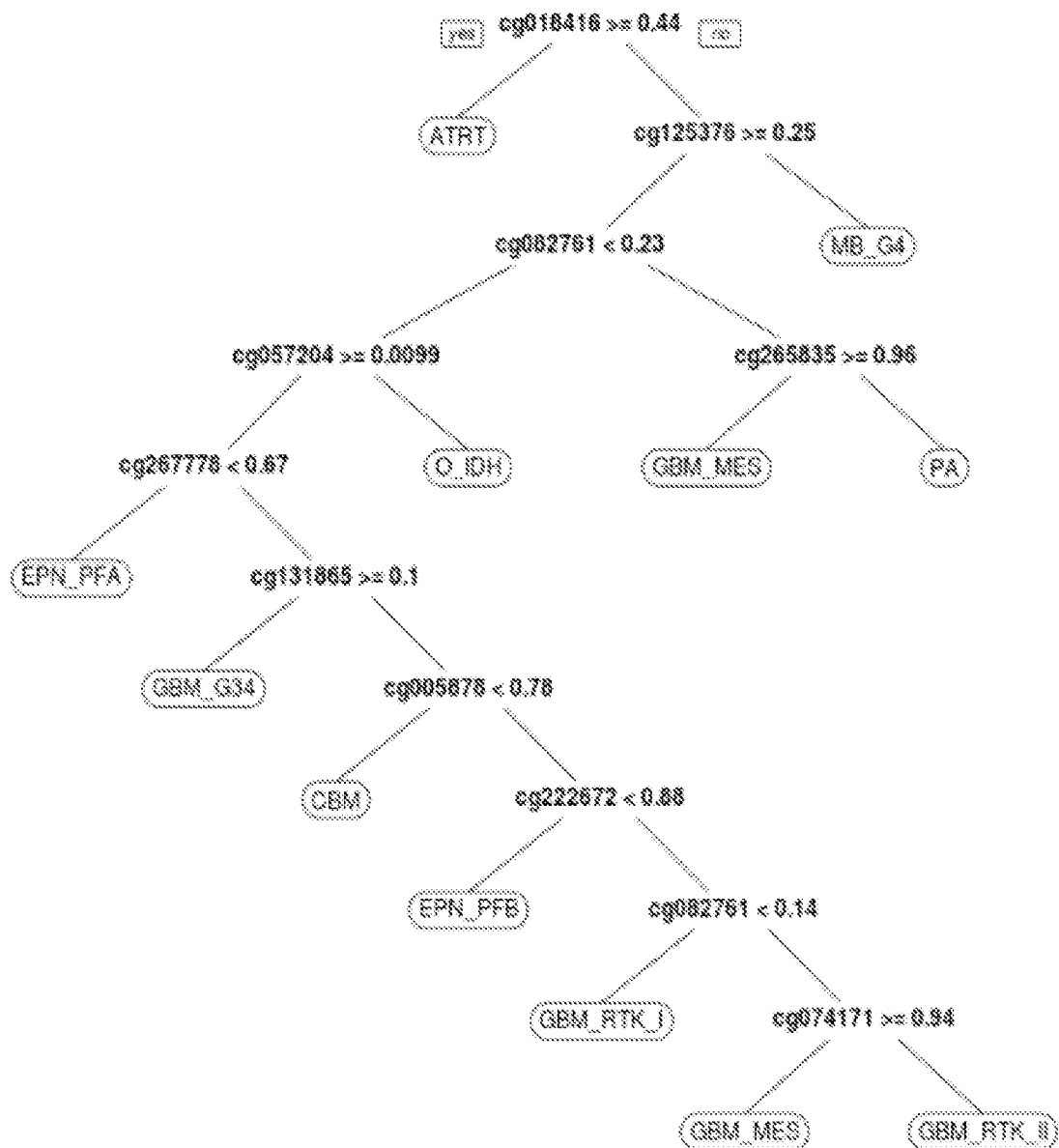


Fig. 2

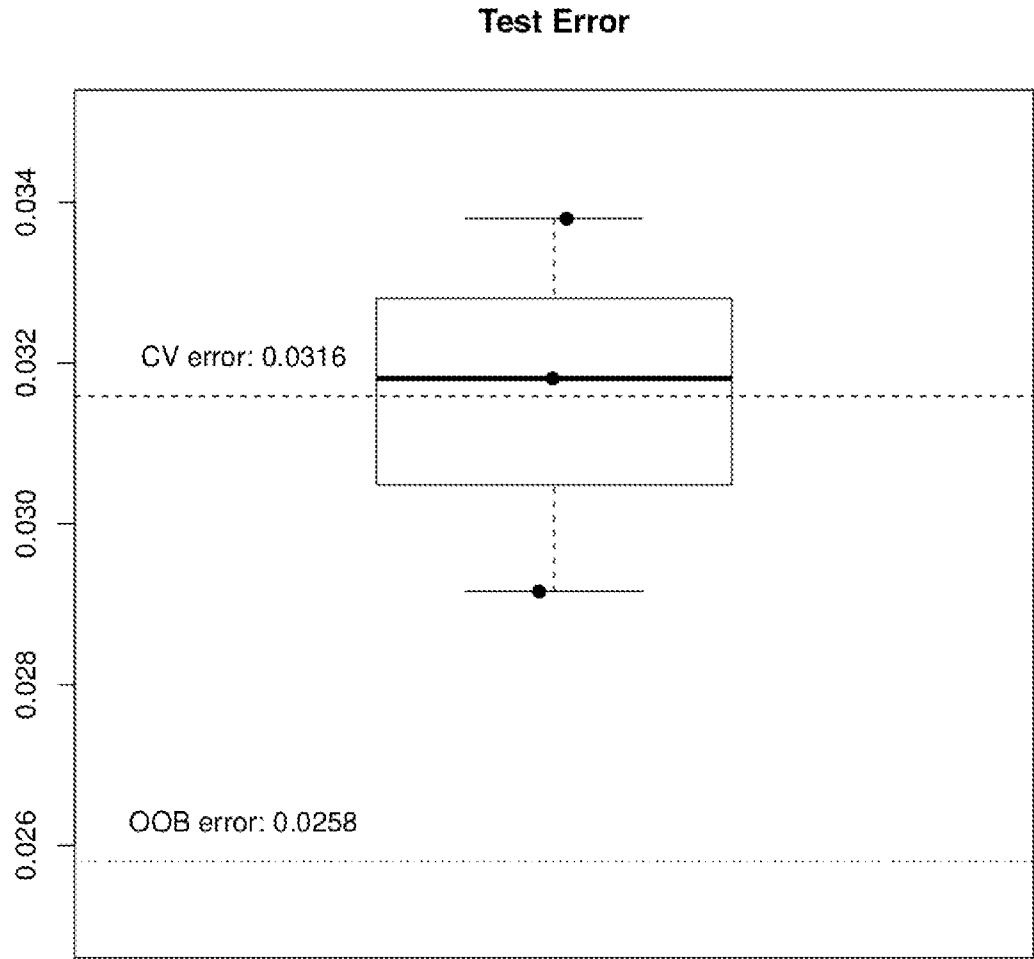
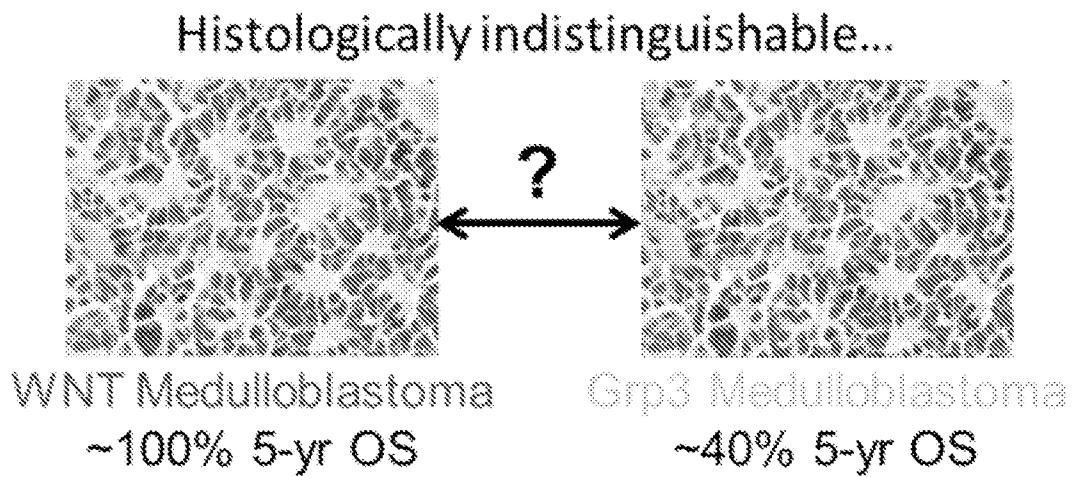


Fig. 3



...molecularly distinct

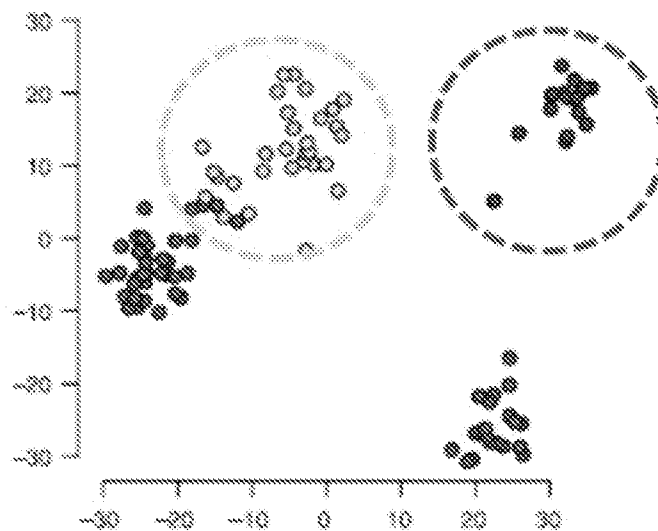


Fig. 4

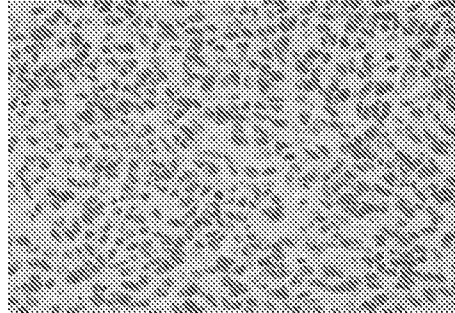


Fig. 5A

Tumor	64082 classifier score
Astrozytom IDH mut	0.017
Angiozent. Gliom	0.117
AT/RT	0.005
Normalgewebe Kleinhirn	0.001
Neurozytom	0.002
Craniopharyngeom adam.	0.000
Craniopharyngeom papill.	0.008
Plexus Papillom	0.001
Dediff. Liposarkom	0.012
Esthesioneuroblastom	0.019
Ependymom Infratentoriell Gruppe A	0.001
Ependymom Infratentoriell Gruppe B	0.008
Ependymom supratentoriell 2 (R-pos)	0.006
ETANTR (ETMR)	0.006
Glioblastom	0.335
Glioblastom H3.3 G34 mut	0.018
Glioblastom H3.3 K27 mut	0.050
Glioblastom RTK1	0.040
Germinom	0.000
Normalgewebe Hemisphäre	0.008
Hämangioblastom	0.004
Hämangioperizytom	0.000
Low grade Gliom (PA, GG, DNT)	0.038
Medulloblastom Gruppe 3	0.001
Medulloblastom Gruppe 4	0.001
Medulloblastom SHH	0.002
Medulloblastom WNT	0.011
Melanom Metastase	0.015
Meningeom	0.000
Spinales Ependymom	0.015
Oligodendrogliom IDH mut	0.017
Primäres ZNS Lymphom	0.040
Paragangliom	0.000
Hypophysenadenom	0.001
PNET (supratentoriell)	0.000
Pinealis Parenchymtumor interm. Diff.	0.001
Papill. Tumor der Pinealis Region	0.005
Pleomorphes Xanthoastrozytom	0.156
Schwannom	0.001
Subependymom	0.026
SEGA	0.013
Solitärer fibröser Tumor	0.000

Fig. 5B

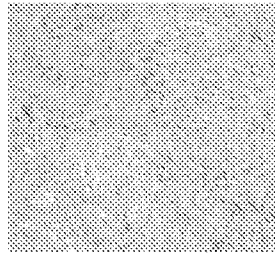


Fig. 6A

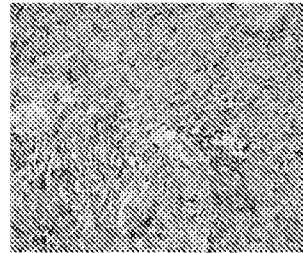


Fig. 6B

Tumor	64780 classifier score
Astrozytom IDH mut	0,000
Angiozent. Gliom	0,003
AT/RT	0,003
Normalgewebe Kleinhirn	0,001
Neurozytom	0,002
Craniopharyngeom adam.	0,002
Craniopharyngeom papill.	0,008
Plexus Papillom	0,009
Dediff. Liposarkom	0,139
Esthesioneuroblastom	0,025
Ependymom Prog. Gruppe A	0,006
Ependymom Prog. Gruppe B	0,005
Ependymom Supratentoriell 1 (R-neg)	0,026
Ependymom Supratentoriell 2 (R-pos)	0,008
ETANTR (ETMR)	0,001
Glioblastom	0,035
Glioblastom H3.3 G34 mut	0,001
Glioblastom H3.3 K27 mut	0,004
Glioblastom RTK I	0,011
Germinom	0,003
Normalgewebe Hemisphere	0,003
Hämangioblastom	0,042
Hämangioperizytom	0,024
Low grade Gliom (PA, GG, DNT)	0,048
Medulloblastom Gruppe 3	0,000
Medulloblastom Gruppe 4	0,002
supratent. PNET	0,001
Medulloblastom SHH	0,001
Medulloblastom WNT	0,002
Meningeom	0,439
Myxopapilläres Ependymom	0,024
Schwannom	0,038
Oligodendrogliom IDH mut	0,000
Primäres ZNS Lymphom	0,000
Paragangliom	0,008
Pinealis Parenchymtumor intern. Diff.	0,004
Papill. Tumor der Pinealis Region	0,007
PXA	0,036
Subependymom	0,015
Solitärer fibröser Tumor (SFT)	0,007

Fig. 6C

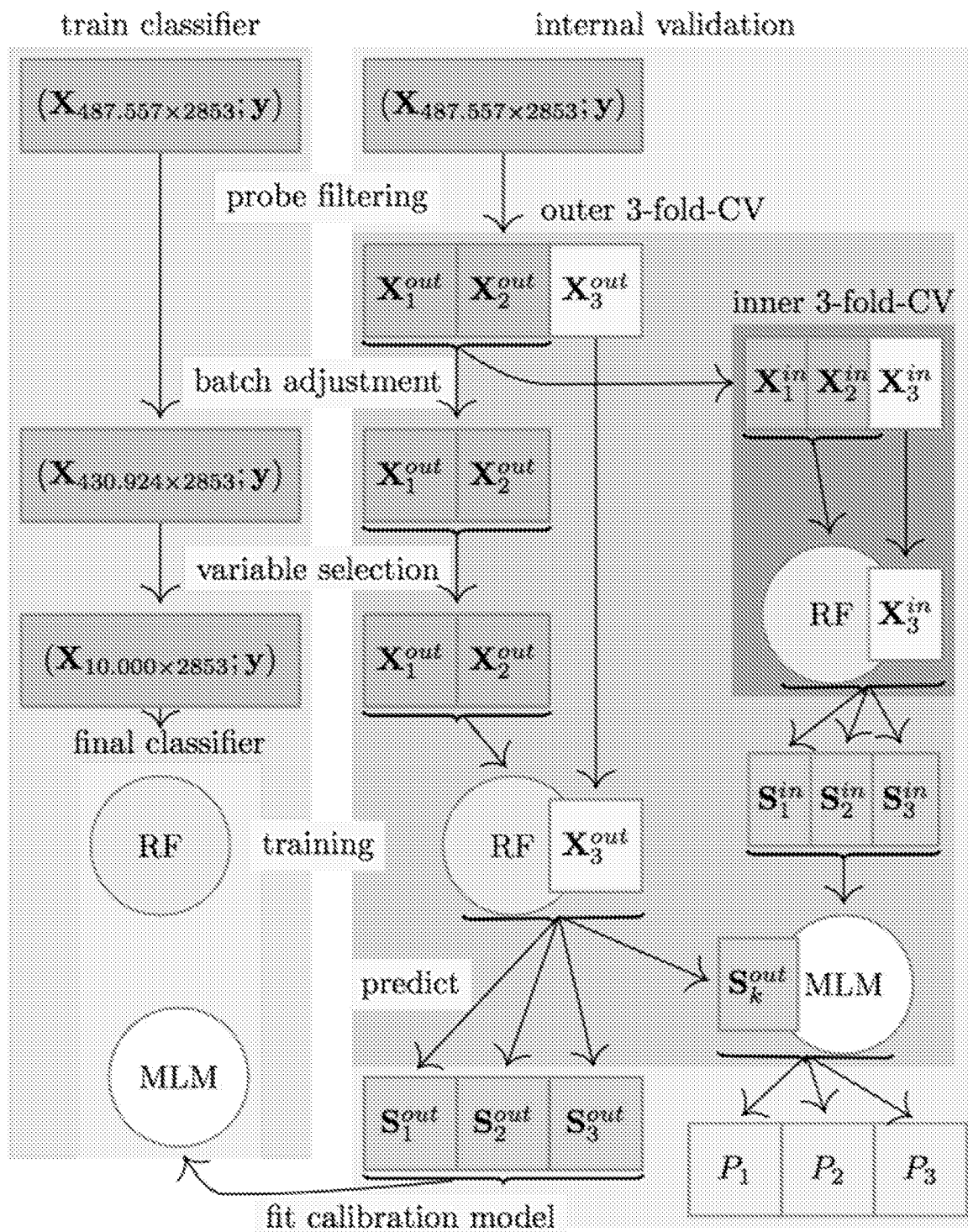


Fig. 7



Fig. 8

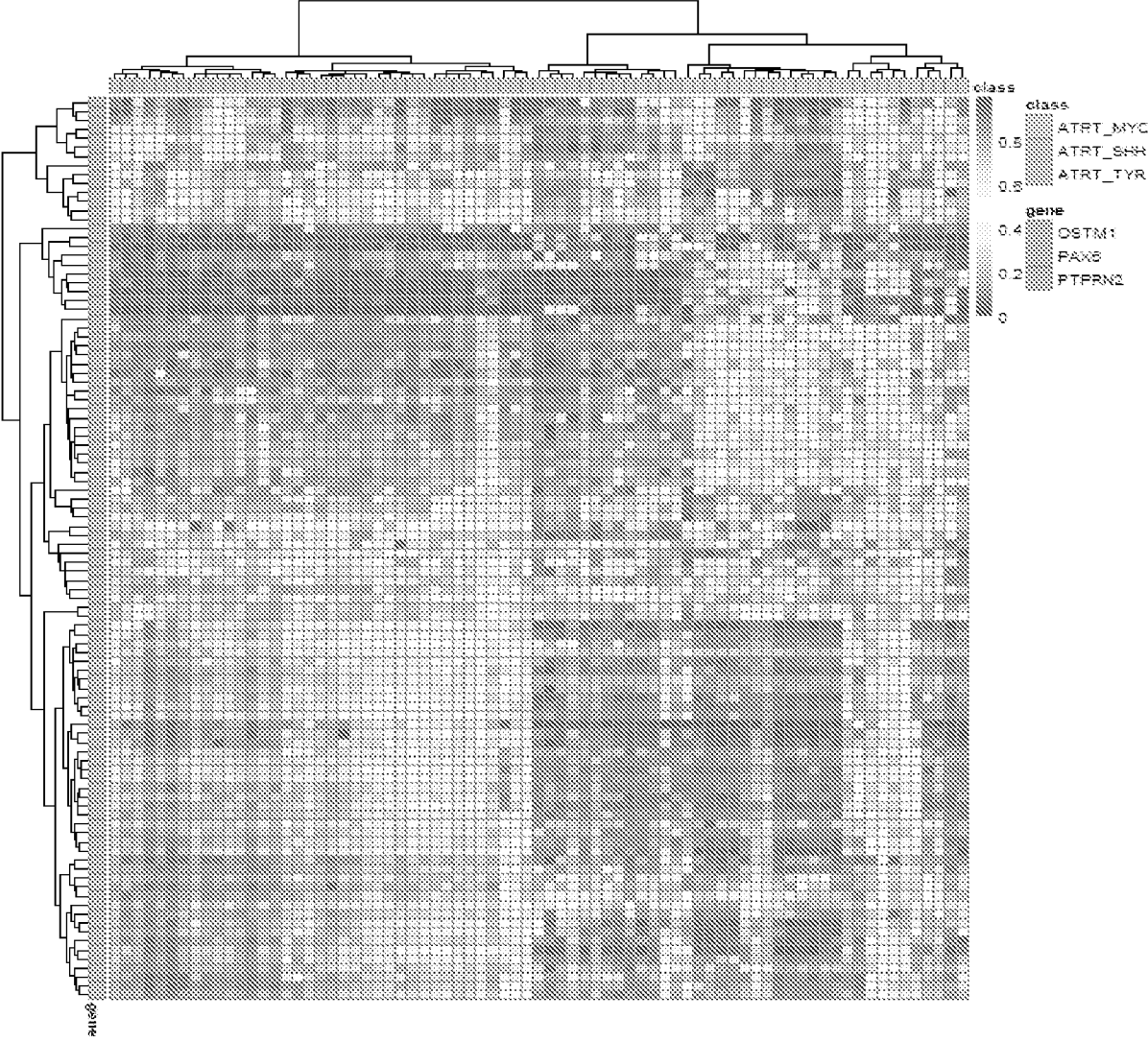


Fig. 9

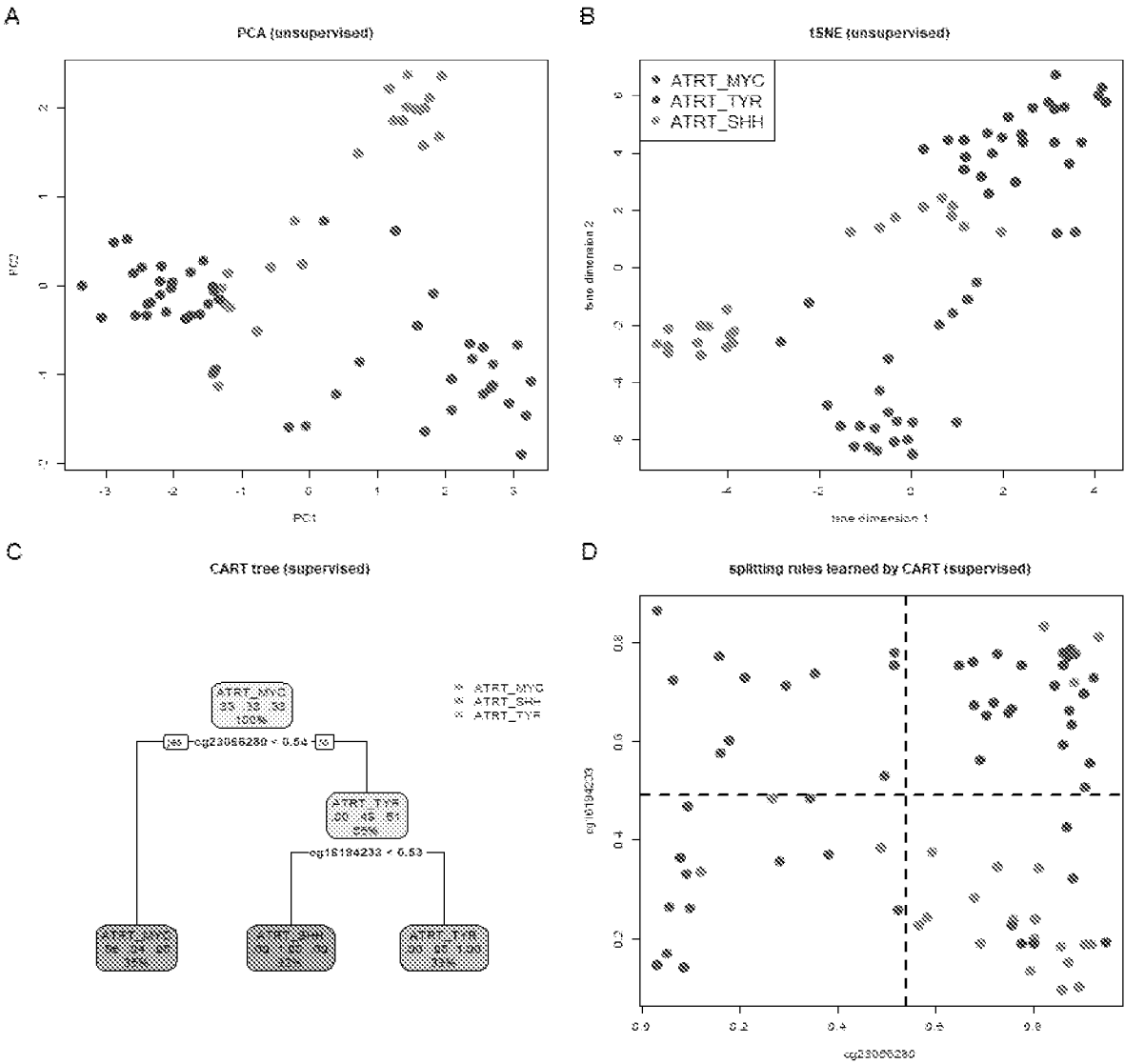
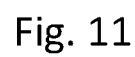
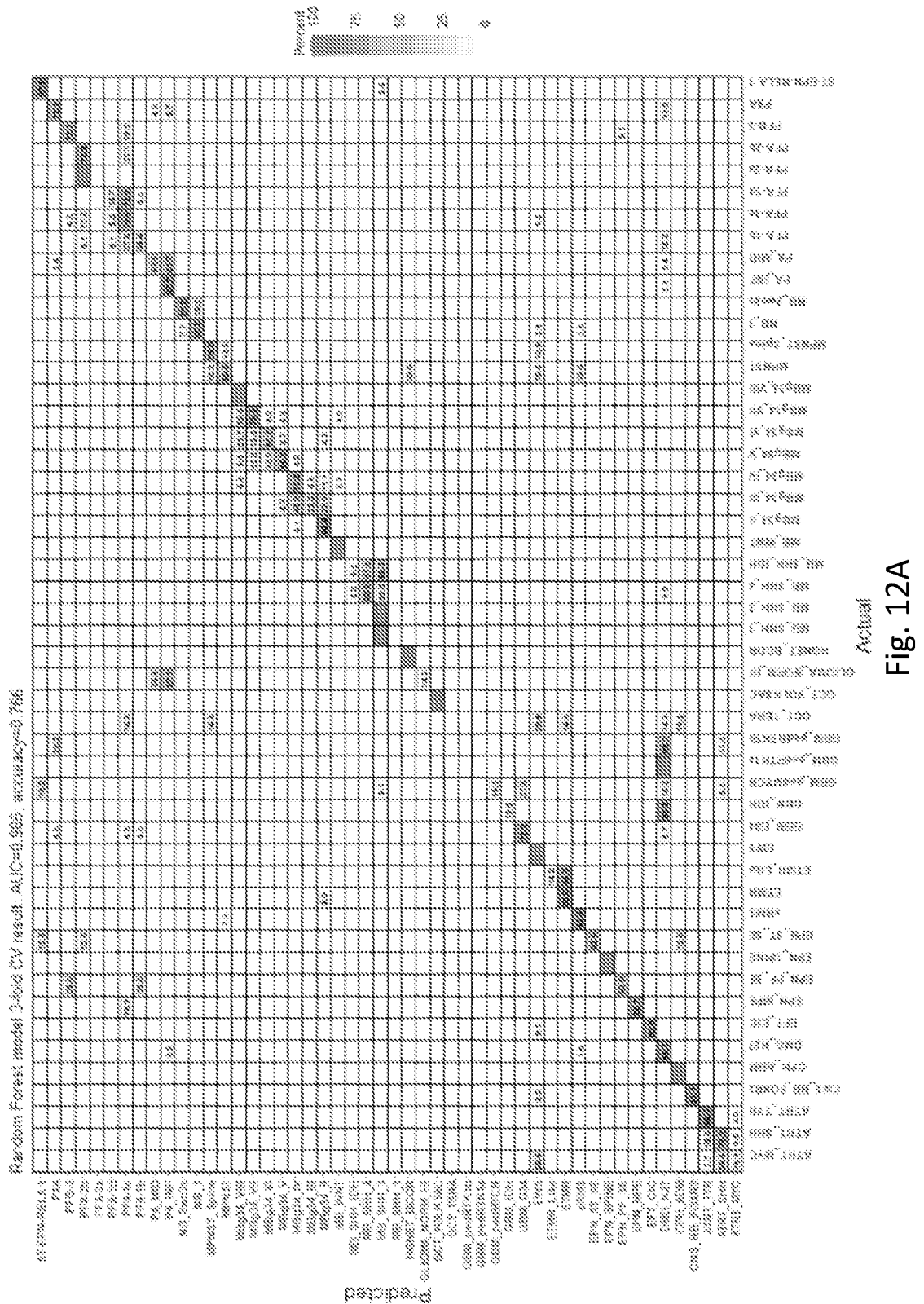
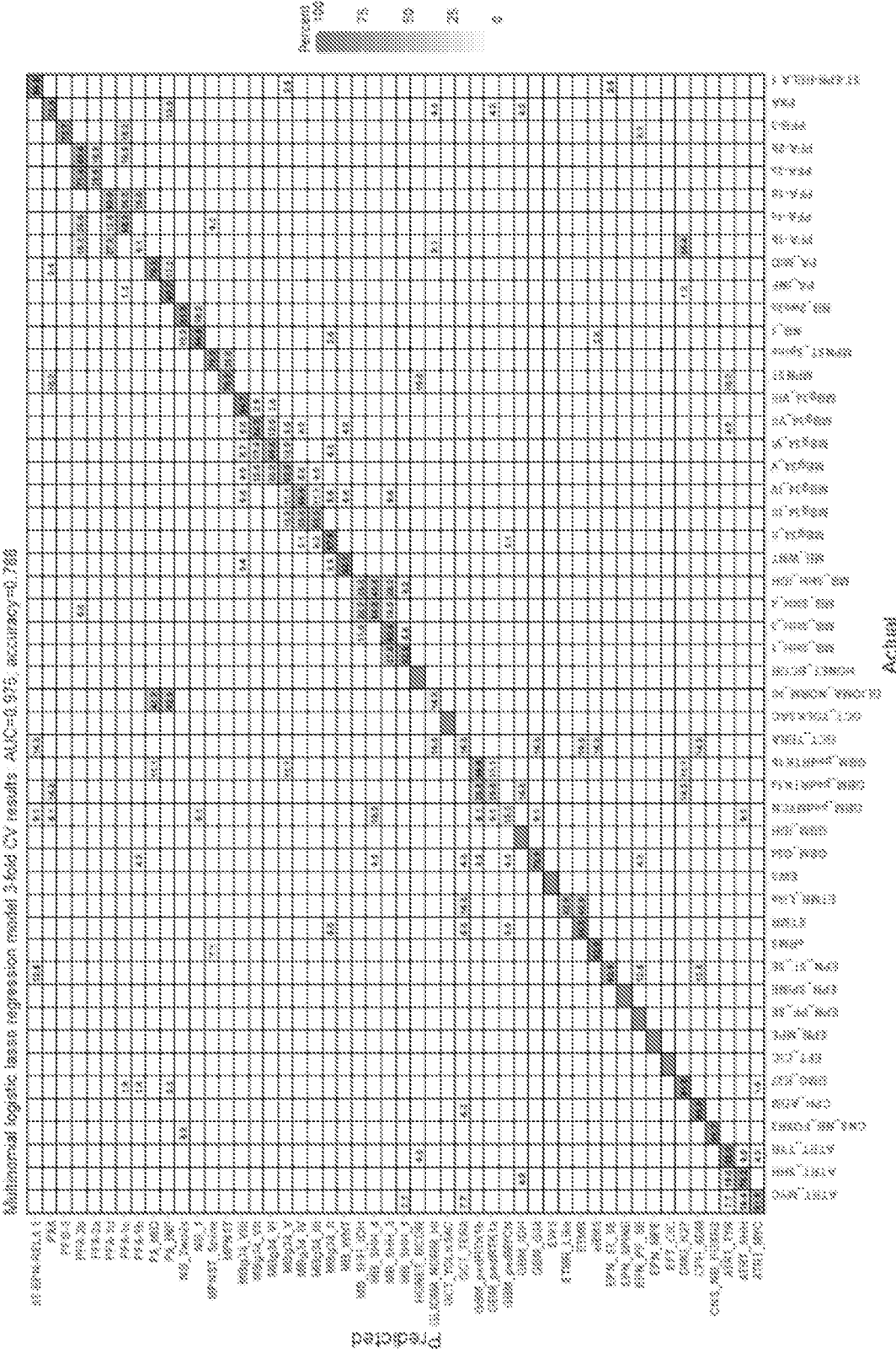


Fig. 10







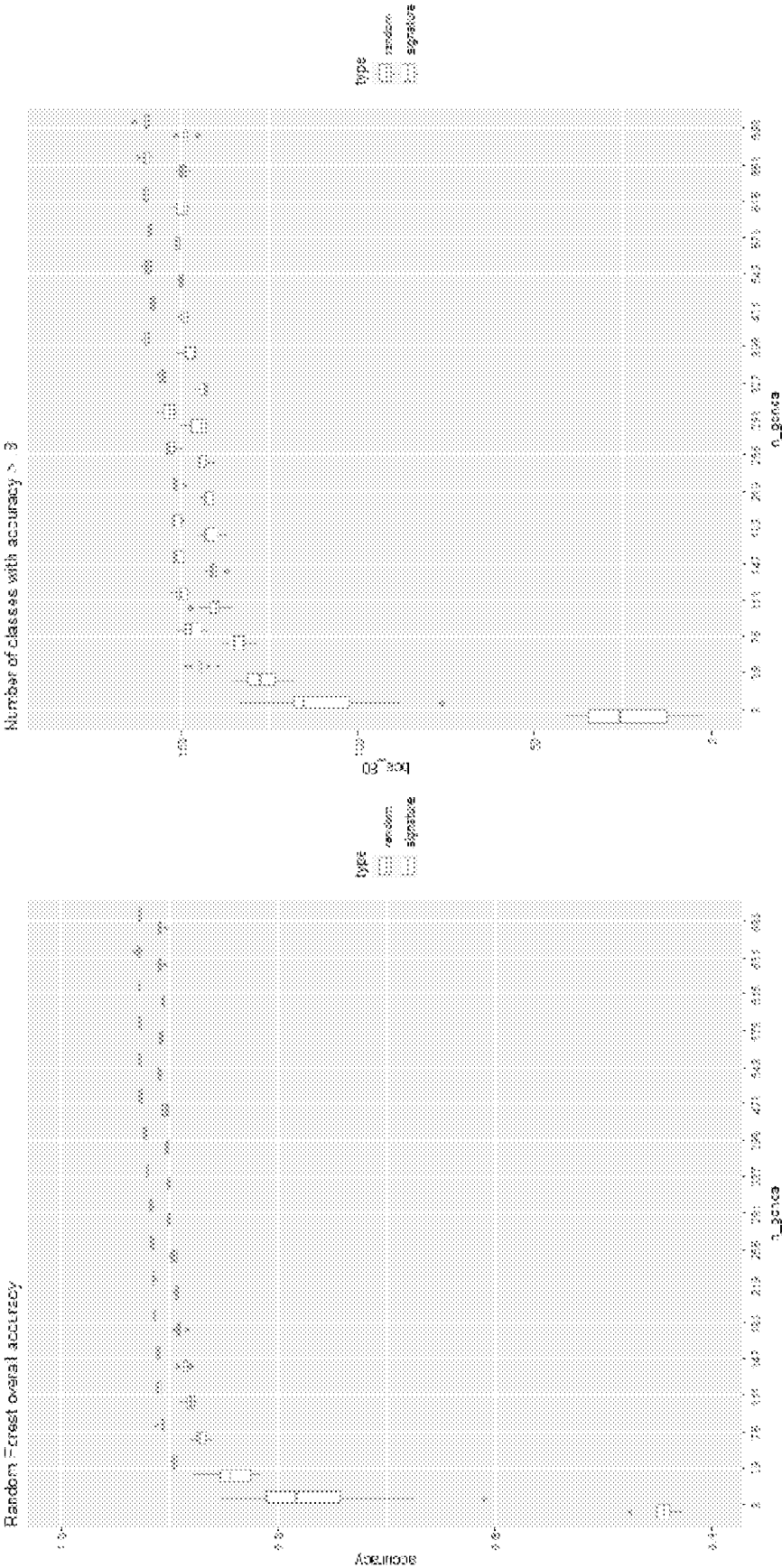


Fig. 13

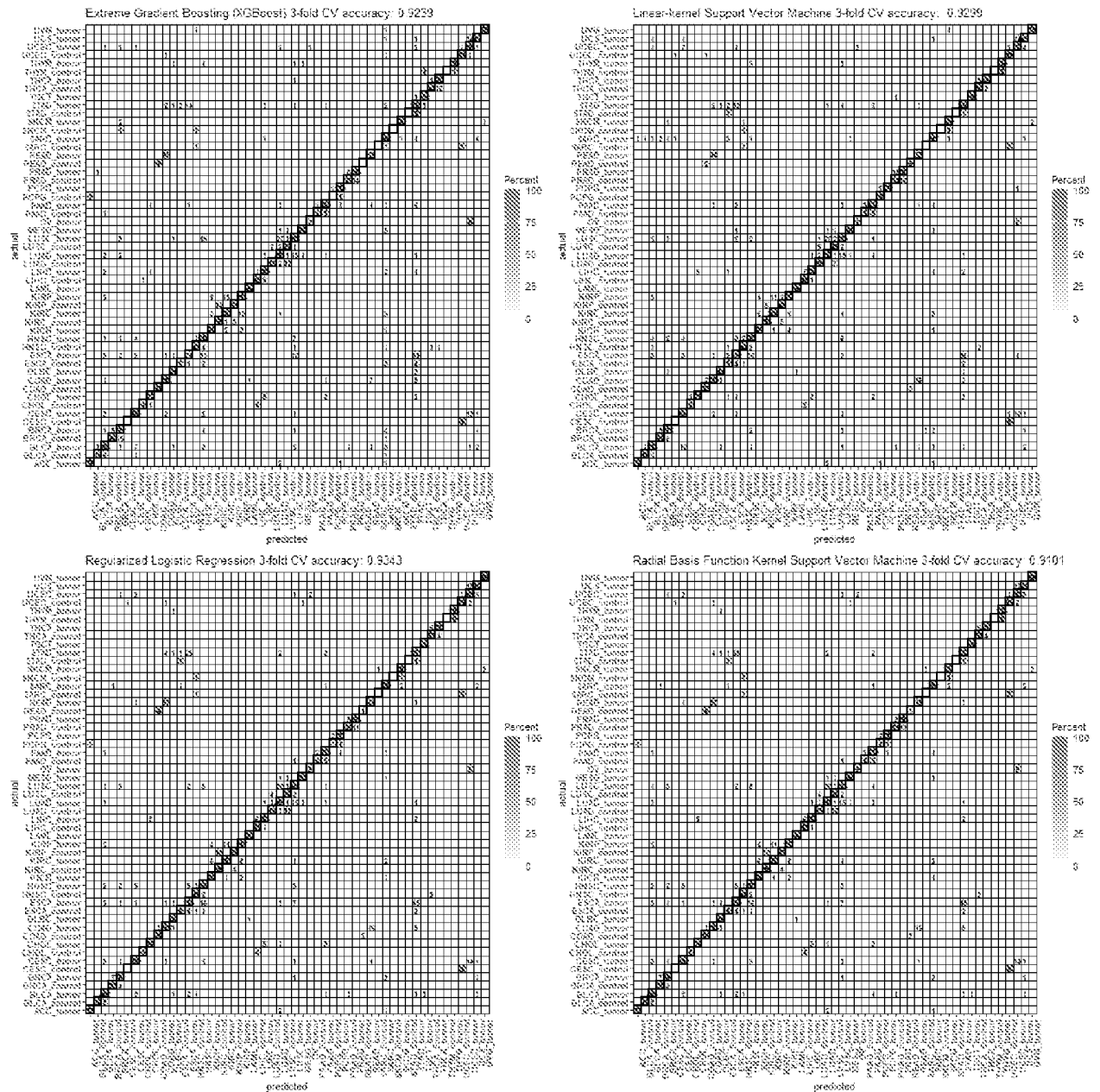


Fig. 16